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OM protein - protein search, using sw model

Run on: August 15, 2002, 11:38:26 ; Search time 73.69 Seconds
(without alignments)
22.610 Million cell updates/sec

Title: US-09-613-092a-7
Perfect score: 79
Sequence: 1 LVRRFVHRPHEQ 15

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A.Geneseq_032802:*
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2: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT:*
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20: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT:*
21: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	100.0	15	20	AAV30353
2	74	93.7	15	20	AAV30354
3	52	65.8	156	22	AAV75292
4	52	65.8	156	22	AAV75293
5	52	65.8	243	22	ABBS8399
6	52	65.8	273	22	ABG18986
7	52	65.8	280	22	ABG10923
8	52	65.8	282	22	ABG10922
9	52	65.8	351	20	AAV59757
10	48	60.8	142	22	ABG18985
11	45	57.0	580	20	AAV34665

12	45	57.0	798	22	ABB62356	Drosophila melanog
13	44	55.7	164	22	AAW83043	Human immune/haema
14	42	53.2	175	22	AAV30377	C glutamicum prote
15	42	53.2	203	22	AAV78872	C. glutamicum SRT
16	42	53.2	316	22	AAV58773	Propionibacterium
17	41	51.9	105	22	AAV64657	Propionibacterium
18	41	51.9	466	19	AAW84355	Talaromyces thermo
19	41	51.9	466	20	AAV39899	T. thermophilus ph
20	40	50.6	1233	20	AAV55954	Mouse Str20-relate
21	40	50.6	1317	22	AAW65167	Drosophila melanog
22	39	49.4	63	21	AAV02947	Human secreted pro
23	39	49.4	76	22	AAV58639	Propionibacterium
24	39	49.4	194	22	AAV25661	G protein-coupled
25	39	49.4	409	22	ABB65172	Drosophila melanog
26	39	49.4	986	20	AAV37617	Protein which is s
27	39	49.4	1792	22	ABB71108	Drosophila melanog
28	38.5	48.7	830	22	ABG28908	Novel human diagno
29	38.5	48.7	973	22	ABG24942	Novel human diagno
30	38	48.1	67	20	AAV29052	T. gondii immunoge
31	38	48.1	67	22	AAV25523	T. gondii immunoge
32	38	48.1	141	22	AAW69191	Drosophila melanog
33	38	48.1	174	22	AAV52994	Propionibacterium
34	38	48.1	177	22	AAW42368	Human polypeptide
35	38	48.1	217	22	ABB65332	Drosophila melanog
36	38	48.1	275	22	AAV62724	Propionibacterium
37	38	48.1	312	22	AAV71996	Human olfactory re
38	38	48.1	312	22	AAV72164	Human olfactory re
39	38	48.1	313	22	ABG14394	Novel human diagno
40	38	48.1	328	22	AAW41174	Human polypeptide
41	38	48.1	414	22	AAV29180	Human PRO polypept
42	38	48.1	414	22	AAW87576	Human PRO3579. Ho
43	38	48.1	571	22	ABG27421	Novel human diagno
44	37.5	47.5	129	22	ABG02129	Novel human diagno
45	37	46.8	69	22	AAV39255	Propionibacterium

ALIGNMENTS

RESULT	1	
AAV30353	AAV30353 standard; Peptide; 15 AA.	
XX	XX	
AC	AAV30353;	
XX	XX	
DT	09-NOV-1999 (first entry)	
XX	XX	
DE	Epitope derived from pneumococcal surface adhesion A protein.	
XX	XX	
KW	Pneumococcal surface adhesion A protein; Psaa; monoclonal antibody;	
KW	vaccine; Streptococcus pneumoniae infection.	
XX	XX	
OS	Streptococcus pneumoniae.	
XX	XX	
PN	WO9945121-A1.	
XX	XX	
PD	10-SEP-1999.	
XX	XX	
PF	26-FEB-1999; 99WO-US04326.	
XX	XX	
PR	02-MAR-1998; 98US-0076565.	
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.	
XX	XX	
PI	Ades EW, Carlone GM, Sampson JS, Tharpe JA, Westerink MAJ;	
PI	Zeller JL;	
XX	XX	
DR	WPI; 1999-540849/45.	
XX	XX	
PT	New peptides corresponding to Streptococcus pneumoniae Psaa, used	
PT	for treating or preventing Streptococcus pneumoniae infection in a	
PT	subject	
XX	XX	

PS Claim 6; Page 43; 58pp; English.

XX AAY30351-54 represent immunogenic peptides which are derived from
CC a pneumococcal surface adhesion A protein (PsaA). The specification
CC describes monoclonal antibodies which bind epitopes of the PsaA protein
CC (e.g. present sequence). The peptides can be used in vaccines to prevent
CC Streptococcus pneumoniae infections. The antibodies of the invention
CC can also be used to detect S. pneumoniae in a sample or individual.

XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 79; DB 20; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVRRFVHRPHVESQ 15
Db 1 LVRRFVHRPHVESQ 15

RESULT 2
AAY30354
ID AAY30354 standard; Peptide: 15 AA.

XX AAY30354;

XX 09-NOV-1999 (first entry)

DE Eptlope derived from pneumococcal surface adhesion A protein.

XX
KM Pneumococcal surface adhesion A protein; PsaA; monoclonal antibody;
KM vaccine; Streptococcus pneumoniae infection.

XX
OS Streptococcus pneumoniae.

XX
PN WO9945121-A1.

XX 10-SEP-1999.

XX 26-FEB-1999; 99WO-US04326.

XX 02-MAR-1998; 98US-0076565.

XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Ades EM, Carlone GW, Sampson JS, Tharpe JA, Westerink MAJ;
PI Zeller JL;
DR WPI; 1999-540849/45.

XX
PT New peptides corresponding to Streptococcus pneumoniae PsaA, used
PT for treating or preventing Streptococcus pneumoniae infection in a
PT subject

XX
PS Claim 6; Page 43; 58pp; English.

XX AAY30351-54 represent immunogenic peptides which are derived from
CC a pneumococcal surface adhesion A protein (PsaA). The specification
CC describes monoclonal antibodies which bind epitopes of the PsaA protein
CC (e.g. present sequence). The peptides can be used in vaccines to prevent
CC Streptococcus pneumoniae infections. The antibodies of the invention
CC can also be used to detect S. pneumoniae in a sample or individual.

XX
SQ Sequence 15 AA;

Query Match 93.7%; Score 74; DB 20; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.5e-06;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LVRRFVHRPHVESQ 15
XXXXXXXXXXXXXXXXXXXX

Db 1 LVRRFVHRPHVESQ 15

RESULT 3
AAB75292
ID AAB75292 standard; Protein: 156 AA.

XX AAB75292;

XX 03-APR-2001 (first entry)

XX
DE Gene 6 human secreted protein homologous amino acid sequence #111.

XX
KW Human; immunosuppressive; antiarthritic; antirheumatic; nootropic;
KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
KW neuroprotective; antibacterial; virucide; fungicide; opthalmological;
KW venereary; autoimmune disease; hyperproliferative disorder; cancer;
KW cardiovascular disorder; cerebrovascular disorder; infection; cancer;
KW nervous system disorder; ocular disorder; chemotaxis; food additive;
KW secreted protein.

XX
OS Homo sapiens.

XX
PN WO200077021-A1.

XX 21-DEC-2000.

XX 01-JUN-2000; 2000WO-US15135.

XX 11-JUN-1999; 99US-0138632.

XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.

XX
PI Rosen CA, Ruben SM, Komatsoulis GA;
DR WPI; 2001-071257/08.

XX
PT Nucleic acid molecules encoding human secreted proteins, used in
PT preventing, treating or ameliorating a disorder, e.g. Alzheimer's and
PT Parkinson's diseases and cancers -

XX
PS Disclosure; Page 18-19; 530pp; English.

XX
CC This invention relates to polynucleotide sequences AAF63789 - AAF63836
CC which encode human secreted proteins AAB75260 - AAB75287. Included in the
CC invention are protein sequences AAB75288 - AAB75341 which are fragments
CC of the secreted proteins and amino acid sequences with which these
CC fragments share homology. Examples of the activities of the proteins and
CC polynucleotides and the activities of their agonists and antagonists
CC include, immunosuppressive; antiarthritic; antirheumatic;
CC antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
CC neuroprotective; antibacterial; virucide; fungicide;
CC opthalmological; and venereary activity. The protein and polynucleotide
CC sequences, their agonists and antagonists may be useful for treating,
CC preventing and diagnosing diseases and disorders such as autoimmune
CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders
CC e.g. neoplasms of the breast or liver, cardiovascular disorders
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischemia,
CC angiogenesis, nervous system disorders e.g. Alzheimer's disease,
CC infections caused by bacteria, viruses and fungi and ocular disorders
CC e.g. corneal infection. The polypeptides can also be used to aid wound
CC healing and epithelial cell proliferation, to prevent skin aging due to
CC sunburn, to maintain organs before transplantation, for supporting cell
CC culture of primary tissues, to regenerate tissues and in chemotaxis. The
CC polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities. Included in the invention are
CC oligonucleotides AAF63780 - AAF63788 and peptide AAB75239 which are used
CC in the identification and characterisation of the DNA and protein
CC sequences of the invention.

XX
SQ Sequence 156 AA;

OY 2 VAREVHRRPHE 13
 |||:||||:
 Db 103 vrfvfhkprhvd 114

RESULT 6
 ABG18986
 ID ABG18986 standard; Protein; 273 AA.
 XX
 AC ABG18986;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #18977.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.

PN WO200175067-A2.
 XX
 PD 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

PI Dmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR N-PSDB; AAS83173.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -

PS Claim 20; SEQ ID NO 49345; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX
 SQ Sequence 273 AA;

Query Match 65.8%; Score 52; DB 22; Length 273;
 Best Local Similarity 75.0%; Pred. No. 0.28;
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 VAREVHRRPHE 13
 |||:||||:
 Db 124 vrfvfhkprhvd 135

RESULT 7
 ABG10923
 ID ABG10923 standard; Protein; 280 AA.
 XX
 AC ABG10923;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #10914.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.

PN WO200175067-A2.
 XX
 PD 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

PI Dmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR N-PSDB; AAS75110.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -

PS Claim 20; SEQ ID NO 41282; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX
 SQ Sequence 280 AA;

Query Match 65.8%; Score 52; DB 22; Length 280;
 Best Local Similarity 75.0%; Pred. No. 0.28;
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 OY 2 VAREVHRRPHE 13

Db 124 vrfvkhkphvd 135

RESULT 8
ID ABG10922 standard; Protein; 282 AA.
XX
AC ABG10922;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #10913.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN MO200175067-A2.
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
DR N-PSDB; AAS75109.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID No 41281; 103pp; English.
XX
XS The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 282 AA;

Query Match 65.8%; Score 52; DB 22; Length 282;
Best Local Similarity 75.0%; Pred. No. 0.29;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 VRRFVRRHPVE 13
II III:IIII:

Db 103 vrfvkhkphvd 114

RESULT 9
ID AAY59757 standard; Protein; 351 AA.
XX
AC AAY59757;
XX
DT 18-JAN-2000 (first entry)
XX
DE Human normal ovarian tissue derived protein 34.
XX
DE Human; ovary; screening; ovarian cancer; treatment.
XX
KW Human; ovary; screening; ovarian cancer; treatment.
XX
OS Homo sapiens.
XX
PN DE19816395-A1.
PD 07-OCT-1999.
XX
PF 03-APR-1998; 98DE-1016395.
XX
PR 03-APR-1998; 98DE-1016395.
XX
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
PI Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;
XX
DR WPI: 1999-552352/47.
DR N-PSDB; AA241237.
XX
PT Nucleic acid sequences potentially useful in diagnosis or therapy of
PT ovarian cancer -
XX
PS Claim 23; Page 229; 274pp; German.
XX
XS This invention describes novel nucleic acid sequences that are highly
CC expressed in normal ovary tissue. Artificial chromosomes and cosmid
CC clones containing the sequences can be used as gene transfer vehicles.
CC The sequences can be used to produce DNA fragments containing
CC full-length genes. Host cells transformed with the sequences can be used
CC to produce polypeptides or polypeptide fragments, which can be used to
CC screen phage displays for polypeptides that bind to them, or as tools for
CC identifying agents active against ovarian cancer, or to prepare
CC medicaments for treating ovarian cancer. The cDNA sequences can be used
CC to obtain genomic genes, their promoters, enhancers, silencers, exon
CC structures, intron structures and their splice variants. AAY59724-Y59837
CC represent protein fragments encoded by the cDNA sequences represented in
CC AA241222-241324 which are derived from normal human ovarian tissue.
XX
SQ Sequence 351 AA;

Query Match 65.8%; Score 52; DB 20; Length 351;
Best Local Similarity 75.0%; Pred. No. 0.36;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 VRRFVRRHPVE 13
II III:IIII:

Db 211 vrfvkhkphvd 222

RESULT 10
ID ABG18985 standard; Protein; 142 AA.
XX
AC ABG18985;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #18976.
XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX Homo sapiens.
XX
XX MO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.
XX
XX 31-MAR-2000; 2000US-0540217.
XX 23-AUG-2000; 2000US-0649167.
XX
XX (HXSE-) HXSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI: 2001-639362/73.
XX N-PSDB; AAS83172.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity -
XX
XX Claim 20; SEQ ID No 49344; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human
XX diagnostic amino acid sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pcl_sequences.
XX
XX Sequence 142 AA:
SQ
Query Match 60.8%; Score 48; DB 22; Length 142;
Best Local Similarity 75.0%; Pred. NO. 0.7;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 VRRVYRRPHE 13
DB 3 vrfvthrpvhd 14
RESULT 11
AAV34665
ID AAV34665 standard; Protein; 580 AA.
XX
XX AAV34665;
XX
XX 13-SEP-1999 (first entry)
XX
XX Chlamydia pneumoniae protein not found in C. trachomatis.
XX
XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW

KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
KW vaccine; neutralising epitope.
XX
XX Chlamydia pneumoniae.
XX
XX MO9927105-A2.
XX
XX 03-JUN-1999.
XX
XX 20-NOV-1998; 98WO-1B01890.
XX
XX 04-NOV-1998; 98US-0107078.
XX 21-NOV-1997; 97FR-0014673.
XX
XX (GEST) GENSET.
XX
XX Griffais R;
XX
XX WPI: 1999-357842/30.
XX
XX Genome sequence of Chlamydia pneumoniae
XX
XX Page 670-671; Disclosure; 1912pp; English.
XX
XX AAY34584-Y35879 represent the proteins encoded by all the open reading
XX frames in the complete genome (see AAX91990) of Chlamydia pneumoniae.
XX C. pneumoniae causes respiratory disease such as pneumonia and
XX bronchitis and is thought to be a contributing factor in heart
XX disease, sarcoidosis, sinusitis, purulent otitis media, erythema
XX nodosum or pharyngitis. The polypeptides encoded by the open reading
XX frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in
XX immunogenic compositions as vaccines. Vectors containing C. pneumoniae
XX nucleotide sequences can also be used as immunogenic compositions,
XX especially where the vector directs the expression of a neutralising
XX epitope of C. pneumoniae.
XX
XX Sequence 580 AA:
SQ
Query Match 57.0%; Score 45; DB 20; Length 580;
Best Local Similarity 80.0%; Pred. NO. 11;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 VRRVYRRPHE 11
DB 570 vrrlvhrp 579
RESULT 12
ABB62356
ID ABB62356 standard; Protein; 798 AA.
XX
XX ABB62356;
XX
XX 26-MAR-2002 (first entry)
XX
XX Drosophila melanogaster polypeptide SEQ ID NO 13860.
XX
XX Drosophila: developmental biology; cell signalling; insecticide;
XX pharmaceutical.
XX
XX Drosophila melanogaster.
XX
XX MO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US09231.
XX
XX 23-MAR-2000; 2000US-191637P.
XX 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE) PE CORP NY.
PA

PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 DR WPI; 2001-483426/52.
 DR N-PSDB; AAK55824.
 XX
 PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating cancers and
 PT metastasis -
 XX
 PS
 PS Claim 11; SEQ ID NO 10636; 3071pp + Sequence Listing; English.
 XX
 CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
 CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patients own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent.

CC diagnose and treat immune/haematopoietic-related diseases, especially
 CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/hematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
 CC represent sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 164 AA:
 QY 1 LVRRFVRRRHVESQ 15
 Db 79 lIrrgtthrqfthq 93
 Query Match 55.7%; Score 44; DB 22; Length 164;
 Best Local Similarity 53.3%; Pred. No. 4.2;
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 RESULT 14
 AAG93077
 ID AAG93077 standard; Protein; 175 AA.
 XX
 AC AAG93077;
 XX
 DI 26-SEP-2001 (first entry)
 XX
 DE C glutamicum protein fragment SEQ ID NO: 6831.
 XX
 KW Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
 KW organic acid synthesis.
 XX
 OS Corynebacterium glutamicum.
 XX
 PN EP1108790-A2.
 XX
 PD 20-JUN-2001.
 XX
 PF 18-DEC-2000; 2000EP-0127688.
 XX
 PR 16-DEC-1999; 99JP-0377484.
 PR 07-APR-2000; 2000JP-0159162.
 PR 03-AUG-2000; 2000JP-0280988.
 XX
 PA (KIOW) KYOWA HAKKO KOGYO KK.
 XX
 PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
 PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
 XX
 DR WPI: 2001-376931/40.
 DR N-PSDB; AAM68296.
 XX
 PT Novel polynucleotides derived from Coryneform bacteria, for identifying
 PT mutation point of a gene, measuring expression of a gene, analysing
 PT expression profile or pattern of a gene and identifying homologous gene
 XX
 PS
 PS Claim 17; SEQ ID NO: 6831; 246bp + Sequence Listing; English.
 XX
 CC The present invention provides a number of nucleotide and protein
 CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These
 CC are useful for identifying the mutation point of a gene derived from a
 CC mutant of coryneform bacterium, measuring expression amount and
 CC analysing the expression profile or expression pattern of a gene derived
 CC from coryneform bacterium, and identifying a homologue of a gene derived
 CC from coryneform bacterium. Coryneform bacteria are useful for producing
 CC amino acids, nucleic acids, vitamins, saccharides and organic acids,
 CC particularly L-lysine. The present sequence is a protein described
 CC in the exemplification of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from the
 CC European Patent Office.
 XX
 SQ Sequence 175 AA;

Query Match 53.2%: Score 42; DB 22; Length 175;
 Best Local Similarity 57.1%; Pred. No. 10;
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVRRFVHRPPHVES 14
 :||| | | | | |
 Db 87 mlrrfnhrpfvret 100

RESULT 15
 AAB78972
 ID AAB78972 standard; Protein; 203 AA.
 XX
 AC AAB78972;
 XX
 DT 30-APR-2001 (first entry)
 XX
 DE C. glutamicum SRT protein sequence SEQ ID NO:204.
 XX
 KW Corynebacterium glutamicum; stress; resistance; tolerance; SRT;
 KW fine chemical production; organic acid; proteinogetic amino acid;
 KW nonproteinogetic amino acid; purine base; pyrimidine base; nucleoside;
 KW nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol;
 KW carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme;
 KW evolutionary study; environmental hazard; fermentation.
 XX
 OS Corynebacterium glutamicum.
 XX
 PN W0200100804-A2.
 XX
 PD 04-JAN-2001.
 XX
 PF 23-JUN-2000; 2000MO-IB00922.
 XX
 PR 25-JUN-1999; 990S-0141031.
 PR 01-JUL-1999; 99DE-1030429.
 PR 01-JUL-1999; 990S-0142692.
 PR 08-JUL-1999; 99DE-1031413.
 PR 08-JUL-1999; 99DE-1031457.
 PR 08-JUL-1999; 99DE-1031541.
 PR 09-JUL-1999; 99DE-1032209.
 PR 09-JUL-1999; 99DE-1032230.
 PR 14-JUL-1999; 99DE-1032914.
 PR 27-AUG-1999; 99DE-1040764.
 PR 27-AUG-1999; 990S-0151214.
 PR 31-AUG-1999; 99DE-1041382.
 XX
 PA (BAD1) BASF AG.
 XX
 PI Pompejus M, Kroeger B, Schroeder H, Zeider O, Habernauer G, Lee H;
 PI Kim H;
 DR N-PDB; AAF71085.
 XX
 DR WPI; 2001-061972/07.
 XX
 PT New isolated Corynebacterium glutamicum nucleic acid encoding a stress,
 PT tolerance or resistance protein, for production or modulation of
 PT production of fine chemicals, such as, e.g. amino acids, lipids,
 PT carbohydrates, or enzymes -
 XX
 PS Claim 20; Page 374; 526pp; English.
 XX
 CC AAF70984 to AAF71133 encode the Corynebacterium glutamicum stress,
 CC resistance, and tolerance (SRT) proteins given in AAB78871 to AAB79020.
 CC The C. glutamicum SRT genes (I) can be used in vectors (II) for
 CC expression in host cells and production of fine chemicals, such as, an
 CC organic acid, a proteinogetic or nonproteinogetic amino acid (preferred),
 CC a purine or pyrimidine base, a nucleoside, a nucleotide, a lipid, a
 CC saturated or unsaturated fatty acid, a diol, a carbohydrate, an aromatic
 CC compound, a vitamin, a cofactor, a polyketide, or an enzyme. The fine
 CC chemical production can be modulated. The presence of (I) or the SRT

CC proteins (III) encoded by them are used for diagnosing the presence
 CC or activity of Corynebacterium diphtheriae. (I), (II), (III) and host
 CC cells containing them can be used to map the genomes of organisms related
 CC to C. glutamicum, to identify and localise C. glutamicum sequences of
 CC interest, in evolutionary studies, in determination of SRT protein
 CC regions required for function, in modulating the SRT protein activity,
 CC and in modulating the activity of an SRT pathway. (II) are used to permit
 CC C. glutamicum to survive in an environment that is normally
 CC environmentally or chemically hazardous to it. (I) and protein molecules
 CC encoded by it increase the survival of C. glutamicum to chemical and
 CC environmental hazards and provide a means for continued growth and
 CC multiplication in large scale fermentative growth conditions. By
 CC increasing the growth rate or maintaining a normal growth rate in poor or
 CC toxic conditions, the yield, production and/or efficiency or production
 CC of fine chemicals from a culture may be increased.

XX
 SQ Sequence 203 AA;
 XX

Query Match 53.2%: Score 42; DB 22; Length 203;
 Best Local Similarity 57.1%; Pred. No. 12;
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVRRFVHRPPHVES 14
 :||| | | | | |
 Db 115 mlrrfnhrpfvret 128

Search completed: August 15, 2002, 11:38:27
 Job time: 268 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 11:38:58 ; Search time 26.88 seconds
(without alignments)
13.630 Million cell updates/sec

Title: US-09-613-092a-7
Perfect score: 79
Sequence: 1 LVRRFVHRPHVESQ 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
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6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	65.8	244	2	US-08-933-750C-23
2	52	65.8	244	4	US-09-234-613-23
3	41	51.9	466	4	US-08-868-435-31
4	41	51.9	466	2	US-08-744-231-31
5	37	46.8	426	2	US-08-852-743-2
6	37	46.8	426	2	US-09-211-930-4
7	37	46.8	426	3	US-09-340-993-4
8	37	46.8	426	3	US-09-185-370-2
9	37	46.8	426	4	US-09-152-406-4
10	37	46.8	426	4	US-09-468-442-4
11	37	46.8	647	1	US-07-894-212A-8
12	37	46.8	649	1	US-07-894-212A-2
13	37	46.8	650	1	US-07-893-928A-1
14	36	45.6	362	1	US-08-415-751-6
15	36	45.6	375	2	US-08-506-864A-1
16	36	45.6	375	2	US-08-851-968-1
17	35	44.3	53	4	US-08-866-545-5
18	35	44.3	169	3	US-08-630-172-11
19	35	44.3	169	4	US-09-375-419-11
20	35	44.3	180	4	US-08-913-159-13
21	35	44.3	213	3	US-08-971-158-4
22	35	44.3	260	4	US-09-006-353A-8
23	35	44.3	462	3	US-08-486-099-117
24	35	44.3	462	3	US-08-360-107A-127
25	35	44.3	462	3	US-08-484-223B-117
26	35	44.3	462	3	US-08-919-597-117
27	35	44.3	462	3	US-08-475-668A-117

28	35	44.3	462	3	US-08-485-551A-117	Sequence 117, App
29	35	44.3	462	3	US-08-471-913A-117	Sequence 117, App
30	35	44.3	462	4	US-08-485-264A-117	Sequence 117, App
31	35	44.3	462	4	US-08-474-349A-117	Sequence 117, App
32	35	44.3	462	4	US-09-311-311C-24	Sequence 24, App
33	35	44.3	2259	4	US-09-413-814-70	Sequence 70, App
34	35	44.3	2439	3	US-09-335-102-7	Sequence 7, App
35	35	44.3	2439	4	US-09-568-102-7	Sequence 7, App
36	35	44.3	2439	4	US-09-567-969-7	Sequence 7, App
37	35	44.3	2439	4	US-09-568-480-7	Sequence 7, App
38	35	44.3	2439	4	US-09-568-486-7	Sequence 7, App
39	35	44.3	2439	4	US-09-568-472-7	Sequence 7, App
40	34.5	43.7	282	2	US-08-997-080-134	Sequence 134, App
41	34.5	43.7	282	2	US-08-997-262-134	Sequence 134, App
42	34.5	43.7	282	4	US-09-095-855-134	Sequence 134, App
43	34.5	43.7	282	4	US-09-324-542-134	Sequence 134, App
44	34.5	43.7	297	2	US-08-997-080-177	Sequence 177, App
45	34.5	43.7	297	2	US-08-997-362-177	Sequence 177, App

ALIGNMENTS

RESULT 1
US-08-933-750C-23
Sequence 23, Application US/08933750C
Patent No. 5932442
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933 750C
FILING DATE: September 23, 1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SPLNNOT04

CLONE: 1561587
US-08-933-750C-23

Query Match 65.8%; Score 52; DB 2; Length 244;
Best Local Similarity 75.0%; Pred. No. 0.1;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 VRFVHRPHVE 13
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DB 104 VRFVHRPHVD 115

RESULT 2
US-09-234-613-23
; Sequence 23, Application US/09234613
; Patent No. 6132973

GENERAL INFORMATION:

APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.

APPLICANT: Bandman, Olga

APPLICANT: Shah, Purvi

APPLICANT: Au-Young, Janice

APPLICANT: Yue, Henry

APPLICANT: Guegler, Karl J.

APPLICANT: Corley, Neil C.

TITLE OF INVENTION: HUMAN REGULATORY MOLECULES

NUMBER OF SEQUENCES: 98

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/234,613

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/933,750

FILING DATE: September 23, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0356 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEFAX: 415-845-4166

TELEX:

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 244 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: SPLNOT04

CLONE: 1561587

US-09-234-613-23

DB 104 VRFVHRPHVD 115

RESULT 3

US-08-868-435-31

; Sequence 31, Application US/08868435

; Patent No. 6291221

GENERAL INFORMATION:

APPLICANT: Van Loon, Adolphus

APPLICANT: Mitchell, David

TITLE OF INVENTION: POLYPEPTIDES WITH PHYTASE ACTIVITY

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hoffmann-La Roche Inc.

STREET: 340 Kingsland Street

CITY: Nutley

STATE: New Jersey

COUNTRY: United States of America

ZIP: 07110

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/868,435

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/744,231

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Kass, Alan P

REGISTRATION NUMBER: 32142

REFERENCE/DOCKET NUMBER: Case Docket 9339

TELECOMMUNICATION INFORMATION:

TELEPHONE: (201) 235-4205

TELEFAX: (201) 235-2363

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 466 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: misc-feature

LOCATION: 204

OTHER INFORMATION: /note="potential N-glycosylation site"

FEATURE:

NAME/KEY: misc-feature

LOCATION: 269

OTHER INFORMATION: /note="potential N-glycosylation site"

FEATURE:

NAME/KEY: misc-feature

LOCATION: 372

OTHER INFORMATION: /note="potential N-glycosylation site"

US-08-868-435-31

Query Match 51.9%; Score 41; DB 4; Length 466;
Best Local Similarity 57.1%; Pred. No. 16;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 LVRFVHRPHVES 14
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Db 12 LVALVSRNPHVDS 25

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RESULT 4
US-08-744-231-31
; Sequence 31, Application US/08744231
; Patent No. 6358722
; GENERAL INFORMATION:
; APPLICANT: Van Loon, Adolphus
; APPLICANT: Mitchell, David
; TITLE OF INVENTION: POLYPEPTIDES WITH PHOSPHATASE ACTIVITY
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/744,231
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/424,757
; FILING DATE: 18-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kass, Alan P
; REGISTRATION NUMBER: 32142
; REFERENCE/DOCKET NUMBER: Case Docket 9339
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-4205
; TELEFAX: (201) 235-2363
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 466 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 204
; OTHER INFORMATION: /note="potential N-glycosylation site"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 269
; OTHER INFORMATION: /note="potential N-glycosylation site"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 335
; OTHER INFORMATION: /note="potential N-glycosylation site"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 348
; OTHER INFORMATION: /note="potential N-glycosylation site"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 372
; OTHER INFORMATION: /note="potential N-glycosylation site"
; US-08-744-231-31
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Best Local Similarity 57.1%; Pred. No. 16;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Oy 1 LVRRVHRRPHVES 14
|| :| | |||:|
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Db 12 LVALVSRNPHVDS 25

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RESULT 5
US-08-852-743-2
; Sequence 2, Application US/08852743
; Patent No. 5830699
; GENERAL INFORMATION:
; APPLICANT: Force, Thomas
; APPLICANT: Kyriakis, John M.
; APPLICANT: Pombo, Celia M.
; APPLICANT: Bonventre, Joseph
; TITLE OF INVENTION: SOK-1 AND METHODS OF USE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,743
; FILING DATE: 7-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/016,774
; FILING DATE: 7-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/327001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200134
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: Internal
; US-08-852-743-2
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Query Match 46.8%; Score 37; DB 2; Length 426;
Best Local Similarity 53.8%; Pred. No. 71;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
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Db 412 VQRFSHRNHLTS 424
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RESULT 6
US-09-211-930-4
; Sequence 4, Application US/09211930
; Patent No. 5962265
; GENERAL INFORMATION:
; APPLICANT: Tyrell E. No. 5962265r1s
; APPLICANT: William Craig Moore
; APPLICANT: David Shay Silberstein
; TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION
; TITLE OF INVENTION: SERINE/THREONINE KINASE
; FILE REFERENCE: PHM.70296
; CURRENT APPLICATION NUMBER: US/09/211,930
; CURRENT FILING DATE: 1998-12-15
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; EARLIER APPLICATION NUMBER: GB 9726851.0
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-211-930-4

Query Match
Best Local Similarity 46.8%; Score 37; DB 2; Length 426;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 2 VRRFVHRPHVES 14
Db 412 VORFSHRNHLTS 424

RESULT 7
US-09-340-993-4
; Sequence 4, Application US/09340993
; Patent No. 6034228
; GENERAL INFORMATION:
; APPLICANT: Tyrell E. No. 6034228rls
; APPLICANT: William Craig Moore
; APPLICANT: David Shay Silberstein
; TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION SERINE/THREONINE KINASE
; FILE REFERENCE: PHM.70296.N1
; CURRENT APPLICATION NUMBER: US/09/340,993
; CURRENT FILING DATE: 1999-06-25
; EARLIER APPLICATION NUMBER: GB 9726851.0 & US 09/211,930
; EARLIER FILING DATE: 1997-12-19 & 1998-12-15
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-340-993-4

Query Match
Best Local Similarity 46.8%; Score 37; DB 3; Length 426;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 2 VRRFVHRPHVES 14
Db 412 VORFSHRNHLTS 424

RESULT 8
US-09-185-370-2
; Sequence 2, Application US/09185370
; Patent No. 6093560
; GENERAL INFORMATION:
; APPLICANT: Force, Thomas
; APPLICANT: Kyriakis, John M.
; APPLICANT: Pombo, Celia M.
; APPLICANT: Bonventre, Joseph
; TITLE OF INVENTION: SOK-1 AND METHODS OF USE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
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; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/185,370
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/852,743
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/327001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: Internal
US-09-185-370-2
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Query Match
Best Local Similarity 46.8%; Score 37; DB 3; Length 426;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
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OY 2 VRRFVHRPHVES 14
Db 412 VORFSHRNHLTS 424
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RESULT 9
US-09-152-406-4
; Sequence 4, Application US/09152406
; Patent No. 6265560
; GENERAL INFORMATION:
; APPLICANT: William Craig Moore
; APPLICANT: Tyrell E. No. 6265560rls
; APPLICANT: David Shay Silberstein
; TITLE OF INVENTION: HUMAN STE20-LIKE STRESS ACTIVATED
; FILE REFERENCE: PHM.70272
; CURRENT APPLICATION NUMBER: US/09/152,406
; CURRENT FILING DATE: 1998-09-14
; EARLIER APPLICATION NUMBER: 9719920.2
; EARLIER FILING DATE: 1997-09-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-152-406-4
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Query Match
Best Local Similarity 46.8%; Score 37; DB 4; Length 426;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
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OY 2 VRRFVHRPHVES 14
Db 412 VORFSHRNHLTS 424
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RESULT 10
US-09-468-442-4
; Sequence 4, Application US/09468442
; Patent No. 6300098
```

```

? GENERAL INFORMATION:
? APPLICANT: Tyrell E. No. 6300098rlts
? APPLICANT: William Craig Moore
? APPLICANT: David Shay Silberstein
? TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION SERINE/THREONINE KINASE
? FILE REFERENCE: PHM. 70296.NI
? CURRENT APPLICATION NUMBER: US/09/468,442
? CURRENT FILING DATE: 1999-12-21
? EARLIER APPLICATION NUMBER: US 09/340,993
? EARLIER FILING DATE: 1999-06-25
? EARLIER APPLICATION NUMBER: GB 9726651.0
? EARLIER FILING DATE: 1997-12-19
? EARLIER APPLICATION NUMBER: US 09/211,930
? EARLIER FILING DATE: 1998-12-15
? NUMBER OF SEQ ID NOS: 14
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 4
? LENGTH: 426
? TYPE: PRP
? ORGANISM: Homo sapiens
? US-09-468-442-4

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Query Match	46.8%;	Score 37;	DB 4;	Length 426;
Best Local Similarity	53.8%;	Pred. No. 71;		
Matches 7; Conservative	2;	Mismatches 4;	Indels 0;	Gaps 0

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QY      2 VRFVHRRPHVES 14
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Db      412 VQFESHNRNHLTS 424
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-894-212A-8

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Query Match	46.8%	Score 37:	DB 1:	Length 647:
Best Local Similarity	53.3%	Pred. No.	1.1e+02:	
Matches	8;	Conservative	2;	Mismatches 5;
				Indels 0;
				Gaps 0;

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QY      1 LVRRFVHRPVESQ 15
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Db      435 LARRWEHYHGYVESQ 449
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RESULT 12
US-07-894-212A-2
? Sequence 2, Application US/07894212A
? Patent No. 5365883
?
GENERAL INFORMATION:
APPLICANT: ASADA, KIYOZO
APPLICANT: UEMORI, TAKASHI
APPLICANT: MUKAI, HIROYUKI
APPLICANT: KATO, IKUNOSHIN
APPLICANT: LADEBMAN, KENNETH
APPLICANT: ANTIENSEN, CHRISTIAN
TITLE OF INVENTION: THE ALPHA-AMYLASE GENE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: CUSHMAN DABRY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON, D.C.
COUNTRY: U.S.A.
ZIP: 20005
?
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/894,212A
FILING DATE:
?
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16773
REFERENCE/DOCKET NUMBER: 95469/C-1195
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
?
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 649 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-894-212A-2

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Query Match	46.8%	Score 37:	DB 1:	Length 649;
Best Local Similarity	53.3%	Pred. No.	1.1e+02;	
Matches	8;	Mismatches	5;	Indels 0;
				Gaps 0;

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QY      1 LVRRFVHRPHE$Q 15
         | | | : | : | | |
Db      437 LARRWEHYHGVE$Q 451

```

RESULT 13
US-07-893-928A-1
; Sequence 1, Application US/07893928A
; Patent No. 5578479

GENERAL INFORMATION:
APPLICANT: LADERMAN, KENNETH
TITLE OF INVENTION: a-AMYLASE FROM HYPERTHERMOPHILIC
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON, D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/893,928A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL, N.
REGISTRATION NUMBER: 16773
REFERENCE/DOCKET NUMBER: 95470/C-1197
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 650 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-893-928A-1

Query Match 46.8%; Score 37; DB 1; Length 650;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 LVRRFVHRPHVRSQ 15
DB 437 LARRMEHYHGYVESQ 451

RESULT 14
US-08-415-751-6
Sequence 6, Application US/08415751
Patent No. 5643772
GENERAL INFORMATION:
APPLICANT: PETERSEN, CAROLYN
APPLICANT: LEECH, JAMES
APPLICANT: NELSON, RICHARD, C.
TITLE OF INVENTION: POLYPEPTIDES BINDING ANTI-
TITLE OF INVENTION: CRYPTOSPORIDIUM ANTIBODIES, DNA
TITLE OF INVENTION: AND RNA ENCODING THEM, HYBRID
TITLE OF INVENTION: VECTOR AND TRANSFORMED HOST AND
TITLE OF INVENTION: METHODS FOR IMMUNOTHERAPY AND
TITLE OF INVENTION: DIAGNOSIS AND KIT
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: PHILLIPS, MOORE, LEMPJO & FINLEY
STREET: 385 Sherman Avenue, Suite 6
CITY: Palo Alto
STATE: California
COUNTRY: United States of America
ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Kb storage

COMPUTER: PC
OPERATING SYSTEM: DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/415,751
FILING DATE: 03-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/071,880
FILING DATE: June 1, 1993
APPLICATION NUMBER: 07/891,301
FILING DATE: May 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Hana Dolezalova
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.19-2 (HND)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-1677
TELEFAX: (415) 324-1678
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORGANISM: Cryptosporidium parvum
FEATURE:
NAME/KEY: Positions coded by nonsense codons are
US-08-415-751-6

Query Match 45.6%; Score 36; DB 1; Length 362;
Best Local Similarity 60.0%; Pred. No. 89;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 VRRFVHRPH 11
DB 328 LRRFVHRSH 337

RESULT 15
US-08-506-864A-1
Sequence 1, Application US/08506864A
Patent No. 5834245
GENERAL INFORMATION:
APPLICANT: NAKAMURA, YUSUKE
TITLE OF INVENTION: FUJIMARA, YOSHIYUKI
TITLE OF INVENTION: PRITS PROTEINS AND DNA'S
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLYNN, THEIL, BOUTELL & TANIS, P.C.
STREET: 2026 Rambling Road
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49008-1699
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
COMPUTER: IBM PC/XT/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: Wordperfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/506,864A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP6-178131
FILING DATE: 29-JULY-1994
ATTORNEY/AGENT INFORMATION:

NAME: Terrence F. Chapman
REGISTRATION NUMBER: 32549
REFERENCE/DOCKET NUMBER: Furuya Case 1334
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 375
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: human fetal lung cDNA library
US-08-506-864A-1

Query Match 45.6%; Score 36; DB 2; Length 375;
Best Local Similarity 53.8%; Pred. NO. 93;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 3 RRFVRRPPHVESQ 15
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Db 229 RGFVYLQPHSEHQ 241

Search completed: August 15, 2002, 11:38:59
Job time: 265 sec

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Result No.	Score	Query Match	Length	DB	ID	Description
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2	45	57.0	377	2	F72122	hypothetical prote
3	45	57.0	577	2	C86499	hypothetical prote
4	44	55.7	546	2	I49636	DNA-binding prote
5	43	54.4	782	2	T12874	hypothetical prote
6	41	51.9	282	2	G70482	panothenate synth
7	41	51.9	485	2	A44498	radial spoke prote
8	41	51.9	481	2	T15372	hypothetical prote
9	40	50.6	138	2	H72534	hypothetical prote
10	40	50.6	1220	2	T42573	DNA-directed DNA p
11	40	50.6	1233	2	T30989	serine/threonine p
12	39	49.4	67	2	S14854	hypothetical prote
13	39	49.4	80	2	G81065	hypothetical prote
14	39	49.4	246	2	T16371	hypothetical prote
15	39	49.4	257	2	E70330	conserved hypotet
16	39	49.4	261	2	T51322	hypothetical prote
17	39	49.4	476	2	T40330	hypothetical prote
18	39	49.4	540	2	JC4816	hypothetical prote
19	39	49.4	548	2	JC4917	signal transducing
20	39	49.4	954	2	G71496	signal transducing
21	39	49.4	1207	2	H87475	hypothetical prote
22	39	49.4	1792	2	T13939	urea am-dolylase-re
23	38	48.1	248	2	S30194	myosin V - fruit f
24	38	48.1	363	2	C86214	ribosomal protein
25	38	48.1	384	2	T24596	hypothetical prote
26	38	48.1	434	2	F75425	hypothetical prote
27	38	48.1	654	2	S75005	tRNA nucleotidyltr
28	38	48.1	688	2	T21641	sensory transducti
29	38	48.1	837	2	T19625	hypothetical prote

30	37.5	47.5	24.1	2	H82072	DNA repair protein
31	37	46.8	167	2	S76074	hypothetical protein
32	37	46.8	225	2	A72594	hypothetical protein
33	37	46.8	244	2	T43958	hypothetical protein
34	37	46.8	274	2	AE1619	hypothetical protein
35	37	46.8	274	2	A11256	hypothetical protein
36	37	46.8	222	2	AD0362	probable lysr-fam1
37	37	46.8	426	2	S71886	Ste20-like protein
38	37	46.8	589	2	T13086	serine/threonine-p
39	37	46.8	590	2	A10094	ABC-transporter tr
40	37	46.8	600	2	D83683	L-glutamine-D-fruc
41	37	46.8	600	2	T14613	hypothetical prote
42	37	46.8	649	2	A49512	alpha-amylase (EC
43	37	46.8	651	2	T03889	Na ⁺ /Ca ²⁺ ,K ⁺ -exch
44	37	46.8	675	1	F0PFB	brown protein - fr
45	37	46.8	1108	2	T17455	translation initia

ALIGNMENTS

RESULT

transcription regulator LysR family homolog ycgK - *Bacillus subtilis*

C;Species: Bacillus subtilis

C:Accession: F69758
#sequence_revision 03-Dec-1997
#lex_change 20-Jul-2000

R;Kunst, F.; Ogasawara, M.

C.: Bron, S.; Grouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997

A;Authors: Foulger,
Josh T.;Harwood

Lech, J. J.; Halwood, Koetter, P. J.; Koning

A;Authors: Lauber,

Y, M.; Ogawa, K.; O
Piero M.; Pivrol

A;Authors: Schleicher

akeuchi, M.; Tamako

T.; Winters, P.; Winters, P.

A:Title: The complete

A;Reference number:

A;Accession: F69758

A;molecule type: DN

A;Residues: 1-324 <

A;Cross-references:

A; experimental source:
C: Genetics:

A;Gene: ycqk

C;Superfamily: prob

Query Match

Best Local Simila

Matches 9; Co

1 LVRRVHRE
OV

—

Db 109 LKQFVARY

RESULT 2

F72122

C:Species: Chlamydo

C; Date: 23-Apr-1999

C;Accession: F72122

R; Kallman, S.; Mutch
Nature Genet. 21: 3

A;Title: Comparatiw

A; Reference number:

A:Accession: F72122
A:Molecule type: DNA
A:Residues: 1-577 <ARN>
A:Cross-references: GB:AE001592; GB:AE001363; NID:94376322; PIDN:AA18219.1; PID:9437632
A:Experimental source: strain CMI029
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwin, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of *Chlamydia trachomatis* Mopn and *Chlamydia pneumoniae* AR39.
A:Reference number: AB1500; MUID:20150255
A:Accession: DB1548
A:Molecule type: DNA
A:Residues: 1-577 <REA>
A:Cross-references: GB:AE002229; GB:AE002161; NID:97189613; PIDN:AAF38516.1; PID:9718962
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: CPn0066; CP0708

Query Match 57.0%; Score 45; DB 2; Length 577;
Best Local Similarity 80.0%; Pred. No. 7;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 VRRFVHRPH 11
|||:|||||
DB 567 VRRNLHRPH 576

RESULT 3
C68499
hypothetical protein CPJ0066 [imported] - *Chlamydia pneumoniae* (strain J138)
C:Species: *Chlamydia pneumoniae*, *Chlamydia pneumoniae*
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C:Accession: C68499
R:Shital, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; IS
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of *chlamydia pneumoniae* J138.
A:Reference number: AB6491; MUID:20330349
A:Accession: C68499
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-577 <STO>
A:Cross-references: GB:BA000008; NID:98978440; PIDN:BA98277.1; GSPDB:GN00142
A:Experimental source: strain J138
C:Genetics:
A:Gene: CPJ0066

Query Match 57.0%; Score 45; DB 2; Length 577;
Best Local Similarity 80.0%; Pred. No. 7;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 VRRFVHRPH 11
|||:|||||
DB 567 VRRNLHRPH 576

RESULT 4
I49636
DNA-binding protein - mouse
C:Species: *Mus musculus* (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 01-Dec-2000
C:Accession: I49636
R:Wick, M.J.; Ann, D.K.; Lee, N.M.; Loh, H.H.
Gene 152, 227-232, 1995
A:Title: Isolation of a cDNA encoding a novel zinc-finger protein from neuroblastoma x
A:Reference number: I49636; MUID:95137933
A:Accession: I49636
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-346 <RES>
A:Cross-references: GB:L20450; NID:9437443; PIDN:AAA65196.1; PID:9437444
C:Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology

Query Match 55.7%; Score 44; DB 2; Length 546;
Best Local Similarity 58.3%; Pred. No. 9.8;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 4 REVHRPHVESQ 15
|:|||||:
DB 117 KOIHRPHTEEK 128

RESULT 5
T12874
hypothetical protein yqjN - *Bacillus subtilis* phage SPBc2
C:Species: *Bacillus subtilis* phage SPBc2
C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 15-Oct-1999
C:Accession: T12874; F69920
R:Lazarevic, V.; Duesterhoeft, A.; Soldo, B.; Hilbert, H.; Mael, C.; Karamata, D.
submitted to the EMBL Data Library, August 1997
A:Description: The complete nucleotide sequence of the *Bacillus subtilis* SPBc2 pro
A:Reference number: Z17583
A:Accession: T12874
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-72 <LAZ>
A:Cross-references: EMBL:AF020713; NID:93025478; PID:93025588; PIDN:AA13083.1
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funai, S.; Galizzi, A.; Gal
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M
Koeltz, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanl
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowaka, A.; Se
kouchi, M.; Tamakoshi, A.; Tanaka, T.; Terperera, P.; Tognoni, A.; Tosato, V.; Uchiya
T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*
A:Reference number: A69580; MUID:98044033
A:Accession: F69920
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-72 <KUN>
A:Cross-references: GB:299114; GB:AL009126; NID:92634230; PIDN:CAB13949.1; PID:el1855
A:Experimental source: strain 168
C:Genetics:
A:Gene: yqjN
A:Note: yqjN

Query Match 54.4%; Score 43; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 FVHRPH 11
|||||
DB 60 FVHRPH 66

RESULT 6
G70482
pantothenate synthetase - *Aquifex aeolicus*
C:Species: *Aquifex aeolicus*
C>Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 29-Sep-1999
C:Accession: G70482
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;
V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium *Aquifex aeolicus*.
A:Reference number: AF0300; MUID:98196666

A:Accession: G70482
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-282 <NOF>
 A:Cross-references: GB:AE000774; NID:g2984324; PIDN:AAC07847.1; PID:g2984326; GB:AE00065
 A:Experimental source: strain VFS
 C:Genetics:
 A:Gene: panc
 C:Superfamily: pantoate-beta-alanine ligase

Query Match 51.9%; Score 41; DB 2; Length 282;
 Best Local Similarity 50.0%; Pred. No. 16;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 VRRFVHRRPHEV 13
 :|:|:|:|:|:
 Db 228 IRAFIERHPHV 239

RESULT 7
 A44498
 radial spoke protein 4 - Chlamydomonas reinhardtii
 C:Species: Chlamydomonas reinhardtii
 C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
 C:Accession: A44498
 R:Curry, A.M.; Williams, B.D.; Rosenbaum, J.L.
 Mol. Cell. Biol. 12, 3967-3977, 1992
 A:Title: Sequence analysis reveals homology between two proteins of the flagellar radial
 A:Reference number: A44498; MUID:92375065
 A:Accession: A44498
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-465 <CUR>
 A:Cross-references: GB:M87526; NID:q167435; PIDN:AAA33092.1; PID:q167436
 A:Note: Sequence extracted from NCBI backbone (NCBIN:111696, NCBIPI:111697)

Query Match 51.9%; Score 41; DB 2; Length 465;
 Best Local Similarity 63.6%; Pred. No. 27;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 FVHRHRRPHEV 15
 :|:|:|:|:|:
 Db 319 WNVHRPHLRKSO 329

RESULT 8
 T15372
 hypothetical protein C01F1.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C:Accession: T15372
 R:Johnson, D.
 submitted to the EMBL Data Library, May 1996
 A:Description: The sequence of C. elegans cosmid C01F1.
 A:Reference number: Z18338
 A:Accession: T15372
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-481 <OH>
 A:Cross-references: EMBL:U58761; NID:g1330391; PID:g1330397; PIDN:AAB00717.1; GSPDB:GN00
 A:Experimental source: strain Bristol N2; clone C01F1
 C:Genetics:
 A:Gene: CESP.C01F1.1
 A:Map position: 2
 A:Insertions: 263/1; 287/2; 428/3

Query Match 51.9%; Score 41; DB 2; Length 481;
 Best Local Similarity 42.9%; Pred. No. 28;
 Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 VRRFVHRRPHEV 15
 :|:|:|:|:|:
 Db 416 VRRYLRRKPHHTTKE 429

RESULT 9
 H72534
 hypothetical protein APE1565 - Aeropyrum pernix (strain K1)
 C:Species: Aeropyrum pernix
 C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
 C:Accession: H72534
 R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Jin-no, K.; Ta
 awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.
 DNA Res. 6, 83-101, 1999
 A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero
 A:Reference number: A72450; MUID:99310339
 A:Accession: H72534
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-138 <KAW>
 A:Cross-references: DDBJ:AF000062; NID:g5105244; PIDN:BAA80565.1; PID:d1044351; PID:g
 A:Experimental source: strain K1
 C:Genetics:
 A:Gene: APE1565

Query Match 50.6%; Score 40; DB 2; Length 138;
 Best Local Similarity 66.7%; Pred. No. 12;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 RRVVHRRPH 11
 :|:|:|:|:|:
 Db 66 RSVVHRQPH 74

RESULT 10
 T42573
 DNA-directed DNA polymerase (EC 2.7.7.7) - equine herpesvirus 4 (strain NS80567)
 C:Species: equine herpesvirus 4
 A:Variety: strain NS80567
 C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
 C:Accession: T42573
 R:Telford, E.A.; Watson, M.S.; Perry, J.; Cullinane, A.A.; Davison, A.J.
 J. Gen. Virol. 79, 1197-1203, 1998
 A:Title: The DNA sequence of equine herpesvirus-4.
 A:Reference number: Z22173; MUID:98264497
 A:Accession: T42573
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1220 <TEL>
 A:Cross-references: EMBL:AF030027; NID:g2605950; PIDN:AAC59546.1; PID:g2605974
 A:Experimental source: strain NS80567
 C:Genetics:
 A:Gene: 30
 C:Superfamily: herpesvirus DNA-directed DNA polymerase
 C:Keywords: DNA binding; DNA replication; nucleotidyltransferase

Query Match 50.6%; Score 40; DB 2; Length 1220;
 Best Local Similarity 50.0%; Pred. No. 11e+02;
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 LVRRFVHRRPHEV 14
 :|:|:|:|:|:
 Db 1165 LKRFIPERPHKTS 1178

RESULT 11
 T30989
 serine/threonine protein kinase NIK - mouse
 N:Alternate names: Nck interacting kinase
 C:Species: Mus musculus (house mouse)
 C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999

C:Accession: T30989
 R:Su, Y.C.; Han, J.; Xu, S.; Cobb, M.; Skolnik, E.Y.
 EMBL J. 16, 1279-1290, 1997
 A:Title: NIK is a new Ste20-related kinase that binds NCK and MEK1 and activates the SA
 A:Reference number: Z20954; MUID:97280817
 A:Accession: T30989
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1233 <SOY>
 A:Cross-references: EMBL:U88984; NID:g1872545; PID:g1872546; PIDN:AAC53165.1
 C:Keywords: protein kinase

Query Match 50.6%; Score 40; DB 2; Length 1233;
 Best Local Similarity 66.7%; Pred. No. 1.1e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 HRRPHVESQ 15
 ||||| : |
 Db 496 HRRPHVQQ 504

RESULT 12
 S14854

hypothetical protein 1 - yeast (*Pichia angusta*)
 C:Species: *Pichia angusta*
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Apr-2000
 C:Accession: S14854
 R:Krutillina, A.I.; Seregina, S.A.; Tikhomirova, L.P.; Kryukov, V.M.
 submitted to the EMBL Data Library, April 1991
 A:Description: Nucleotide sequence of *Hansenula polymorpha* DNA region complementing DAK.
 A:Reference number: S14854
 A:Accession: S14854
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-67 <RRU>
 A:Cross-references: EMBL:X58862; NID:g2762; PIDN:CAA1665.1; PID:g2763

Query Match 49.4%; Score 39; DB 2; Length 67;
 Best Local Similarity 77.8%; Pred. No. 8.2;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 HRRPHVESQ 15
 ||||| : |
 Db 12 HRRVHEAQ 20

RESULT 13
 G81065

hypothetical protein NMB1589 [imported] - *Neisseria meningitidis* (strain MC58 serogroup
 C:Species: *Neisseria meningitidis*
 C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
 C:Accession: G81065
 R:Rettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
 Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
 Li, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masiagnani, V.; Pizza, M.
 Science 287, 1809-1815, 2000
 A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V
 A:Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
 A:Reference number: A81000; MUID:20175755
 A:Accession: G81065
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-80 <RET>
 A:Cross-references: GB:AE002509; GB:AE002098; NID:g7226832; PIDN:AAFA1942.1; PID:g722683
 A:Experimental source: serogroup B, strain MC58
 C:Genetics:
 A:Gene: NMB1589

Query Match 49.4%; Score 39; DB 2; Length 80;
 Best Local Similarity 70.0%; Pred. No. 9.8;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 2 VRRFVHRRPH 11
 ||:||||| :
 Db 62 VRQFVHRRQY 71

RESULT 14
 T16371

hypothetical protein F45E12.1 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C:Accession: T16371
 R:Latreille, P.
 submitted to the EMBL Data Library, June 1995
 A:Description: The sequence of *C. elegans* cosmid F45E12.
 A:Reference number: Z18501
 A:Accession: T16371
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-246 <LAT>
 A:Cross-references: EMBL:U29536; NID:g868261; PID:g868266; PIDN:AAA68794.1; CESP:F45E
 A:Experimental source: strain Bristol N2
 C:Genetics:
 A:Gene: CESP:F45E12.1
 A:Introns: 29/3; 53/1; 92/3; 120/2; 151/2; 193/1

Query Match 49.4%; Score 39; DB 2; Length 246;
 Best Local Similarity 58.3%; Pred. No. 31;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 VRRFVHRRPHE 13
 | : ||||| :
 Db 100 VKRFVHERPHVD 111

RESULT 15
 E70330

conserved hypothetical protein aq_342 - *Aquifex aeolicus*
 C:Species: *Aquifex aeolicus*
 C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 20-Aug-1999
 C:Accession: E70330
 R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;
 V.
 Nature 392, 353-358, 1998
 A:Title: The complete genome of the hyperthermophilic bacterium *Aquifex aeolicus*.
 A:Reference number: A70300; MUID:98196666
 A:Accession: E70330
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-257 <AOE>
 A:Cross-references: GB:AE00684; NID:g2983009; PIDN:AAC06636.1; PID:g2983025; GB:AE00
 A:Experimental source: strain VFS
 C:Genetics:
 A:Gene: aq_342
 C:Superfamily: beta-lactamase regulatory protein; beta-lactamase regulatory protein h
 F.17-248/Domain: beta-lactamase regulatory protein homology <BLR>

Query Match 49.4%; Score 39; DB 2; Length 257;
 Best Local Similarity 50.0%; Pred. No. 33;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVRRFVHRRPHV 12
 ||: : |||||
 Db 89 LVKRLIERPHV 100

Search completed: August 15, 2002, 11:39:42
 Job time: 203 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 11:47:41 ; Search time 18.67 seconds
(without alignments)
31.108 Million cell updates/sec

Title: US-09-613-092a-7
Perfect score: 79
Sequence: 1 LVRRFVHRHPHVESQ 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	45	57.0	YBL1_STRCI	P33653 streptomyc
2	41	51.9	PANC_AOUAE	O67891 aquilex aeo
3	41	51.9	RSP4_CHLRE	Q01656 chlamydomon
4	38	48.1	RS6_DROME	P29327 drosophila
5	38	48.1	04F3_HUMAN	O95013 homo sapien
6	38	48.1	CGB3_CAREL	O10654 caenorhabdi
7	38	48.1	YLB5_CAREL	P46941 caenorhabdi
8	37	46.8	VCOM_ADECC	O65932 canine aden
9	37	46.8	VCOM_ADECR	O96685 canine aden
10	37	46.8	ST25_HUMAN	O00506 homo sapien
11	37	46.8	SHK2_SCHPO	O10056 schistosach
12	37	46.8	GLMS_PACHD	O9K945 b glucosami
13	37	46.8	AMTA_PYRFU	P49067 pyrococcus
14	37	46.8	BROW_DROME	P12428 drosophila
15	37	46.8	E2K3_RAT	O92121 ratius norv
16	37	46.8	E2K3_MOUSE	O92285 mus musculi
17	36.5	46.2	YCPI1_STNRY	O02188 synecococc
18	35	45.6	RS15_PVRHO	O57805 pyrococcus
19	36	45.6	EXPI1_ERMCA	P33882 erwilia car
20	36	45.6	PGY2_STNEL	P30040 synecococc
21	36	45.6	Y152_HALHA	P04137 halobacteri
22	36	45.6	ST25_MOUSE	O92285 mus musculi
23	36	45.6	YB28_MYCTU	O06580 mycobacteri
24	36	45.6	YGO2_YEAST	P30777 saccharomyc
25	36	45.6	NEL1_RAT	O62919 ratius norv
26	36	45.6	MOTS_TREPA	O83348 treponema p
27	36	45.6	E2K3_HUMAN	P09215 homo sapien
28	36	45.6	RPCL1_TRYBB	P08968 trypanosoma
29	36	45.6	PEPL_MOUSE	P12659 mus musculi
30	36	45.6	MY10_BOVIN	P79114 bos taurus
31	36	45.6	MY10_HUMAN	Q9H667 homo sapien
32	36	45.6	TOR1_YEAST	P35169 saccharomyc
33	36	45.6	POLG_DEN3	P27915 d genome po

34	35.5	44.9	102	1	RS10_CAUCR	O9a8v4 caulobacter
35	35.5	44.9	236	1	RECO_HAEIN	P44642 haemophilus
36	35	44.3	60	1	YB61_ARCFU	O29105 archaeoglob
37	35	44.3	110	1	RK23_PORPU	P51312 porphyra pu
38	35	44.3	125	1	YN25_CAREL	P34584 caenorhabdi
39	35	44.3	140	1	YK24_PSEAE	P23205 pseudomonas
40	35	44.3	183	1	RL6_CHLPN	O92781 chlamydia p
41	35	44.3	213	1	GRPE_DROME	P48604 drosophila
42	35	44.3	250	1	TNR7_MOUSE	P41272 mus musculi
43	35	44.3	260	1	TNR7_HUMAN	P26842 homo sapien
44	35	44.3	352	1	URIC_DROME	P16163 drosophila
45	35	44.3	354	1	CARX_BACST	P54324 bacillus st

ALIGNMENTS

RESULT	ID	YBL1_STRCI	STANDARD;	PRT;	242 AA.
AC	P33653;				
DT	01-FEB-1994 (Rel. 28, Created)				
DT	01-FEB-1994 (Rel. 28, Last sequence update)				
DT	01-FEB-1994 (Rel. 28, Last annotation update)				
DE	Hypothetical 26.1 kDa protein in blaB 3'region.				
OS	Streptomyces cacaoi.				
OC	Bacteria: Firmicutes; Actinobacteria; Actinobacteridae;				
OC	Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.				
OX	NCBI_TaxID=1898;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=KCC S0352;				
RX	MEDLINE=92244939; PubMed=1569015;				
RA	Urahe H., Ogawara H.;				
RT	"Nucleotide sequence and transcriptional analysis of				
RT	activator-regulator proteins for beta-lactamase in Streptomyces				
RT	cacaoi.";				
RL	J. Bacteriol. 174:2834-2842(1992).				
CC	-I- SIMILARITY: TO E. COLI MAGZ AND TO PLASMID PIP1100 ERYTHROMYCIN				
CC	ESTERASE.				
CC	-----				
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CC	-----				
DR	EMBL: D00937; BAA00775.1; -				
KW	Hypothetical protein.				
SO	SEQUENCE 242 AA; 26051 MW; 286B53C75AF90063 CRC64;				
Query Match	57.0%; Score 45; DB 1; Length 242;				
Best Local Similarity	66.7%; Pred. No. 1;				
Matches	8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;				
OY	1 LVRRFVHRHPH 12				
Db	126 LVTKLVHRHPHV 137				
RESULT 2					
ID	PANC_AOUAE	STANDARD;	PRT;	282 AA.	
AC	O67891;				
DT	30-MAY-2000 (Rel. 39, Created)				
DT	30-MAY-2000 (Rel. 39, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Pantoate--beta-alanine ligase (EC 6.3.2.1) (Pantothenate synthetase)				
DE	(Pantoate activating enzyme).				
GN	PANC OR AO_2132.				

```

OS Aquifex aeolicus.
OC Bacteria; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320;
RA Decker G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Sneed M.A., Keller M., AuJay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus".
RL Nature 392:353-358(1998).
CC -I- CATALYTIC ACTIVITY: ATP + (R)-pantoate + beta-alanine = AMP +
CC -I- phosphate + (R)-pantothenate.
CC -I- PATHWAY: Pantothenate biosynthesis; last step.
CC -I- SIMILARITY: BELONGS TO THE PANTOTHENATE SYNTHETASE FAMILY.
CC -----
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CC -----
DR EMBL: AE000774; AAC07847.1; -
DR InterPro: IPR003721; Pantoate_ligase.
DR Pfam: PF02569; Pantoate_ligase; 1.
KW Pantothenate biosynthesis; Ligase; Complete proteome.
SQ SEQUENCE 282 AA; 32433 MW; 7E71B941C158DCB CRC64;

Query Match 51.9%; Score 41; DB 1; Length 282;
Best Local Similarity 50.0%; Pred. No. 5.9;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 VRFVRRRHVE 13
: |||: |||:
DB 228 IRAFIERHPVK 239

RESULT 3
RSP4_CHLRE STANDARD; PRT; 465 AA.
ID RSP4_CHLRE Q01656;
AC 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-1993 (Rel. 27, Last annotation update)
DE Flagellar radial spoke protein 4.
GN RSP4.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=21GR;
RX MEDLINE=92375065; PubMed=1508197;
RA Curry A.M., Williams B.D., Rosenbaum J.L.;
RT "Sequence analysis reveals homology between two proteins of the
RT flagellar radial spoke."
RL Mol. Cell. Biol. 12:3967-3977(1992).
CC -I- FUNCTION: FLAGELLAR RADIAL SPOKES CONTRIBUTE TO THE REGULATION
CC OF DYNEIN ARM ACTIVITY AND THUS THE PATTERN OF FLAGELLAR BENDING.
CC THEY CONSIST OF A THIN STALK, WHICH IS ATTACHED TO THE A SUBTIBER
CC OF THE OUTER DOUBLET MICROTUBULE, AND A BULBOUS HEAD, WHICH IS
CC ATTACHED TO THE STALK AND APPEARS TO INTERACT WITH THE
CC PROTECTIONS FROM THE CENTRAL PAIR OF MICROTUBULES.
CC -I- SUBUNIT: THE RADIAL SPOKE HEAD IS MADE OF FIVE DIFFERENT
CC POLYPEPTIDES (RSP1, RSP4, RSP6, RSP9, AND RSP10).
CC -I- SUBCELLULAR LOCATION: RADIAL SPOKE.
CC -I- SIMILARITY: TO THE FLAGELLAR RADIAL SPOKE PROTEIN 6.

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CC -----
DR EMBL: M87526; AAA33092.1; -
DR PIR: A44498; A44498.
KW Flagella.
SQ SEQUENCE 465 AA; 49798 MW; A23AFB030CDB3E29 CRC64;

Query Match 51.9%; Score 41; DB 1; Length 465;
Best Local Similarity 63.6%; Pred. No. 10;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 FVHRPHVESQ 15
: || |||: ||
DB 319 VWHVRPHLKSQ 329

RESULT 4
RS6_DROME STANDARD; PRT; 248 AA.
ID RS6_DROME P29327; Q9W3N4;
AC 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 40S ribosomal protein S6.
GN RPS6 OR L(1)AIR8 OR HEN OR CG10944.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93087515; PubMed=1454811;
RA Watson K.L., Konrad K.D., Woods D.F., Bryant P.J.;
RT "Drosophila homolog of the human S6 ribosomal protein is required for
RT tumor suppression in the hematopoietic system."
RL Proc. Natl. Acad. Sci. U.S.A. 89:11302-11306(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93192329; PubMed=8448211;
RA Spencer T.A., Mackie G.A.;
RT "The nucleotide sequence of a cloned cDNA encoding ribosomal protein
RT S6 from Drosophila melanogaster."
RL Biochim. Biophys. Acta 1172:332-334(1993).
RN [3]
RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
RX MEDLINE=94018587; PubMed=8412647;
RA Stewart M.J., Denell R.;
RT "The Drosophila ribosomal protein S6 gene includes a 3' triplication
RT that arose by unequal crossing-over."
RL Mol. Biol. Evol. 10:1041-1047(1993).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM A).
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,

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RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahke C., Davenport L.B., Davies P.,
 RA de Pallos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Domes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howard T.J., Wei M.-H., Ibeigwan C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., Moleod M.P., Moperson D.,
 RA Merklov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Slier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Sytkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 CC -1- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN CONTROLLING CELL GROWTH
 AND PROLIFERATION THROUGH THE SELECTIVE TRANSLATION OF PARTICULAR
 CC CLASSES OF MRNA.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B/C; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- PTM: RIBOSOMAL PROTEIN S6 IS THE MAJOR SUBSTRATE OF PROTEIN
 CC KINASES IN EUKARYOTE RIBOSOMES. THE PHOSPHORYLATION IS STIMULATED
 CC BY GROWTH FACTORS, TUMOR PROMOTING AGENTS, AND MITOGENS. IT IS
 CC DEPHOSPHORYLATED AT GROWTH ARREST.
 CC -1- SIMILARITY: BELONGS TO THE S6E FAMILY OF RIBOSOMAL PROTEINS.
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 CC -----
 DR EMBL: L01658; AAC36306.1; -;
 DR EMBL: L07881; AAA28871.1; -;
 DR EMBL: L02074; AAB05982.1; -;
 DR EMBL: L02074; AAB05983.1; -;
 DR EMBL: L02074; AAB05984.1; -;
 DR EMBL: L02075; AAB05985.1; -;
 DR EMBL: AEO03442; AAF46288.1; ALT_SEQ.
 DR PIR: A47240; A47240.
 DR PIR: S30194; S30194.
 DR FLYBase: FBgn0004922; Rp56.
 DR InterPro: IPR001377; Ribosomal_S6e.
 DR Pfam: PF01092; Ribosomal_S6e; 1.
 DR ProDom: PD003460; Ribosomal_S6e; 1.
 DR PROSITE: PS00578; RIBOSOMAL_S6e; 1.
 DR Ribosomal protein; Phosphorylation.
 FT VARSPLIC 73 200
 FT VRLKKGSGCYPRPRGCKRRKSRVCIIDANNVYALVY
 FT LKGGKNDIPGLTPTTIRRIAGPRASIRKLYNLSKEDVR
 FT RFVVRRLPAKDKKAKSRAPKIORLTLPVIOKRHRRL
 FT KKKRQ -> LRLKTIHSCPRPCNCRKCKTYAKTIVEAN
 FT VSAVLTVLKNSPCLGVRSSNLSIKTYLLEDEDEVIP
 FT VKLQRRHQRKRONATKEALVYKLVLRKRKESKANGRVY
 FT TIRKPKSSVFSGKK (IN ISOFORM B).
 FT MISSING (IN ISOFORM B).
 VARSPLIC 201 248
 SEQUENCE 248 AA; 28407 MW; 4E78127C33B3BD CRC64;

Query Match 48.1%; Score 38; DB 1; Length 248;
 Best Local Similarity 88.9%; Pred. No. 17;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 2 VRRFVRRP 10
 Db 153 VRRFVRRP 161
 RESULT 5
 04F3_HUMAN
 ID 04F3_HUMAN STANDARD; PRT; 312 AA.
 AC 095013;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Olfactory receptor 4F3.
 GN 04F3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Courtney L., Langston Y., Stoneking T., Drone K., Shih K.;
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PUTATIVE ODOURANT RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 DR EMBL: AC004908; AAD05195.1; -;
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCRHOOPS.
 DR PROSITE: PS00237; G_PROTEIN_RECPT-FL_1; 1.
 DR PROSITE: PS50262; G_PROTEIN_RECPT-FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KM Multigene family; Olfaction.
 FT DOMAIN 1 25
 FT TRANSMEM 26 49
 FT DOMAIN 50 57
 FT TRANSMEM 58 79
 FT DOMAIN 80 100
 FT TRANSMEM 101 120
 FT DOMAIN 121 139
 FT TRANSMEM 140 158
 FT DOMAIN 159 195
 FT TRANSMEM 196 219
 FT DOMAIN 220 235
 FT TRANSMEM 236 258
 FT DOMAIN 259 269
 FT TRANSMEM 270 289
 FT DOMAIN 290 312
 FT DISULFID 97 189
 FT CARBOHYD 5 5
 SEQUENCE 312 AA; 35087 MW; ABEE3F4ABA43F86 CRC64;
 Query Match 48.1%; Score 38; DB 1; Length 312;
 Best Local Similarity 63.6%; Pred. No. 21;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Oy 5 FVYRPHVNSQ 15
 Db 256 FVYRPHVNSQ 266

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RESULT 6
ID CGB3_CAEEL STANDARD; PRT; 385 AA.
AC 010654;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE G2/mitotic-specific cyclin B3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxId=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2.
RX MEDLINE=95403581; PubMed=7545687;
RA Kreutzer M.A., Richards J.P., de Silva-Udawatta M.N.,
RA Temenak J.J., Knoblich J.A., Lehner C.F., Bennett K.L.;
RT "Caenorhabditis elegans cyclin A- and B-type genes: a cyclin A
RT multigene family, an ancestral cyclin B3 and differential germline
RT expression."
RT J. Cell Sci. 108:2415-2424(1995).
CC -!- FUNCTION: COULD BE INVOLVED AT THE G2/M (MITOSIS) TRANSITION.
CC INTERACTS WITH THE CDC2 AND CDK2 PROTEIN KINASES. G2/M CYCLINS
CC ACCUMULATE STEADILY DURING G2 AND ARE ABRUPTLY DESTROYED AT
CC MITOSIS.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
CC -----
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CC -----
CC EMBL; U21282; AAA84395.1; -.
CC InterPro: IPR000553; Cyclin.
CC Pfam: PF00134; cyclin; 1.
CC SMART: SM00385; cyclin; 2.
CC PROSITE: PS00292; CYCLINS; FALSE_NEG.
CC Cyclin; Cell cycle; Cell division; Mitosis; Nuclear protein.
CC KW PROSITE: PS00292; CYCLINS; FALSE_NEG.
CC SEQUENCE 385 AA; 44757 MW; 74CEDA847A76B695 CRC64;
SQ

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RC STRAIN-BRISTOL N2;
RA Coles L.;
RL Submitted (OCT-1994) to the EMBL/Genbank/DBJ databases.
CC -!- SIMILARITY: C-TERMINAL TO CHIMAERIN.
CC -!- SIMILARITY: CONTAINS 1 MW DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 PH DOMAIN.
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CC -----
CC EMBL; Z46241; CAA86318.1; -.
CC Wormpep: C38D4.5; CE00918.
CC InterPro: IPR001849; PH.
CC InterPro: IPR00198; RhogAP.
CC InterPro: IPR001202; WW.
CC Pfam: PF00169; PH; 1.
CC Pfam: PF00620; RhogAP; 1.
CC Pfam: PF00397; WW; 1.
CC SMART: SM00233; PH; 1.
CC SMART: SM00324; RhogAP; 1.
CC SMART: SM00456; WW; 1.
CC PROSITE: PS01159; WW_DOMAIN_1; 1.
CC PROSITE: PS50020; WW_DOMAIN_2; 1.
CC PROSITE: PS50003; PH_DOMAIN_1.
CC Hypothetical protein.
CC KW DOMAIN 36 129
CC DOMAIN 386 505
CC PH.
CC SEQUENCE 837 AA; 94196 MW; D1895E622D1F5997 CRC64;
SQ

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Query Match 48.1%; Score 38; DB 1; Length 385;
Best Local Similarity 41.7%; Pred. No. 27;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

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Query Match 48.1%; Score 38; DB 1; Length 837;
Best Local Similarity 61.5%; Pred. No. 60;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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RESULT 7
ID YLE5_CAEEL STANDARD; PRT; 837 AA.
AC P46941;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 94.2 kDa protein C38D4.5 in chromosome III.
GN C38D4.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxId=6239;
RN [1]
RP SEQUENCE FROM N.A.

```

```

RESULT 8
ID VCOM_ADECC STANDARD; PRT; 421 AA.
AC 065952;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Minor core protein (Protein V).
GN PV.
OS Canine adenovirus type 1 (strain CLL).
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxId=69150;
RN [1]
RP SEQUENCE FROM N.A.
RA Campbell J.B., Zhao Y.;
RL Submitted (AUG-1996) to the EMBL/Genbank/DBJ databases.
CC -----
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CC or send an email to license@sib-sib.ch.)
CC -----
CC EMBL; U55001; AAB05440.1; -.
CC Core protein; Late protein.
CC KW CORE PROTEIN; Late protein.
CC SEQUENCE 421 AA; 47538 MW; C84536291CDDDEF9 CRC64;
SQ

```


Query Match 46.8%; Score 37; DB 1; Length 421;
 Best Local Similarity 70.0%; Pred. No. 43;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 VRRFVHRRPH 11
 |||||
 DB 66 VRRFAPRRPY 75

RESULT 9
 VCOM_ADECR STANDARD; PRT; 421 AA.
 AC 096685;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Minor core protein (Protein V).
 GN PV.
 OS Canine adenovirus type 1 (strain RI261).
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
 OX NCBI_TaxID=69151;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97275900; Pubmed=9129661;
 RA Morrison M.D., Onions D.E., Nicolson L.;
 RT "Complete DNA sequence of canine adenovirus type 1.";
 RL J. Gen. Virol. 78:873-876(1997).
 CC -----
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 CC -----
 KM EMBL: Y07760; CAA69063.1; -
 DR Core protein: Late protein.
 SQ SEQUENCE 421 AA; 47649 MW; A5F53E18748211F CRC64;

Query Match 46.8%; Score 37; DB 1; Length 421;
 Best Local Similarity 70.0%; Pred. No. 43;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 VRRFVHRRPH 11
 |||||
 DB 66 VRRFAPRRPY 75

RESULT 10
 ST25_HUMAN STANDARD; PRT; 426 AA.
 AC 000506; Q15522;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Serine/threonine protein kinase 25 (EC 2.7.1.37) (Sterile 20/oxidant
 DE stress-response kinase 1) (Ste20/oxidant stress response kinase-1)
 DE (SOK-1) (Ste20-like kinase).
 GN STK25 OR SOK1 OR YSK1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97042345; Pubmed=8887545;
 RA Pombo C.M., Bonventre J.V., Molnar A., Kyriakis J., Force T.;
 RT "Activation of a human Ste20-like kinase by oxidant stress defines a
 RT novel stress response pathway.";
 RL EMBO J. 15:4537-4546(1996).

RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97304522; Pubmed=9160885;
 RA Osada S.-I., Izawa M., Saito R., Mizuno K., Suzuki A., Hirai S.-I.,
 RA Ohno S.;
 RT "YSK1, a novel mammalian protein kinase structurally related to Ste20
 RT and SPK1, but is not involved in the known MAPK pathways.";
 RL Oncogene 14:2047-2057(1997).
 CC -----
 CC -1- FUNCTION: OXIDANT STRESS-ACTIVATED SERINE/THREONINE KINASE THAT
 CC MAY PLAY A ROLE IN THE RESPONSE TO ENVIRONMENTAL STRESS.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- ENZYME REGULATION: ACTIVATED BY PHOSPHORYLATION, PROBABLY
 CC AUTOPHOSPHORYLATION. THE C-TERMINAL NON-CATALYTIC REGION INHIBITS
 CC THE KINASE ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: UBIGUOUSLY EXPRESSED. HIGHEST LEVELS ARE
 CC FOUND IN TESTIS, LARGE INTESTINE, BRAIN AND STOMACH FOLLOWED BY
 CC HEART AND LUNG.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC -----
 CC STE20 SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: X99325; CAA67700.1; -
 DR EMBL: D63780; BAA20420.1; -
 DR HSSP: 000534; 1B17.
 DR MIM: 602255; -
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR002290; Ser_Thr_Pkinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR SMART: SM00220; S_TKC; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_SF; FALSE_NEG.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR KW Transferrase; Serine/threonine-protein kinase; ATP-binding;
 KM phosphorylation.
 FT DOMAIN 20 270 PROTEIN KINASE.
 FT NP_BIND 26 34 ATP (BY SIMILARITY).
 FT BINDING 49 49 ATP (BY SIMILARITY).
 FT ACT_SITE 140 140 BY SIMILARITY.
 FT CONFLICT 347 348 EP -> DA (IN REF. 1).
 SQ SEQUENCE 426 AA; 48111 MW; 183CE5700FCEA716 CRC64;

Query Match 46.8%; Score 37; DB 1; Length 426;
 Best Local Similarity 53.8%; Pred. No. 44;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 VRRFVHRRPH 14
 |||||
 DB 412 VQRFSHNRNHLTS 424

RESULT 11
 SHK2_SCHPO STANDARD; PRT; 589 AA.
 AC 010056;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Serine/threonine-protein kinase shk2 (EC 2.7.1.1).
 GN SHK2 OR SPACIF5.09C.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;

```

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98325061; PubMed-9660817;
RA Yang P., Kanstra S., Pimental R.A., Gilbreth M., Marcus S.;
RT "Cloning and characterization of shk2, a gene encoding a novel p21-
RT activated protein kinase from fission yeast.";
RL J. Biol. Chem. 273:18481-18489(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-972;
RA Gentles S., Odell C., Churcher C.M., Barrell B.G., Rajandream M.A.,
RA Walsh S.V.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBD databases.
CC -1- FUNCTION: FORMS AN ACTIVATED COMPLEX WITH GTP-BOUND RAS-LIKE
CC CDC42. PARTICIPATES IN RAS-DEPENDENT MORPHOLOGICAL CONTROL AND
CC MATING RESPONSE PATHWAYS.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC STE20 SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 GBD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
CC -----
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CC -----
DR EMBL; U45981; AAA87575.1; -
DR EMBL; Z68136; CAA92237.1; -
DR HSSP; P00518; LPHK.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR000095; PAK_box_P21_Rho_binding.
DR InterPro; IPR001849; PH.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00069; pkinase; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS50108; GBD; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_SF; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 23 125
FT DOMAIN 129 186
FT DOMAIN 309 566
FT NP_BIND 315 323
FT BINDING 343 343
FT ACT_SITE 434 434
SQ SEQUENCE 589 AA; 66765 MW; CABE2190925EC31 CRC64;

```

Query Match 46.8%; Score 37; DB 1; Length 589;
 Best Local Similarity 42.9%; Pred. No. 62;
 Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 LVREFVHRRPHVES 14
 DB 251 IIRPTEKSHVES 264

RESULT 12
 GLMS_BACHD STANDARD; PRT; 599 AA.
 AC Q9KG45;
 DT 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)

```

DE Glucosamine-6-phosphate aminotransferase [isomerizing]
DE (EC 2.6.1.16) (Hexosephosphate aminotransferase) (D-fructose-6-
DE phosphate amidotransferase) (GPA) (L-glutamine-D-fructose-6-phosphate
DE amidotransferase) (Glucosamine-6-phosphate synthase).
GN GLMS OR BH0268.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
ON NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C-125 / JCM 9153;
RX MEDLINE-20512582; PubMed-11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fujii F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.",
RT Nucleic Acids Res. 28:4317-4331(2000).
CC -1- FUNCTION: Catalyzes the first step in hexosamine metabolism,
CC converting fructose-6P into glucosamine-6P using glutamine as a
CC nitrogen source (By similarity).
CC -1- CATALYTIC ACTIVITY: L-glutamine + D-fructose 6-phosphate -> L-
CC glutamate + D-glucosamine 6-phosphate.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE TYPE-2
CC GATASE DOMAIN.
CC -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE SIS FAMILY.
CC GLMS SUBFAMILY.
CC -----
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CC -----
DR EMBL; AP001507; BAB03987.1; -
DR HSSP; P17169; IMOG.
DR InterPro; IPR000583; GATase_2.
DR InterPro; IPR001347; SIS.
DR Pfam; PF000310; GATase_2; 1.
DR Pfam; PF01380; SIS; 2.
DR PROSITE; PS00443; GATASE_TYPE_II; 1.
DR PROSITE; PS00443; GATASE_TYPE_II; 1.
KW Complete proteome.
FT INIT_MET 0 0
FT DOMAIN 1 239
FT ACT_SITE 594 594
FT ACT_SITE 594 594
SQ SEQUENCE 599 AA; 65746 MW; DE9C2667EA70C285 CRC64;

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Query Match 46.8%; Score 37; DB 1; Length 599;
 Best Local Similarity 57.1%; Pred. No. 63;
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 LVREFVHRRPHVES 14
 DB 129 LVREFVHRRPHVES 142

RESULT 13
 AMYA_PYRFU STANDARD; PRT; 648 AA.
 AC P49067;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alpha-amylase (EC 3.2.1.1).
 GN AMYA OR PF0272.
 OS Pyrococcus furiosus.

```

OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
ON NCBI_TaxID=2261;
RX MEDLINE=94043280; Pubmed=8226990.
RP MEDLINE=94043280; Pubmed=8226990.
RX Laderman K.A., Asada K., Uemori T., Mukai H., Taguchi Y., Kato I.,
RA Anfinsen C.B.;
RT "Alpha-amylase from the hyperthermophilic archaeobacterium Pyrococcus
RT furiosus. Cloning and sequencing of the gene and expression in
RT Escherichia coli";
RL J. Biol. Chem. 268:24402-24407(1993).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=94043279; Pubmed=8226989;
RA Laderman K.A., Davis B.R., Kruttsch H.C., Lewis M.S., Griko V.V.,
RA Privakov P.L., Anfinsen C.B.;
RT "The purification and characterization of an extremely thermostable
RT alpha-amylase from the hyperthermophilic archaeobacterium Pyrococcus
RT furiosus.";
RL J. Biol. Chem. 268:24394-24401(1993).
CC -1- FUNCTION: DISPLAYS A BROAD RANGE OF SUBSTRATE SPECIFICITY. WITH
CC THE CAPACITY TO HYDROLYSE CARBOHYDRATES AS SIMPLE AS MALTOSE.
CC -1- CATALYTIC ACTIVITY: Endo-hydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- PATHWAY: POLYSACCHARIDE DEGRADATION.
CC -1- SUBUNIT: HOMODIMER.
CC -1- MISCELLANEOUS: THE ISOELECTRIC POINT IS 4.3. THE ENZYME DISPLAYS
CC OPTIMAL ACTIVITY, WITH SUBSTANTIAL THERMAL STABILITY, AT 100
CC DEGREES CELSIUS, WITH THE ONSET OF ACTIVITY AT APPROXIMATELY 40
CC DEGREES CELSIUS.
CC -1- SIMILARITY: BELONGS TO FAMILY 57 OF GLYCOSYL HYDROLASES.
CC -----
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CC -----
DR EMBL: L22346; AAA72035.1; -
DR InterPro: IPR004300; Glyco_hydro_57.
DR Pfam: PF03065; Glyco_hydro_57.1.
KW Hydrolyase; Glycosidase; Carbohydrate metabolism.
FT INIT MET 0
FT SEQUENCE 648 AA; 76178 MW; BF7A495F084E0FB1 CRC64;
SQ

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Query Match 46.8%; Score 37; DB 1; Length 648;
Best Local Similarity 53.3%; Pred. No. 68;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

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QY 1 LVRFVHRRPVEQ 15
DB 436 LARMEHYGVESQ 450

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RESULT 14
BROW_DROME STANDARD; PRT: 675 AA.
AC P12428; Q24264;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Brown protein.
GN BW.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.

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```

RX MEDLINE=89218981; Pubmed=3149712;
RA Dreesen T.D., Johnson D.H., Henikoff S.;
RT "The brown protein of Drosophila melanogaster is similar to the white
RT protein and to components of active transport complexes.";
RL Mol. Cell. Biol. 8:5206-5215(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95044127; Pubmed=7956072;
RA Martin-Morris L.E., Loughney K., Kershinsnik E.O., Poorlinga G.,
RA Henikoff S.;
RT "Characterization of sequences responsible for trans-inactivation of
RT the Drosophila brown gene.";
RL Cold Spring Harb. Symp. Quant. Biol. 58:577-584(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=10281;
RA Nitasaka E., Green M.W., Yamazaki T.;
RL Submitted (NOV-1992) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PART OF A MEMBRANE-SPANNING PERMEASE SYSTEM NECESSARY
CC FOR THE TRANSPORT OF PIGMENT PRECURSORS INTO PIGMENT CELLS
CC RESPONSIBLE FOR EYE COLOR. BROWN AND WHITE DIMERIZE FOR THE
CC TRANSPORT OF GUANINE.
CC -1- SUBUNIT: HETERODIMER OF BROWN WITH WHITE.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
CC -----
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CC -----
DR EMBL: M20630; AAA28397.1; -
DR EMBL: L23543; AAC37214.1; -
DR EMBL: L05635; AAA28398.1; -
DR PIR: A31399; FYFEB.
DR FlyBase: FBgn0000241; bw.
DR InterPro: IPR003439; ABC_transportr.
DR InterPro: IPR001687; ATP_GTP_A.
DR Pfam: PF00005; ABC_tran; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
KW Pigment; ATP-binding; Transmembrane; Transport.
FT NP BIND 66
FT TRANSMEM 423 441
FT TRANSMEM 454 474
FT TRANSMEM 504 522
FT TRANSMEM 531 552
FT TRANSMEM 565 583
FT TRANSMEM 645 665
FT TRANSMEM 28 28
FT VARIANT 274 274
FT VARIANT 331 331
FT VARIANT 407 407
FT VARIANT 638 638
FT CONFLICT 44 44
FT SEQUENCE 675 AA; 75943 MW; 81DEBD8F56FAF174 CRC64;
SQ

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Query Match 46.8%; Score 37; DB 1; Length 675;
Best Local Similarity 75.0%; Pred. No. 71;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LVRFVHR 8
DB 664 LVRRYIHR 671

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RESULT 15
E2K3_RAT STANDARD; PRT: 1108 AA.
ID E2K3_RAT
AC Q92121;

```

DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Eukaryotic translation initiation factor 2-alpha kinase 3 precursor
 DE (EC 2.7.1.-) (PKR-like endoplasmic reticulum kinase) (Pancreatic
 DE eIF2-alpha kinase).
 GN EIF2AK3 OR PERK OR PERK.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP TISSUE: PANCREATIC ISLETS; AND CHARACTERIZATION.
 RC MEDLINE=99038253; PubMed=9819435;
 RX Shi Y., Valtem K.M., Sood R., An J., Liang J., Stramm L.E., Wek R.C.;
 RA "Identification and characterization of pancreatic eukaryotic
 RA initiation factor 2 alpha-subunit kinase, PERK, involved in
 RA translational control".
 RL Mol. Cell. Biol. 18:7499-7509(1998).
 RN [2]
 RP MUTAGENESIS OF LYS-614.
 RX MEDLINE=99150360; PubMed=10026192;
 RA Shi Y., An J., Liang J., Hayes S.E., Sandusky G.E., Stramm L.E.,
 RA Yang N.N.;
 RT "Characterization of a mutant pancreatic eIF-2alpha kinase, PERK, and
 RT co-localization with somatostatin in islet delta cells.";
 RL J. Biol. Chem. 274:5723-5730(1999).
 RN [3]
 RP SUBUNIT.
 RX MEDLINE=20313073; PubMed=10854322;
 RA Bertolotti A., Zhang Y., Hendershot L.M., Harding H.P., Ron D.;
 RT "Dynamic interaction of BiP and ER stress transducers in the
 RT unfolded-protein response.";
 RL Nat. Cell Biol. 2:326-332(2000).
 CC -1- FUNCTION: PHOSPHORYLATES THE ALPHA SUBUNIT OF EUKARYOTIC
 CC TRANSLATION-INITIATION FACTOR 2 (EIF2), LEADING TO ITS
 CC INACTIVATION AND THUS TO A RAPID REDUCTION OF TRANSLATIONAL
 CC INITIATION AND REPRESSION OF GLOBAL PROTEIN SYNTHESIS. SERVES AS A
 CC CRITICAL EFFECTOR OF UNFOLDED PROTEIN RESPONSE (UPR)-INDUCED G1
 CC GROWTH ARREST DUE TO THE LOSS OF CYCLIN D1 (BY SIMILARITY).
 CC -1- ENZYME REGULATION: PERTURBATION IN PROTEIN FOLDING IN THE
 CC ENDOPLASMIC RETICULUM (ER) PROMOTES REVERSIBLE DISSOCIATION FROM
 CC HSP45/BIP AND OLIGOMERIZATION, RESULTING IN
 CC TRANSAUTOPHOSPHORYLATION AND KINASE ACTIVITY INDUCTION.
 CC -1- SUBUNIT: FORMS DIMERS WITH HSP45/BIP IN RESTING CELLS.
 CC OLIGOMERIZES IN ER-STRESSED CELLS.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Endoplasmic
 CC reticulum.
 CC -1- TISSUE SPECIFICITY: UNBOUTOUS.
 CC -1- INDUCTION: BY ER STRESS.
 CC -1- DOMAIN: THE LUMENAL DOMAIN SENSES PERTURBATIONS IN PROTEIN FOLDING
 CC IN THE ER, PROBABLY THROUGH REVERSIBLE INTERACTION WITH HSP45/BIP.
 CC -1- PTM: AUTOPHOSPHORYLATED.
 CC -1- PTM: N-GLYCOSYLATED (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC GCN2 SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL: AF096835; AAC83801.1; -;
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase; 2.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.

KW Serine/threonine-protein kinase; Transferase; ATP-binding;
 KW Translation regulation; Unfolded protein response;
 KW Endoplasmic reticulum; Phosphorylation; Glycoprotein; Signal;
 KW Transmembrane.
 FT SIGNAL 1 27
 FT CHAIN 28 1108
 FT
 FT DOMAIN 28 506
 FT TRANSMEM 507 527
 FT DOMAIN 528 1108
 FT DOMAIN 585 1069
 FT NP_BIND 591 599
 FT BINDING 614 614
 FT ACT_SITE 929 929
 FT DOMAIN 47 50
 FT DOMAIN 223 228
 FT CARBOHYD 253 253
 FT MUTAGEN 614 614
 SQ SEQUENCE 1108 AA: 124769 MW: 83716BIPD26ED32B CRC64;

Query Match 46.8%; Score 37; DB 1; Length 1108;
 Best local Similarity 54.5%; Pred. No. 1.2e+02;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 LVRRFVRRPH 11
 :||| |:
 Db 531 IYRRLFPQPH 541

Search completed: August 15, 2002, 11:47:42
 Job time: 518 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 11:47:17 ; Search time 58.4 Seconds
(without alignments)
44.434 Million cell updates/sec

Title: US-09-613-092a-7
Perfect score: 79
Sequence: 1 LVRRFVRRPHVESQ 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	52	65.8	243	5	09VRG7	09VRG7 drosophila
2	52	65.8	244	4	095476	095476 homo sapien
3	52	65.8	244	4	096G09	096G09 homo sapien
4	46	58.2	324	16	P94387	P94387 bacillus su
5	45	57.0	577	16	0929B5	0929B5 chlamydia p
6	45	57.0	798	5	09U4H1	09U4H1 drosophila
7	45	57.0	798	5	09V865	09V865 drosophila
8	44	55.7	546	11	061491	061491 mus musculu
9	43	54.4	72	9	064123	064123 bacterioph
10	43	54.4	72	16	031924	031924 bacillus su
11	42	53.2	325	2	09F2P9	09F2P9 streptomyce
12	41	51.9	168	11	09D9D6	09D9D6 mus musculu
13	41	51.9	254	5	095XU1	095XU1 caenorhabdi
14	41	51.9	466	3	000086	000086 talatomyces
15	41	51.9	481	5	017558	017558 caenorhabdi
16	40	50.6	138	17	09YBN3	09YBN3 aeropyrum p

17	40	50.6	439	2	09Z4R6	09Z4R6 elkenella c
18	40	50.6	542	5	0960K4	0960K4 drosophila
19	40	50.6	1087	5	09B104	09B104 caenorhabdi
20	40	50.6	1220	12	039272	039272 equine heip
21	40	50.6	1233	11	P97820	P97820 mus musculu
22	40	50.6	1255	5	095VU9	095VU9 drosophila
23	40	50.6	1317	5	09VLK6	09VLK6 drosophila
24	39	49.4	67	3	004334	004334 pichia angu
25	39	49.4	80	16	09YXH1	09YXH1 nelisseria m
26	39	49.4	148	10	004427	004427 chlamydomon
27	39	49.4	181	4	096N68	096N68 homo sapien
28	39	49.4	183	16	092KK8	092KK8 rhizobium m
29	39	49.4	232	12	099GPO	099GPO culex nigrl
30	39	49.4	246	5	020432	020432 caenorhabdi
31	39	49.4	257	16	066673	066673 aquifex aeo
32	39	49.4	261	3	09P390	09P390 neurospora
33	39	49.4	409	5	09VND6	09VND6 drosophila
34	39	49.4	410	5	0906M0	0906M0 drosophila
35	39	49.4	476	3	059718	059718 schizosacch
36	39	49.4	540	4	092783	092783 homo sapien
37	39	49.4	548	11	P70297	P70297 mus musculu
38	39	49.4	564	10	09FR00	09FR00 oryza sativ
39	39	49.4	954	16	084594	084594 chlamydia t
40	39	49.4	1207	16	09A797	09A797 caulobacter
41	39	49.4	1792	5	097417	097417 drosophila
42	39	49.4	1792	5	09V4M6	09V4M6 drosophila
43	39	49.4	1927	5	09G9Y5	09G9Y5 leishmania
44	38	48.1	141	5	09VD20	09VD20 drosophila
45	38	48.1	217	5	095TP9	095TP9 drosophila

ALIGNMENTS

RESULT	1	ALIGNMENTS
09VRG7	PRELIMINARY;	PRT; 243 AA.
AC 09VRG7	01-MAY-2000 (TREMBlrel. 13, Created)	
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)		
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)		
DE CG1696 PROTEIN.		
GN CG1696.		
OS Drosophila melanogaster (Fruit fly).		
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;		
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC Ephydroidea; Drosophilidae; Drosophila.		
OX NCBI_TaxID=7227;		
RN NCBI_TaxID=7227;		
RP SEQUENCE FROM N.A.		
RC STRAIN=BERKELEY;		
RX MEDLINE=20196006; PubMed=10731132;		
RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,		
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,		
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,		
RA Sutton G.G., Mortan J.R., Vandel M.D., Zhang Q., Chen L.X.,		
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,		
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,		
RA Adair J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,		
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,		
RA Beson K.Y., Benos P.V., Berman B.P., Bhattacharya D., Bolshakov S.,		
RA Bokova D., Botchan M.R., Bouck J., Brockstein P., Brothier P.,		
RA Burdick K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,		
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,		
RA de Paulis B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,		
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunov B.C., Dunn P.,		
RA Durbin K.J., Evangelista C.C., Ferriaz C., Ferriera S., Fleischmann W.,		
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,		
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,		
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,		
RA Hostin D., Houston K.A., Howland T.J., Mei M.H., Idagagam C.,		
RA Jaitani M., Kailash F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,		
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,		

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mallet B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merulov G., Mishina N.V., Mobarry C., Morris J., Mostrelil A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Murzyn D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spirdling A.C., Stapleton M., Strong R., Sun E.,
 RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003568; AAF50833.1; -
 DR FLYBASE: FBgn0031173; CG1696.
 DR InterPro: IPR004274; NIF.
 DR Pfam: PF03031; NIF.
 SQ SEQUENCE 243 AA; 28486 MW; 1E278DD18DF60C6 CRC64;

Query Match 65.8%; Score 52; DB 5; Length 243;
 Best Local Similarity 75.0%; Pred. No. 0.33;
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 VRFVHRRPHE 13
 |||||:
 DB 103 VRFVHRRPHE 114

RESULT 2
 ID 095476 PRELIMINARY; PRT; 244 AA.
 AC 095476;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE HYPOTHETICAL. 28.3 KDA PROTEIN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RA Keen J., Inghearn C.;
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ011916; CAA09865.1; -
 DR InterPro: IPR004274; NIF.
 DR Pfam: PF03031; NIF.
 DR Hypothetical protein.
 KW SEQUENCE 244 AA; 28347 MW; E23843B815DEFDF0 CRC64;

Query Match 65.8%; Score 52; DB 4; Length 244;
 Best Local Similarity 75.0%; Pred. No. 0.33;
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 VRFVHRRPHE 13
 |||||:
 DB 104 VRFVHRRPHE 115

RESULT 3
 ID 096609 PRELIMINARY; PRT; 244 AA.
 AC 096609;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE UNKNOWN (PROTEIN FOR MCC:16648).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MUSCLE, AND RHABDOMYOSARCOMA;
 RA Strausberg R.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC009295; AAH09295.1; -
 SQ SEQUENCE 244 AA; 28377 MW; 062952A90F74575A CRC64;

Query Match 65.8%; Score 52; DB 4; Length 244;
 Best Local Similarity 75.0%; Pred. No. 0.33;
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 VRFVHRRPHE 13
 |||||:
 DB 104 VRFVHRRPHE 115

RESULT 4
 ID P94387 PRELIMINARY; PRT; 324 AA.
 AC P94387;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE HOMOLOGUE OF REGULATORY PROTEIN OXIR OF E. COLI.
 GN YCGK.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168.
 RL MEDLINE=97124189; PubMed=8969502;
 RA Yamane K., Kumano M., Kurita K.;
 RT "The 25 degrees-36 degrees region of the Bacillus subtilis chromosome:
 RT determination of the sequence of a 146 kb segment and identification
 RT of 113 genes.";
 RL Microbiology 142:3047-3056(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168.
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bertolo M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Borst R., Boursier L., Brans A., Braun M., Brigneau S.C., Bron S.,
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Conerton I.F., Cummins N.J., Daniel R.A.,
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Eutlian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Gallizzi A., Galleron N.,
 RA Ghim S.Y., Glaser P., Goffeau A., Golligly E.J., Grandi G.,
 RA Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henauf A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Iraya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klaerr-blanchard M., Klein C.,
 RA Kobayashi Y., Koeltter P., Koningsstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 RA Moore D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 RA Prescan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Roche A., Roche B., Rose M., Sadate Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Serron P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takekura K.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,

RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzengrger T.,
 RA Winters P., Wipet A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
 RT "The complete genome sequence of the gram-positive bacterium *Bacillus*
 RT *subtilis*,"
 RL Nature 390:249-256(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.,
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO THE LYSR FAMILY OF TRANSCRIPTIONAL REGULATORS.
 DR EMBL: D50453; BAA08951.1; -;
 DR EMBL: Z99105; CAB2111.1; -;
 DR Interpro: IPR000847; HTH_LysR.
 DR Pfam: PF00126; HTH_1; 1.
 DR PRINTS: PR00039; HTHLYSR.
 DR PROSITE: PS00044; HTH_LYSR_FAMILY; UNKNOWN.1.
 KM Complete proteome: DNA-binding; Transcription regulation.
 SQ SEQUENCE 324 AA; 36406 MW; C0C8FD25C3E08D97 CRC64;

Query Match 58.2%; Score 46; DB 16; Length 324;
 Best Local Similarity 60.0%; Pred. No. 4.6;
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVRFVHRHRRPVSQ 15
 Db 109 LKQFVARYPHVEVO.123

RESULT 5
 0929B5 PRELIMINARY; PRT; 577 AA.
 AC 0929B5;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE HYPOHETICAL 65.1 KDA PROTEIN.
 GN CPN0066 OR CPJ0066 OR CPJ0708.
 OS Chlamydia pneumoniae (Chlamydia pneumoniae).
 OC Bacteria; Chlamydiales; Chlamydiales; Chlamydiales.
 NCBI_TaxID=83558;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CWL029;
 RX Kaiman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
 RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
 RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis,"
 RL Nat. Genet. 21:385-389(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AR39;
 RX MEDLINE=20150255; Pubmed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
 RA White O., Hickey E.K., Peterson J., Uterback T., Berry K., Bass S.,
 RA Linher K., Weidman J., Knouri H., Craven B., Bowman C., Dodson R.,
 RA Gwin M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
 RA Eisen J., Fraser C.M.;
 RT "Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
 RT pneumoniae AR39,"
 RL Nucleic Acids Res. 28:1397-1406(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=J138;
 RX MEDLINE=20330349; Pubmed=10871362;
 RA Shira T., Ishii K., Hattori M., Tabuchi M., Kishi F., Ouchi K.,
 RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
 RT from Japan and CWL029 from USA,"
 RL Nucleic Acids Res. 28:2311-2314(2000).

DR EMBL: AE001592; AAD18219.1; -;
 DR EMBL: AE002229; AAF38516.1; -;
 DR EMBL: AP002545; BAA98277.1; -;
 DR TIGR: CP0708; -;
 KM Hypothetical protein; Complete proteome.
 SQ SEQUENCE 577 AA; 65110 MW; FC436FA530116A8F CRC64;

Query Match 57.0%; Score 45; DB 16; Length 577;
 Best Local Similarity 80.0%; Pred. No. 12;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VRFVHRHRRP 11
 Db 567 VRRRLHRRPH 576

RESULT 6
 0904H1 PRELIMINARY; PRT; 798 AA.
 AC 0904H1;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE BCDNA:GH05095.
 GN BCDNA:GH05095 OR CG6424.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rudin G.M., Wan K.H., Harvey D., Lewis S.E., Brokstein P., Tsang G.,
 RA Agbayani A., Arcalata T.T., Baxter E., Blazej R.G., Butenhof C.,
 RA Champe M., Chavez C., Chew M., Doyle C.M., Farfan D.E., Frise E.,
 RA Galle R., George R.A., Harris N.L., Hoskins R.A., Evans-Holm M.,
 RA Houston K.A., Hummasti S.R., Kim E., Li P., Moshrefi M., Pacleb J.M.,
 RA Park S., Sequelira A., Sethi H., Snir E., Svitskas R.R., Weinburg T.,
 RA Celinker S.E.;
 RT "Full Length Drosophila melanogaster cDNA sequence,"
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF181632; AAD5418.1; -;
 DR FlyBase: FBgn0028494; BCDNA:GH05095.
 SQ SEQUENCE 798 AA; 88467 MW; OD1B9DB99243752A CRC64;

Query Match 57.0%; Score 45; DB 5; Length 798;
 Best Local Similarity 58.3%; Pred. No. 17;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVRFVHRHRRPV 12
 Db 374 LSRRAHSHRPHI 385

RESULT 7
 09V866 PRELIMINARY; PRT; 798 AA.
 AC 09V866;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE BCDNA:GH05095 OR CG6424.
 GN BCDNA:GH05095 OR CG6424.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;

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RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,
RA Abril J.F., Abdayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borikova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burks K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dletz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mostreli A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Switskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL: AE003802; AAF57810.2; -
DR Flybase: FBgn0028494; BCDNA:GH05095.
SQ SEQUENCE 798 AA; 88472 MW; 82CA52PACF00BA6 CRC64;

Query Match 57.0%; Score 45; DB 5; Length 798;
Best Local Similarity 58.3%; Pred. No. 17;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVRRFVRRPHV 12
DB 374 LSRRAHRRPH 385

RESULT 8
O61491 PRELIMINARY; PRT; 546 AA.
AC O61491:
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE DNA-BINDING PROTEIN.
GN ZFP97.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=95137393; PubMed=7835705;
RA Wick M.-J., Ann D.K., Lee N.M., Loh H.H.;
RT "Isolation of a cDNA encoding a novel zinc-finger protein from
RT neuroblastoma x glioma NG108-15 cells.";
RL Gene 152:227-232(1995).
```

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CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL: L20450; AAA65196.1; -.
DR HSSP: P08047; ISP2.
DR MGD: MGI:105921; Zfp97.
DR InterPro: IPR001909; KRAB.
DR InterPro: IPR000822; Znf-C2H2.
DR Pfam: PF01352; KRAB.1.
DR Pfam: PF00096; Zf-C2H2; 13.
DR PRINTS: PR00048; ZINCFINGER.
DR SMART: SM00349; KRAB.1.
DR SMART: SM00355; ZNF_C2H2; 13.
DR PROSITE: PS50805; KRAB.1.
DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 13.
DR PROSITE: PS50157; ZINC_FINGER_C2H2_2; 14.
KW DNA-binding; Metal-binding; Nuclear protein; Zinc-finger.
SQ SEQUENCE 546 AA; 64148 MW; BEA735BAF5C5528B CRC64;

Query Match 55.7%; Score 44; DB 11; Length 546;
Best Local Similarity 58.3%; Pred. No. 17;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 4 REVRRRHVESQ 15
DB 117 RQIRRRPHTEK 128

RESULT 9
O64123 PRELIMINARY; PRT; 72 AA.
AC O64123:
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 8.4 KDA PROTEIN.
GN YOON.
OS Bacteriophage SPBc2.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=66797;
RN [1]
RP SEQUENCE FROM N.A.
RA Lazarevic V., Dueterhoeft A., Soldo B., Hilbert H., Mauel C.,
RA Karamata D.;
RT "The complete nucleotide sequence of the Bacillus subtilis SPbetac2
RT prophage.";
RL Submitted (AUG-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF020713; AAC13083.1; -.
KW Hypothetical protein.
SQ SEQUENCE 72 AA; 8382 MW; 11178AF395985ED8 CRC64;

Query Match 54.4%; Score 43; DB 9; Length 72;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 FVRRPH 11
DB 60 FVRRPH 66

RESULT 10
O31924 PRELIMINARY; PRT; 72 AA.
AC O31924:
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DE 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE YOON PROTEIN.
GN YOON.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuno V., Carter N.M.,
RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fadre C., Ferrari E., Foidger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Gilm S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holzapfel S., Hosono S., Hulio M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klauer-Blanchard M., Klein C.,
RA Kobayashi Y., Koelter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapius A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Paro V., Pohl T.M., Portetelle D., Portwolik S., Prescott A.M.,
RA Prescean E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Takoshi A., Tanaka T., Terpsita P., Tognoni A.,
RA Tosato V., Uchlyama S., Vandenbol M., Vannier F., Vassartoli A.,
RA Varti A., Wandt R., Wedler E., Wedler H., Weltzenegger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the gram-positive bacterium Bacillus
RT subtilis."
RL Nature 390:249-256(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: 299114; CAB13949.1; -.
KW Complete proteome.
SQ SEQUENCE 72 AA; 8382 MW; 11178AF395985ED8 CRC64;

Query Match 54.4%; Score 43; DB 16; Length 72;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FVHRPH 11
Db 60 FVHRPH 66

RESULT 11
Q9F2P9 PRELIMINARY; PRT; 325 AA.
ID Q9F2P9;
AC Q9F2P9;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE CONSERVED HYPOTHETICAL PROTEIN.
GN SCF41.09C.
OS Streptomyces coelicolor.
OC Bacteria: Firmicutes: Actinobacteria: Actinobacteridae;
OC Actinomycetales: Streptomycineae; Streptomycetaceae; Streptomycetes.
ON NCBI_TaxID=1902;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Saunders D.C., Harris D.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [2]

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RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Cerdano A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapate D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome."
RL Mol. Microbiol. 21:77-96(1996).
DR EMBL: AL442120; CAC09541.1; -.
KW Hypothetical protein.
SQ SEQUENCE 325 AA; 34793 MW; 993E789D3B2ADD2C CRC64;

Query Match 53.2%; Score 42; DB 2; Length 325;
Best Local Similarity 58.3%; Pred. No. 22;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LVRFVHRPHV 12
Db 211 LVDFVHRPHV 222

RESULT 12
Q9D9D6 PRELIMINARY; PRT; 168 AA.
ID Q9D9D6;
AC Q9D9D6;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE 1700095D18RIK PROTEIN.
GN 1700095D18RIK.
OS Mus musculus (Mouse).
OC Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi;
OC Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TESTIS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirni L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsi G.,
RA Blake J., Botfield D., Boujunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitlaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai J., Kotsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL: AK007076; BAB24851.1; -.
DR MGD: MGI:1920805; 1700095D18RIK.
DR InterPro: IPR000504; RRM.
DR PROSITE: PS00030; RRM_NP_1; UNKNOWN_1.
SQ SEQUENCE 168 AA; 17964 MW; 144EA0BA9238359 CRC64;

Query Match 51.9%; Score 41; DB 11; Length 168;
Best Local Similarity 50.0%; Pred. No. 17;

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Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 3 RRFVHRRPHVES 14
1:1:1 11:1
Db 65 RQFHSLSLPHNQS 76

RESULT 13
O95XU1 PRELIMINARY; PRT; 254 AA.
ID 095XU1
AC 095XU1;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 27.6 KDA PROTEIN.
GN Y67D8A.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None.
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Edwards J., Lamar B., Mlnx P., Du H., Kemp K., Wohlmann P.,
Walker C.;
RT "The sequence of C. elegans cosmid Y67D8A.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC024848; AK68545.1; -
KW Hypothetical protein
SQ SEQUENCE 254 AA; 27600 MW; 32895C8BDF425785 CRC64;

Query Match 51.9%; Score 41; DB 5; Length 254;
Best Local Similarity 70.0%; Pred. No. 26;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 LVRRFVHRRP 10
1:111 11:1
Db 71 LIRFRHRNP 80

RESULT 14
ID 000096 PRELIMINARY; PRT; 466 AA.
AC 000096;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PHYBASE (EC 3.1.3.8).
OS Talaromyces thermophilus.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; Talaromyces.
OX NCBI_TaxID=28565;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98007872; PubMed=9349716;
RA Pasamontes L., Halker M., Henriquez-Huecas M., Mitchell D.B.,
van Loon A.P.;
RT "Cloning of the phytases from Emericella nidulans and the thermophilic

RT fungus Talaromyces thermophilus.";
RL Biochim. Biophys. Acta 1353:217-223(1997).
DR EMBL: U59802; AAB96873.1; -
DR HSSP: P34752; 1HP.
DR InterPro: IPR000560; His_acid_phosphatase.
DR Pfam: PF00328; acid_phosphat_1.
DR PROSITE: PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE: PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
KW Hydrolyase.
SQ SEQUENCE 466 AA; 51450 MW; FC4575B521A5C929 CRC64;

Query Match 51.9%; Score 41; DB 3; Length 466;
Best Local Similarity 57.1%; Pred. No. 47;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 1 LVRRFVHRRPHVES 14
1:1:1 11:1
Db 12 LVALLYSRNPVDS 25

RESULT 15
ID 017558 PRELIMINARY; PRT; 481 AA.
AC 017558;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE C01F1.1 PROTEIN.
GN C01F1.1
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Murray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
Smaison N., Smith A., Sonhammer E., Staden R., Sulston J.,
Watson A., Weinstock L., Thomas K., Vaubin M., Vaughan K., Waterston R.,
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
RT Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Johnson D.;
RT "The sequence of C. elegans cosmid C01F1.";
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U58761; AAB00717.1; -
SQ SEQUENCE 481 AA; 54463 MW; 00FDE20C409BCC9A CRC64;

Query Match 51.9%; Score 41; DB 5; Length 481;
Best Local Similarity 42.9%; Pred. No. 49;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Oy 2 VRRFVHRRPHVESQ 15
111:1 11:1
Db 416 VRRYLRKRPPTKE 429

• Fri Aug 16 10:36:06 2002

us-09-613-092a-7.rspt

Page 7

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Job time: 529 sec

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residue residue residue

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 11:50:25 ; Search time 51.96 Seconds
(without alignments)
96.196 Million cell updates/sec

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Title:          DEVI-613-COMB
Perfect score:  257
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	91	35.4	15	20	AAV30351	Epitope derived from
2	87	33.9	15	20	AAV30352	Epitope derived from
3	79	30.7	15	20	AAV30353	Epitope derived from
4	74	28.8	15	20	AAV30354	Epitope derived from
5	63	24.5	257	21	AAV68864	Amino acid sequence
6	63	24.5	281	21	AAW93592	Mouse caspase-14 p
7	63	24.5	281	21	AAV93213	Amino acid sequence
8	58.5	22.8	398	20	AAW78169	Human secreted prote
9	58.5	22.8	404	22	AAU14277	Human novel proteol
10	55.5	22.0	459	21	AAV75223	Neisseria gonorrhoe
11	56.5	22.0	459	21	AAV75225	Neisseria meningit

12	56	21.8	214	21	AAV93216	Amino acid sequenc
13	56	21.8	229	21	AAV68865	Amino acid sequenc
14	56	21.8	242	21	AAV93214	Amino acid sequenc
15	56	21.8	731	22	AAAG91100	C glutamicum prote
16	56	21.8	731	22	AAAB79423	Corynebacterium gl
17	55	21.4	43	21	AAAG19038	Zea mays protein f
18	55	21.4	50	21	AAAG19037	Zea mays protein f
19	55	21.4	285	19	AAAB80736	Amino acid sequenc
20	54.5	21.2	125	21	AAAB33276	Pinus radiata tran
21	54.5	21.2	422	22	AAAB76548	Corynebacterium gl
22	54.5	21.2	500	22	AAAG92760	C glutamicum prote
23	54.5	21.2	951	20	AAAY34536	Porphorymonas gln
24	54.5	21.2	953	20	AAAY34403	Porphorymonas gln
25	54	21.0	117	22	AAAG65510	Human reproductive
26	54	21.0	631	22	ABBB63273	Drosophila melanog
27	54	21.0	631	22	AAU38950	Drosophila G-prote
28	53.5	20.8	1182	22	ABBG23897	Novel human diagn
29	53.5	20.8	1216	22	AAE08076	Human transporter-
30	53.5	20.8	1247	22	AAE08077	Human transporter-
31	53.5	20.8	1332	22	AAE08078	Human transporter-
32	53.5	20.8	1363	22	AAE08075	Human transporter-
33	53	20.6	138	22	AAAG75185	Human colon cancer
34	53	20.6	197	22	ABG082446	Novel human diagn
35	53	20.6	197	22	ABAB47135	CDJFF-16, Incyte I
36	53	20.6	215	18	AAAM17522	Human beta-A3-crys
37	52	20.2	66	19	AAAW7616	Staphylococcus aur
38	52	20.2	156	22	AAAB75292	Gene 6 human secre
39	52	20.2	156	22	AAAB75293	Human secreted pro
40	52	20.2	224	22	AAU34219	Staphylococcus aur
41	52	20.2	230	22	AAU36682	Staphylococcus aur
42	52	20.2	243	22	ABBS8399	Drosophila melanog
43	52	20.2	273	22	ABGI19886	Novel human diagn
44	52	20.2	280	22	ABGI19923	Novel human diagn
45	52	20.2	282	22	ABGI19922	Novel human diagn

ALIGNMENTS

RESULT 1

ID AAY30351 standard; Peptide; 15 AA

AC AAY30351

DT 09-NOV-1999 (first entry)

Epitope derived from pneumococcal surface adhesion A protein.

KW vaccine: *Streptococcus pneumoniae* infection

Streptococcus pneumoniae

PN W09945121-A1

PD 10-SEP-1999.

PF 26-FEB-1999; 99WO-US04326.

PR 02-MAR-1998; 98US-0076565.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Ades EW, Carlone GM, Sampson JS, Tharpe JA, Westerink MAJ,

XX
XX
EFT: 1000-540940 /45

DT	XX	XX	Now parties cover
----	----	----	-------------------

PT
subject
for creating or preventing streptococcus pneumoniae infection in a

```

PS Claim 6; Page 43; 58pp; English.
XX
XX AAY30351-54 represent immunogenic peptides which are derived from
CC a pneumococcal surface adhesion A protein (PsaA). The specification
CC describes monoclonal antibodies which bind epitopes of the PsaA protein
CC (e.g present sequence). The peptides can be used in vaccines to prevent
CC Streptococcus pneumoniae infections. The antibodies of the invention
CC can also be used to detect S. pneumoniae in a sample or individual.
XX
SQ Sequence 15 AA;

Query Match 35.4%; Score 91; DB 20; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TVSRVPMWTAMAFHGY 15
   |||||
DB 1 tvsrvpwtawafngy 15

RESULT 2
AAY30352
ID AAY30352 standard; Peptide; 15 AA.
XX
XX AAY30352;
XX
XX 09-NOV-1999 (first entry)
XX
XX Epitope derived from pneumococcal surface adhesion A protein.
XX
XX Pneumococcal surface adhesion A protein; PsaA; monoclonal antibody;
XX vaccine; Streptococcus pneumoniae infection.
XX
XX Streptococcus pneumoniae.
XX
XX WO9945121-A1.
XX
XX 10-SEP-1999.
XX
XX 26-FEB-1999; 99WO-US04326.
XX
XX 02-MAR-1998; 98US-0076565.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Ades EW, Carlone GM, Sampson JS, Tharpe JA, Westerink MAJ;
XX Zeiler JL;
XX
XX WPI; 1999-540849/45.
XX
XX New peptides corresponding to Streptococcus pneumoniae PsaA, used
XX for treating or preventing Streptococcus pneumoniae infection in a
XX subject
XX
XX Claim 6; Page 43; 58pp; English.
XX
XX AAY30351-54 represent immunogenic peptides which are derived from
CC a pneumococcal surface adhesion A protein (PsaA). The specification
CC describes monoclonal antibodies which bind epitopes of the PsaA protein
CC (e.g present sequence). The peptides can be used in vaccines to prevent
CC Streptococcus pneumoniae infections. The antibodies of the invention
CC can also be used to detect S. pneumoniae in a sample or individual.
XX
XX
SQ Sequence 15 AA;

Query Match 33.9%; Score 87; DB 20; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 RSYQHDLRAYGFWRL 30
   |||||

```

```

DB 1 rsyqhdlraygfwrl 15

RESULT 3
AAY30353
ID AAY30353 standard; Peptide; 15 AA.
XX
XX AAY30353;
XX
XX 09-NOV-1999 (first entry)
XX
XX Epitope derived from pneumococcal surface adhesion A protein.
XX
XX Pneumococcal surface adhesion A protein; PsaA; monoclonal antibody;
XX vaccine; Streptococcus pneumoniae infection.
XX
XX Streptococcus pneumoniae.
XX
XX WO9945121-A1.
XX
XX 10-SEP-1999.
XX
XX 26-FEB-1999; 99WO-US04326.
XX
XX 02-MAR-1998; 98US-0076565.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Ades EW, Carlone GM, Sampson JS, Tharpe JA, Westerink MAJ;
XX Zeiler JL;
XX
XX WPI; 1999-540849/45.
XX
XX New peptides corresponding to Streptococcus pneumoniae PsaA, used
XX for treating or preventing Streptococcus pneumoniae infection in a
XX subject
XX
XX Claim 6; Page 43; 58pp; English.
XX
XX AAY30351-54 represent immunogenic peptides which are derived from
CC a pneumococcal surface adhesion A protein (PsaA). The specification
CC describes monoclonal antibodies which bind epitopes of the PsaA protein
CC (e.g present sequence). The peptides can be used in vaccines to prevent
CC Streptococcus pneumoniae infections. The antibodies of the invention
CC can also be used to detect S. pneumoniae in a sample or individual.
XX
XX
SQ Sequence 15 AA;

Query Match 30.7%; Score 79; DB 20; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 31 LVRRFVHRHRYVESQ 45
   |||||
DB 1 lvrrfvhrhrpvesq 15

RESULT 4
AAY30354
ID AAY30354 standard; Peptide; 15 AA.
XX
XX AAY30354;
XX
XX 09-NOV-1999 (first entry)
XX
XX Epitope derived from pneumococcal surface adhesion A protein.
XX
XX Pneumococcal surface adhesion A protein; PsaA; monoclonal antibody;
XX vaccine; Streptococcus pneumoniae infection.
XX
XX Streptococcus pneumoniae.
XX

```


PN MO9945121-A1.
 XX 10-SEP-1999.
 PD 26-FEB-1999; 99WO-US04326.
 XX 02-MAR-1998; 98US-0076565.
 PR (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA Ades EW, Carlone GW, Sampson JS, Tharpe JA, Westerink MAJ;
 PI Zeller JI;
 DR WPI: 1999-540849/45.
 XX New peptides corresponding to Streptococcus pneumoniae Psaa, used
 PT for treating or preventing Streptococcus pneumoniae infection in a
 PS subject
 PS Claim 6; Page 43; 58pp; English.
 CC AAY30351-54 represent immunogenic peptides which are derived from
 CC a pneumococcal surface adhesion A protein (psaa). The specification
 CC describes monoclonal antibodies which bind epitopes of the psaa protein
 CC (e.g present sequence). The peptides can be used in vaccines to prevent
 CC Streptococcus pneumoniae infections. The antibodies of the invention
 CC can also be used to detect S. pneumoniae in a sample or individual.
 XX
 SQ Sequence 15 AA:
 Query Match 28.8%; Score 74; DB 20; Length 15;
 Best Local Similarity 93.3%; Pred. No. 0.0013;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 31 LVRRFVRRPVESSQ 45
 DB 1 LVRRFVRRPVESSQ 15
 RESULT 5
 AAY68864
 ID AAY68864 standard; Protein; 257 AA.
 XX
 AC AAY68864;
 XX
 DT 16-MAY-2000 (first entry)
 XX
 DE Amino acid sequence of a murine caspase-like polypeptide.
 XX
 KW Mouse; caspase-like polypeptide; human; caspase; apoptosis;
 KW skin disease; keratinisation; wound healing.
 XX
 OS Mus musculus.
 XX
 PN WO200004169-A1.
 PD 27-JAN-2000.
 XX
 PF 12-JUL-1999; 99WO-EP04939.
 XX
 PR 17-JUL-1998; 98EP-0202422.
 XX
 PA (VLAAR-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
 XX
 PI Van De Craen M, Declercq W, Vandenaabeele P, Fliers W;
 XX
 DR WPI: 2000-182433/16.
 DR N-PSDB: AAZ60683.
 XX
 PT New murine and human caspase homologues useful for treating skin
 PT related disorders -
 XX

PS Claim 1; Page 51-52; 68pp; English.
 XX
 CC The present sequence represents a murine caspase-like polypeptide. The
 CC specification also describes a human caspase-like polypeptide.
 CC Caspases are cysteinyl aspartate-specific proteinases which play a
 CC central role in apoptosis. The polypeptides of the invention are related
 CC to human and murine caspase-2 and human caspase-9, and possess all of
 CC the typical amino acids involved in catalysis, including the QACRG box,
 CC and contain no or only a very short prodomain. mRNA expression of the
 CC homologues of the invention is predominant in the skin. The caspase-like
 CC polypeptides are useful for treating human or animal diseases, such
 CC as skin diseases. They are also useful for screening for compounds that
 CC modulate its activity, i.e. agonists, antagonists, and inhibitors. The
 CC caspase-like polypeptides and polynucleotides are useful for modulating
 CC keratinisation, for diagnosing and treating inappropriate wound
 CC healing.
 XX
 SQ Sequence 257 AA:
 Query Match 24.5%; Score 63; DB 21; Length 257;
 Best Local Similarity 42.3%; Pred. No. 1;
 Matches 11; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
 QY 14 GYRSYQHDLRAYGFWRLLVRRFVRR 39
 DB 169 GYLSYRDEKSGSFIQTLTDFTHKK 214
 RESULT 6
 AAW93592
 ID AAW93592 standard; Protein; 281 AA.
 XX
 AC AAW93592;
 XX
 DT 21-JUN-1999 (first entry)
 XX
 DE Mouse caspase-14 protein.
 XX
 KW Caspase-14; murine; protease; treatment; apoptotic-related disease;
 KW autoimmune disease; cancer; acquired immunodeficiency syndrome; AIDS;
 KW neurodegenerative disease; ischaemic injury; anti-idiotypic antibody;
 KW caspase-14 processing activity; epitope; competitor; modulator.
 XX
 OS Mus sp.
 XX
 PN WO9910504-A2.
 PD 04-MAR-1999.
 XX
 PF 26-AUG-1998; 98WO-US17715.
 XX
 PR 26-AUG-1997; 97US-0056986.
 XX
 PA (IDUN-) IDUN PHARM INC.
 XX
 PI Alnemrl ES, Fernandes-Alnemrl T;
 XX
 DR WPI: 1999-204670/17.
 DR N-PSDB: AAX23515.
 XX
 PT Newly isolated polynucleotide encoding a caspase-14 polypeptide
 PT useful for identifying (ant)agonists that are useful in the
 PT diagnosis and treatment of apoptosis-related diseases
 XX
 PS Claim 4; Fig 1; 59pp; English.
 XX
 CC This invention describes a novel murine caspase-14 which has protease
 CC activity. The caspase-14 polypeptide is useful for identifying
 CC (ant)agonists of the polypeptide, where enzyme activity is measured
 CC with a fluorescent substrate (especially DEVD-AMC or IVAD-AMC. Activated
 CC caspase-14 is useful for identifying inhibitors or enhancers of
 CC caspase-14 activity. The compounds identified by both methods

CC form pharmaceutical compositions for treating apoptotic-related diseases,
 CC including autoimmune disease, cancer, acquired immunodeficiency syndrome
 CC (AIDS), neurodegenerative diseases and ischemic injury. The
 CC anti-caspase-14 antibody is useful for measuring the level of caspase-14
 CC in a tissue sample. An antibody that binds to a caspase-14 polypeptide is
 CC useful for isolating the polypeptide, and an antibody that binds to the
 CC large or small subunit the polypeptide is useful for identifying samples
 CC with caspase-14 processing activity. An antibody that binds to caspase-14
 CC heterodimer or heterotetramer is useful for isolating caspase-14 with
 CC apoptotic activity or in a screening assay to identify (ant)agonists. The
 CC antibodies form kits for such purposes. The anti-caspase-14 antibody is
 CC also useful for preparing anti-idiotypic antibodies, which mimic a
 CC caspase-14 epitope recognized by the anti-caspase-14 antibody. Therefore,
 CC the antibody is useful as a competitor of caspase-14 in reducing the
 CC level of caspase-14 activity, which reduces the level of apoptotic
 CC activity. Oligonucleotides made from the polynucleotides are useful as
 CC polymerase chain reaction (PCR) primers or probes to screen genomic or
 CC cDNA libraries for similar caspase-14 encoding polynucleotides, or for
 CC diagnosis of diseases associated with enhanced or inhibited apoptosis.
 CC The isolated caspase-14 gene permits methods of modulating apoptosis
 CC for the treatment of human diseases.

CC Sequence 281 AA;

Query Match 24.5%; Score 63; DB 20; Length 281;
 Best Local Similarity 42.3%; Pred. No. 1.1;
 Matches 11; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 14 GYRSYQHDLRAYGFWRLLVRRFVHRR 39
 Db 208 gylsyrndeksgsfqfcltdvflnkk 233

RESULT 7
 AAY93213
 ID AAY93213 standard; Protein; 281 AA.

AC AAY93213;

DT 04-SEP-2000 (first entry)

DE Amino acid sequence of a murine caspase-14.

KW Caspase-14; cell death specific protease; apoptosis stimulator;
 KW apoptosis; AIDS; neurodegenerative disease; ischemic injury.

OS Mus sp.

FH Key Location/Qualifiers

FT Region 1..156
 FT Active-site /note="large subunit"
 FT Cleavage-site 156..157
 FT Cleavage-site 162..163
 FT Region 163..257
 FT /note="small subunit"

PN WO200028047-A1.

PD 18-MAY-2000.

PE 29-OCT-1999; 99WO-US25523.

PR 06-NOV-1998; 98US-0187789.

PA (UYJE-) UNIV JEFFERSON THOMAS.

PI Alnemri ES, Fernandez-Alnemri T;

DR WPI; 2000-376558/32.

DR N-PDB; AAA15163.

PT Novel nucleic acids encoding cell death specific protease termed
 PT caspase-14 useful for treating cancers by stimulating apoptosis -
 PS Claim 52; Fig 1; 78pp; English.

CC The present sequence represents a murine caspase-14 polypeptide. The
 CC polypeptide is a cell death specific protease, and is an apoptosis
 CC stimulator. Caspase-14 polynucleotides and polypeptides, and
 CC anti-caspase-14 antibodies are useful for treating or reducing the
 CC severity of pathological conditions associated with increased or
 CC decreased levels of apoptosis. Apoptosis mediated diseases such as
 CC AIDS, neurodegenerative diseases and ischemic injury are treated by
 CC administering anti-caspase-14 antibodies. The antibody is useful for
 CC determining the presence or the level of caspase-14 in tissue sample
 CC and also for the isolation of caspase-14 with apoptotic activity or
 CC in screening assay to identify an agent that inhibits heterodimer or
 CC heterotetramer formation and therefore, apoptosis.

CC Sequence 281 AA;

Query Match 24.5%; Score 63; DB 21; Length 281;
 Best Local Similarity 42.3%; Pred. No. 1.1;
 Matches 11; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 14 GYRSYQHDLRAYGFWRLLVRRFVHRR 39
 Db 208 gylsyrndeksgsfqfcltdvflnkk 233

RESULT 8

AAW78169
 ID AAW78169 standard; Protein; 398 AA.

AC AAW78169;

DT 13-APR-1999 (first entry)

DE Human secreted protein encoded by gene 44 clone HEPFJ05.

KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
 KW developmental abnormality; foetal deficiency; blood; allergy; renal;
 KW immune system; asthma; lymphocytic disease; brain; hepatitis; lymphoma;
 KW inflammation; ischemic shock; Alzheimer's disease; restenosis; AIDS;
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Misc-difference 13 /label= unknown
 FT Misc-difference 258 /label= unknown
 FT Misc-difference 398 /label= unknown
 FT /label= unknown

PN WO9856804-A1.

PD 17-DEC-1998.

PE 11-JUN-1998; 98WO-US12125.

PR 02-OCT-1997; 97US-0061060.

PR 13-JUN-1997; 97US-0049547.

PR 13-JUN-1997; 97US-0049548.

PR 13-JUN-1997; 97US-0049549.

PR 13-JUN-1997; 97US-0049550.

PR 13-JUN-1997; 97US-0049606.

PR 13-JUN-1997; 97US-0049607.

PR 13-JUN-1997; 97US-0049609.
 PR 13-JUN-1997; 97US-0049610.
 PR 13-JUN-1997; 97US-0049611.
 PR 13-JUN-1997; 97US-0050566.
 PR 13-JUN-1997; 97US-0050901.
 PR 13-JUN-1997; 97US-0052989.
 PR 08-JUL-1997; 97US-0051919.
 PR 18-AUG-1997; 97US-0055984.
 PR 12-SEP-1997; 97US-0058665.
 PR 12-SEP-1997; 97US-0058668.
 PR 12-SEP-1997; 97US-0058669.
 PR 12-SEP-1997; 97US-0058750.
 PR 12-SEP-1997; 97US-0058971.
 PR 12-SEP-1997; 97US-0058972.
 PR 12-SEP-1997; 97US-0058975.
 PR 02-OCT-1997; 97US-0060834.
 PR 02-OCT-1997; 97US-0060841.
 PR 02-OCT-1997; 97US-0060844.
 PR 02-OCT-1997; 97US-0060865.
 PR 02-OCT-1997; 97US-0061059.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Brewer LA, Ebner R, Ferrie AM, Feng P, Greene JM, Lafleur DW;
 PI Moore PA, Ni J, Olsen HS, Rosen CA, Ruben SM, Shi Y, Young P;
 PI Yu GL;
 XX
 DR WPI: 1999-080881/07.
 DR N-PSDB: AAX04354.
 XX
 PT New isolated human genes and the secreted polypeptides they encode -
 PT useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders
 PS
 XX Claim 11; Page 288-289; 380pp; English.
 CC This sequence represents a secreted human protein encoded by the gene
 CC clone detailed in the descriptor line. The gene can be used to generate
 CC fusion proteins by linking to the gene to a human immunoglobulin Fc
 CC portion (e.g. AAX04302) for increasing the stability of the fused
 CC protein as compared to the human protein only.
 CC The invention relates to 86 novel genes and their fragments (nucleic
 CC acid sequences: AAX04311-X04410; amino acid sequences AAW78126-W78225)
 CC which are useful for preventing, treating or ameliorating medical
 CC conditions e.g. by protein or gene therapy. Also, pathological
 CC conditions can be diagnosed by determining the amount of the new
 CC polypeptides in a sample or by determining the presence of mutations in
 CC the new polynucleotides. Specific uses are described for each of the 86
 CC polynucleotides, based on which tissues they are most highly expressed in
 CC (see AAX04311 for described uses).
 XX
 SQ Sequence 398 AA;
 Query Match 22.8%; Score 58.5; DB 20; Length 398;
 Best Local Similarity 40.0%; Pred. No. 6.8;
 Matches 12; Conservative 5; Mismatches 8; Indels 5; Gaps 1;
 QY 6 PWTAMAFHGYSYQHDLRATG-----FWRL 30
 Db 36 pgsawawpfgfqlqeqilaagaalskrywcl 65
 RESULT 9
 AAU14277
 ID AAU14277 standard; Protein; 404 AA.
 AC AAU14277;
 XX
 XX 24-OCT-2001 (first entry)
 XX Human novel protein #148.
 DE
 XX

KW Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
 KW immunomodulatory; cytoskeletal; neuroprotective; vulnerrary; nootropic;
 KW anticonvulsant; antihypertic; cerebroprotective; antifungal; antiviral;
 KW antibacterial; antiallergic; dermatological; haemostatic; antitastmatic;
 KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
 KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
 KW tissue regeneration; immune disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200155437-A2.
 PD
 PD 02-AUG-2001.
 PE 25-JAN-2001; 2001WO-US02623.
 PF
 PR 25-JAN-2000; 2000US-0491404.
 PR
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 PI
 DR WPI: 2001.451939/48.
 DR N-PSDB: AAS22582.
 XX
 PT Isolated polypeptides useful for treating anti-inflammatory diseases,
 PT nervous system disorders, and for regenerating bone and cartilage -
 PS
 XX Example 4; Page 606-607; 894pp; English.
 XX
 CC The invention relates to polynucleotides encoding novel human
 CC proteins or their active domains. The polypeptides, polynucleotides and
 CC antibodies raised against the polypeptides are used in a method of
 CC treatment of a mammal and prevention of disorders caused by the aberrant
 CC protein expression or activity. The polypeptides can be used as
 CC molecular weight markers, food supplements, and in antibody production.
 CC The polypeptides are used to identify compounds which bind to the
 CC polypeptides. Polynucleotides of the invention are used as probes and
 CC primers, for sequencing, for chromosome or gene mapping, in the
 CC production of recombinant proteins, and in generating anti-sense DNA or
 CC RNA and in gene therapy. Polypeptides of the invention can be used to
 CC target drugs to a tumour, in assays to determine biological activity, to
 CC raise antibodies/elicit an immune response, to determine quantitative
 CC protein levels, as tissue markers, and to isolate receptors or ligands.
 CC Polypeptides of the invention may also be useful in treating platelet
 CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,
 CC ligament and/or nerve tissue, wound healing, treating burns, promoting
 CC the proliferation, differentiation and survival of stem cells, as a
 CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,
 CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
 CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
 CC fungal infection or from autoimmunity, cancer, allergy, asthma,
 CC graft-versus-host disease, eczema, haemophilia, thrombosis,
 CC anti-inflammatory diseases, nervous system disorders, and infection.
 CC The present sequence represents a protein of the invention.
 XX
 SQ Sequence 404 AA;
 Query Match 22.8%; Score 58.5; DB 22; Length 404;
 Best Local Similarity 40.0%; Pred. No. 7;
 Matches 12; Conservative 5; Mismatches 8; Indels 5; Gaps 1;
 QY 6 PWTAMAFHGYSYQHDLRATG-----FWRL 30
 Db 43 pgsawawpfgfqlqeqilaagaalskrywcl 72
 RESULT 10
 AAY75223
 ID AAY75223 standard; Protein; 459 AA.
 AC AAY75223;
 XX
 XX

```
XX 21-MAR-2000 (first entry)
XX
XX Neisseria gonorrhoeae ORF 607 protein sequence SEQ ID NO:1920.
DE
XX
XX Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KM antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
KW antibacterial; gene therapy.
XX
XX Neisseria meningitidis.
OS
XX
XX Neisseria gonorrhoeae.
PN
XX WO957280-A2.
PD
XX 11-NOV-1999.
XX
XX 30-APR-1999; 99WO-US09346.
PF
XX
XX 01-MAY-1998; 98US-0083758.
PR 31-JUL-1998; 98US-0094869.
PR 02-SEP-1998; 98US-0098994.
PR 02-SEP-1998; 98US-0099062.
PR 09-OCT-1998; 98US-0103749.
PR 09-OCT-1998; 98US-0103794.
PR 09-OCT-1998; 98US-0103796.
PR 25-FEB-1999; 99US-0121528.
XX
XX (CHIR ) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX
XX Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;
PI Petersen J, Pizze M, Rappuoli R, Ratti G, Scalato E, Scarselli M;
PI Tettelin H, Venter JC;
XX
XX WPI: 2000-062150/05.
DR N-PSDB: AA53985.
XX
XX Novel Neisserial polypeptides predicted to be useful antigens for
PT vaccines and diagnostics -
XX
XX Claim 2: Page 967; 1453pp; English.
PS
XX AA53015 to AA54536, AA54577 to AA54615, and AAY74253 to AAY75941
CC represent novel Neisseria meningitis and N. gonorrhoeae polynucleotides
CC and polypeptides. AA54537 to AA54576 and AA54616 to AA5473 represent
CC PCR primers used in the exemplification of the present invention. The
CC polypeptides, the polynucleotides, antibodies and compositions of
CC the invention can be used as vaccines, as diagnostic reagents, and as
CC immunogenic compositions. The polypeptides can be used in the
CC manufacture of medicaments for treating or preventing infection due to
CC Neisserial bacteria (e.g. meningitis and septicemia), to detect the
CC presence of Neisseria bacteria, or to raise antibodies. They may also
CC be used to screen for agonists or antagonists, which may themselves
CC have use as antibacterial agents. The polynucleotides of the invention
CC may also be used in gene therapy protocols.
XX
XX
SQ Sequence 459 AA;
```

```
Query Match 22.0%; Score 56.5; DB 21; Length 459;
Best Local Similarity 32.5%; Pred. No. 15;
Matches 13; Conservative 6; Mismatches 12; Indels 9; Gaps 2;
```

```
OY 2 VSRVP-----WTAMAFHGY-RSYQHDLRAGFWRRLV 32
|::|| |::|| |::|| |::|| |::|| |::|| |::|| |
Db 392 vtkvpmfhaaafwgcgllpgyllayfdmglygfwtail 431
```

```
RESULT 11
AA75225
ID AAY75225 standard; Protein; 459 AA.
XX
XX AC AAY75225;
XX
```

```
DT 21-MAR-2000 (first entry)
XX
XX Neisseria meningitidis ORF 607 protein sequence SEQ ID NO:1924.
DE
XX
XX Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KM antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
KW antibacterial; gene therapy.
XX
XX Neisseria meningitidis.
OS
XX
XX Neisseria gonorrhoeae.
PN
XX WO957280-A2.
PD
XX 11-NOV-1999.
XX
XX 30-APR-1999; 99WO-US09346.
PF
XX
XX 01-MAY-1998; 98US-0083758.
PR 31-JUL-1998; 98US-0094869.
PR 02-SEP-1998; 98US-0098994.
PR 02-SEP-1998; 98US-0099062.
PR 09-OCT-1998; 98US-0103749.
PR 09-OCT-1998; 98US-0103794.
PR 09-OCT-1998; 98US-0103796.
PR 25-FEB-1999; 99US-0121528.
XX
XX (CHIR ) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX
XX Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;
PI Petersen J, Pizze M, Rappuoli R, Ratti G, Scalato E, Scarselli M;
PI Tettelin H, Venter JC;
XX
XX WPI: 2000-062150/05.
DR N-PSDB: AA53987.
XX
XX Novel Neisserial polypeptides predicted to be useful antigens for
PT vaccines and diagnostics -
XX
XX Claim 2: Page 969; 1453pp; English.
PS
XX AA53015 to AA54536, AA54577 to AA54615, and AAY74253 to AAY75941
CC represent novel Neisseria meningitis and N. gonorrhoeae polynucleotides
CC and polypeptides. AA54537 to AA54576 and AA54616 to AA5473 represent
CC PCR primers used in the exemplification of the present invention. The
CC polypeptides, the polynucleotides, antibodies and compositions of
CC the invention can be used as vaccines, as diagnostic reagents, and as
CC immunogenic compositions. The polypeptides can be used in the
CC manufacture of medicaments for treating or preventing infection due to
CC Neisserial bacteria (e.g. meningitis and septicemia), to detect the
CC presence of Neisseria bacteria, or to raise antibodies. They may also
CC be used to screen for agonists or antagonists, which may themselves
CC have use as antibacterial agents. The polynucleotides of the invention
CC may also be used in gene therapy protocols.
XX
XX
SQ Sequence 459 AA;
```

```
Query Match 22.0%; Score 56.5; DB 21; Length 459;
Best Local Similarity 32.5%; Pred. No. 15;
Matches 13; Conservative 6; Mismatches 12; Indels 9; Gaps 2;
```

```
OY 2 VSRVP-----WTAMAFHGY-RSYQHDLRAGFWRRLV 32
|::|| |::|| |::|| |::|| |::|| |::|| |::|| |
Db 392 vtkvpmfhaaafwgcgllpgyllayfdmglygfwtail 431
```

```
RESULT 12
AA93216
ID AAY93216 standard; Protein; 214 AA.
XX
XX AC AAY93216;
XX
XX DT 04-SEP-2000 (first entry)
```

[illegible]

```

XX 06-NOV-1998: 98US-0187789.
PR (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX Alnemri ES, Fernandez-Alnemri T;
PI
XX WPI: 2000-376558/32.
DR N-PSDB: AAA15164.
XX
PT Novel nucleic acids encoding cell death specific protease termed
PS caspase-14 useful for treating cancers by stimulating apoptosis -
XX
XX Claim 13; Fig 7; 78pp: English.
XX
XX The present sequence represents a human caspase-14 polypeptide. The
CC polypeptide is a cell death specific protease, and is an apoptosis
CC stimulator. Caspase-14 polynucleotides and polypeptides, and
CC anti-caspase-14 antibodies are useful for treating or reducing the
CC severity of pathological conditions associated with increased or
CC decreased levels of apoptosis. Apoptosis mediated diseases such as
CC AIDS, neurodegenerative diseases and ischemic injury are treated by
CC administering anti-caspase-14 antibodies. The antibody is useful for
CC determining the presence or the level of caspase-14 in tissue sample
CC and also for the isolation of caspase-14 with apoptotic activity or
CC in screening assay to identify an agent that inhibits heterodimer or
CC heterotrimer formation and therefore, apoptosis.
XX
SQ Sequence 242 AA;

Query Match 21.8%; Score 56; DB 21; Length 242;
Best Local Similarity 31.8%; Pred. No. 8.7;
Matches 14; Conservative 7; Mismatches 17; Indels 6; Gaps 1;

QY 5 VPTAWAFH-----GYRSYQHDLRAYGEWRLVRRFVRRPRV 42
   || || || || || || || || || || || || || || ||
DB 159 ipytdalhyvstvegyiayrhdkgscfiqltldvftkixhni 202

RESULT 15
AAG91100
ID AAG91100 standard; protein; 731 AA.
XX
AC AAG91100;
XX
DT 26-SEP-2001 (first entry)
XX
DE C glutamicum protein fragment SEQ ID NO: 4854.
XX
KW Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
KW organic acid synthesis.
XX
OS Corynebacterium glutamicum.
XX
PN EP1108790-A2.
XX
PD 20-JUN-2001.
XX
PF 18-DEC-2000; 2000EP-0127688.
XX
PR 16-DEC-1999; 99JP-0377484.
PR 07-APR-2000; 2000JP-0159162.
PR 03-AUG-2000; 2000JP-0280988.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
PI Tateishi N, Senon A, Ikeda M, Ozaki A;
XX
DR WPI: 2001-376931/40.
DR N-PSDB: AAH66319.
XX

```

```

PT Novel polynucleotides derived from Coryneform bacteria, for identifying
PT mutation point of a gene, measuring expression of a gene, analysing
PT expression profile or pattern of a gene and identifying homologous gene
XX
XX Claim 17; SEQ ID NO: 4854; 246pp + Sequence Listing; English.
XX
XX The present invention provides a number of nucleotide and protein
CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These
CC are useful for identifying the mutation point of a gene derived from a
CC mutant of coryneform bacterium, measuring expression amount and
CC analysing the expression profile or expression pattern of a gene derived
CC from Coryneform bacterium, and identifying a homologue of a gene derived
CC from coryneform bacterium. Coryneform bacteria are useful for producing
CC amino acids, nucleic acids, vitamins, saccharides and organic acids,
CC particularly L-lysine. The present sequence is a protein described
CC in the exemplification of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the
CC European Patent Office.
XX
SQ Sequence 731 AA;

Query Match 21.8%; Score 56; DB 22; Length 731;
Best Local Similarity 28.3%; Pred. No. 30;
Matches 13; Conservative 7; Mismatches 12; Indels 14; Gaps 2;

QY 1 TVSRVPWTAWA-----FHGYSYQHDLRAY---GEWRLV 32
   || || || || || || || || || || || || || || ||
DB 140 tvrgtaftwapaigcavvgfngwmasqpmrsmgsgslwelfi 185

Search completed: August 15, 2002, 11:59:15
Job time: 530 sec

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REFERENCE/DOCKET NUMBER: ARCD:058
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-312-744-0090
TELEFAX: 1-312-755-4489
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 144 amino acids
TYPE: Amino acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Peptide
US-08-485-607-89

Query Match 22.2%; Score 57; DB 1; Length 144;
Best Local Similarity 34.1%; Pred. No. 1.2;
Matches 15; Conservative 8; Mismatches 19; Indels 2; Gaps 2;

OY 4 RVPW-TAMAFHGYR-SYQHDLRAYGFWRLLVRRFVHRRPHVESQ 45
Db 32 RIPMDEETRDGFRSSQEAASSFDODRLLEKFIIDNRHIEIQ 75

RESULT 6
US-08-475-879-89
Sequence 89, Application US/08475879
Patent No. 5972644
Patent No. 5972644 5786170
GENERAL INFORMATION:
APPLICANT: Robert Haselkorn and Piotr Gornicki
TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: 321 No. 5972644 5786170th Clark Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60610
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,879
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/956,700
FILING DATE: 10/21/92
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. No. 5972644 5786170thrup
REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: ARCD:058
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-312-744-0090
TELEFAX: 1-312-755-4489
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 144 amino acids
TYPE: Amino acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Peptide
US-08-475-879-89

Query Match 22.2%; Score 57; DB 2; Length 144;
Best Local Similarity 34.1%; Pred. No. 1.2;
Matches 15; Conservative 8; Mismatches 19; Indels 2; Gaps 2;

OY 4 RVPW-TAMAFHGYR-SYQHDLRAYGFWRLLVRRFVHRRPHVESQ 45
Db 32 RIPMDEETRDGFRSSQEAASSFDODRLLEKFIIDNRHIEIQ 75

RESULT 7
US-09-187-789-9
Sequence 9, Application US/09187789
Patent No. 6340740
GENERAL INFORMATION:
APPLICANT: Alnemrl, Emdad S.
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
FILE REFERENCE: 480140.434C1
CURRENT APPLICATION NUMBER: US/09/187,789
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 9
LENGTH: 214
TYPE: PRT
ORGANISM: Homo sapien
US-09-187-789-9

Query Match 21.8%; Score 56; DB 4; Length 214;
Best Local Similarity 31.8%; Pred. No. 2.5;
Matches 14; Conservative 7; Mismatches 17; Indels 6; Gaps 1;

OY 5 VPMWTAMAFH-----GYRSYQHDLRAYGFWRLLVRRFVHRRPHV 42
Db 131 IPTYTDALHYSTVGTYAIRHDOKGSCFIQTVDFVFTKRKGI 174

RESULT 8
US-09-187-789-5
Sequence 5, Application US/09187789
Patent No. 6340740
GENERAL INFORMATION:
APPLICANT: Alnemrl, Emdad S.
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
FILE REFERENCE: 480140.434C1
CURRENT APPLICATION NUMBER: US/09/187,789
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 5
LENGTH: 242
TYPE: PRT
ORGANISM: Homo sapien
US-09-187-789-5

Query Match 21.8%; Score 56; DB 4; Length 242;
Best Local Similarity 31.8%; Pred. No. 2.9;
Matches 14; Conservative 7; Mismatches 17; Indels 6; Gaps 1;

OY 5 VPMWTAMAFH-----GYRSYQHDLRAYGFWRLLVRRFVHRRPHV 42
Db 159 IPTYTDALHYSTVGTYAIRHDOKGSCFIQTVDFVFTKRKGI 202

RESULT 9
US-08-729-152-1
Sequence 1, Application US/08729152
Patent No. 5871739
GENERAL INFORMATION:
APPLICANT: Inoue, Eri
TITLE OF INVENTION: Pharmaceutical Composition
NUMBER OF SEQUENCES: 47

```

CORRESPONDENCE ADDRESS:
ADDRESS: Wenderoth, Lind & Ponack
STREET: Southern Building, Suite 700, 805 Fifteenth
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE:

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,152
FILING DATE: 11-OCT-1996
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 291993/1995
FILING DATE: 13-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Mairen M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:

TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: protein
US-08-729-152-1

Query Match      20.6%; Score 53; DB 2; Length 215;
Best Local Similarity 34.5%; Pred. No. 6.5;
Matches 10; Conservative 4; Mismatches 9; Indels 6; Gaps 1;

QY 7 WTMAFHGRSYOHDIRA-----YGFWR 29
DB 168 WVCYHYLGKRGYQYILKCDHHEGDYKRW 196

RESULT 10
US-08-936-165A-376
Sequence 376, Application US/08936165A
Patent No. 6348582
GENERAL INFORMATION:
APPLICANT: Black, Michael
APPLICANT: Burnham, Martin
APPLICANT: Hodgson, John
APPLICANT: Knowles, David
APPLICANT: Lonetto, Michael
APPLICANT: Nicholas, Richard
APPLICANT: Pratt, Julie
APPLICANT: Reichard, Richard
APPLICANT: Rosenberg, Martin
APPLICANT: Ward, Judith
TITLE OF INVENTION: NO. 6348582el Prokaryotic Polynucleotides,
TITLE OF INVENTION: Polypeptides and Their Uses
NUMBER OF SEQUENCES: 534
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
```

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936,165A
FILING DATE: 24-SEP-1997
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 60/027,032
FILING DATE: 24-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimm1, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P50549
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 376:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-936-165A-376

Query Match      20.2%; Score 52; DB 4; Length 66;
Best Local Similarity 32.4%; Pred. No. 2.4;
Matches 11; Conservative 6; Mismatches 11; Indels 6; Gaps 1;

QY 17 SYOHLEKAVGFWRLVLR-----FWRRPHVPS 44
DB 25 SYEPLEACGTWRYQRLKALEVLTENHVEN 58

RESULT 11
US-08-933-750C-23
Sequence 23, Application US/08933750C
Patent No. 5932442
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750C
FILING DATE: September 23, 1997
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0356 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 244 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SPLNOT04
; CLONE: 1561587
; US-08-933-750C-23

```

```

Query Match      20.2%; Score 52; DB 2; Length 244;
Best Local Similarity 75.0%; Pred. No. 10;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 32 VRREVHRRPVE 43
DB 104 VRFVHRRPVD 115

```

```

RESULT 12
US-09-234-613-23
; Sequence 23, Application US/09224613
; Patent No. 6132973
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Bandman, Olga
; APPLICANT: Shah, Purvi
; APPLICANT: Au-Young, Janice
; APPLICANT: Yue, Henry
; APPLICANT: Guebler, Karl J.
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,613
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,750
; FILING DATE: September 23, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0356 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 244 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SPLNOT04
; CLONE: 1561587
; US-09-234-613-23

```

```

Query Match      20.2%; Score 52; DB 4; Length 244;
Best Local Similarity 75.0%; Pred. No. 10;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 32 VRREVHRRPVE 43
DB 104 VRFVHRRPVD 115

```

```

RESULT 13
US-09-247-155-173
; Sequence 173, Application US/09247155A
; Patent No. 6312922
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Ducleret, Lydie
; APPLICANT: Bougueret, Lydie
; TITLE OF INVENTION: Complementary DNAs
; FILE REFERENCE: GENSET.021A
; CURRENT APPLICATION NUMBER: US/09/247,155A
; EARLIER FILING DATE: 1999-02-09
; EARLIER APPLICATION NUMBER: 60/074,121
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/081,563
; EARLIER FILING DATE: 1998-04-13
; EARLIER APPLICATION NUMBER: 60/096,116
; EARLIER FILING DATE: 1998-08-10
; EARLIER APPLICATION NUMBER: 60/099,273
; EARLIER FILING DATE: 1998-10-04
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patent.pm
; SEQ ID NO 173
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -36..-1
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: -26..-25, -24
; OTHER INFORMATION: Xaa = any one of the twenty amino acids
; US-09-247-155-173

```

```

Query Match      19.8%; Score 51; DB 4; Length 84;
Best Local Similarity 32.6%; Pred. No. 4.3;
Matches 14; Conservative 4; Mismatches 17; Indels 8; Gaps 1;

```

```

QY 5 VPTMAFHGYSYQHDLRVGFWR-----LVRVFRHRR 39
DB 27 VSWAACHGAGTQSPGVAGPWRPRPCVGSLLAARSLHKQ 69

```

```

RESULT 14
US-07-956-700B-79
; Sequence 79, Application US/07956700B
; Patent No. 5539092
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; CARBOXYLASE
; NUMBER OF SEQUENCES: 116

```

```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5539092th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/956,700B
; FILING DATE: 19921002
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5539092thrup
; REGISTRATION NUMBER: 33,268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
;
; INFORMATION FOR SEQ. ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 144 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
;
; US-07-956-700B-79

Query Match          19.6%; Score 50.5; DB 1; Length 144;
Best Local Similarity 36.4%; Pred. No. 9.2;
Matches 12; Conservative 7; Mismatches 13; Indels 1; Gaps 1;

QY 14 GYR-STQHDIRATGFWRLVRRFVHRPRVSEQ 45
      |:| | | | | | | | | | | | | | | | | | |
DB 43 GFRLSSQEAASSFGDDRLLEKFIIDNPRIHQ 75

RESULT 15
US-08-476-537-79
; Sequence 79, Application US/08476537
; Patent No. 5756290
; GENERAL INFORMATION:
; APPLICANT: Robert Haselkorn and Piotr Gornicki
; TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoA
; TITLE OF INVENTION: Carboxylase
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5756290th Clark Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII-DOS
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,537
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,700
; FILING DATE: 10/21/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas E. No. 5756290thrup
; REGISTRATION NUMBER: 33,268
```

```
;
; REFERENCE/DOCKET NUMBER: ARCD:058
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-312-744-0090
; TELEFAX: 1-312-755-4489
;
; INFORMATION FOR SEQ. ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 144 amino acids
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
;
; US-08-476-537-79
```

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Query Match          19.6%; Score 50.5; DB 1; Length 144;
Best Local Similarity 36.4%; Pred. No. 9.2;
Matches 12; Conservative 7; Mismatches 13; Indels 1; Gaps 1;

QY 14 GYR-STQHDIRATGFWRLVRRFVHRPRVSEQ 45
      |:| | | | | | | | | | | | | | | | | | |
DB 43 GFRLSSQEAASSFGDDRLLEKFIIDNPRIHQ 75
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Search completed: August 15, 2002, 11:59:42
Job time: 247 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 11:56:50 ; Search time 25.35 seconds
(without alignments)
170.573 Million cell updates/sec

Title: DEVI-613-COMB

Perfect score: 257
Sequence: 1 TVSRVPMWTAMAFHGYSYOH.....GFWRLVRRFVRRPHEVSEQ 45

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	66.5	25.9	249	1	CYRPM1	beta-crystallin B1
2	61.5	23.9	537	2	T45634	hypothetical prote
3	61.5	23.7	724	2	T16187	hypothetical prote
4	60.5	23.5	253	2	S07264	beta-crystallin B1
5	59.5	23.2	288	2	T42847	replication protei
6	59.5	23.0	292	2	T43618	repa protein homol
7	59.5	23.0	322	2	C70905	hypothetical prote
8	58	22.6	1175	2	T20346	pyruvate carboxyla
9	58	22.6	1178	2	A47255	pyruvate carboxyla
10	58	22.6	1178	1	JC2460	pyruvate carboxyla
11	58	22.6	1178	2	JC4391	pyruvate carboxyla
12	57.5	22.4	215	2	JC1231	beta-crystallin A3
13	57	22.2	704	2	A34337	propionyl-CoA carb
14	57	22.2	771	2	H72410	hypothetical prote
15	56.5	22.0	459	2	D81950	probable transmemb
16	56	21.8	242	2	JC7517	casepase-14/a - hum
17	56	21.8	278	2	S46681	hypothetical prote
18	55.5	21.6	232	2	JC7706	beta crystallin B1
19	55.5	21.6	300	2	T37759	c-5 sterol desatur
20	54.5	21.2	151	2	AC0495	probable acetyltra
21	54	21.0	198	2	S01608	beta-crystallin A1
22	54	21.0	198	2	S55512	beta-A1-2 crystal
23	54	21.0	198	2	S55513	beta-A1-1 crystal
24	54	21.0	215	2	S55514	beta-A3-2 crystal
25	54	21.0	215	2	S55515	beta-A3-1 crystal
26	54	21.0	398	2	B82894	conserved hypotnet
27	54	21.0	976	2	S40697	processing endopro
28	53.5	20.8	291	2	T01241	probable MYB famil
29	53	20.6	32	2	I46165	beta-A3/A1 crystal

30	53	20.6	149	2	C27898	beta-crystallin A3
31	53	20.6	177	2	S10088	beta-crystallin A3
32	53	20.6	197	2	JH0602	beta-crystallin A2
33	53	20.6	215	1	CYHMB3	beta-crystallin A3
34	53	20.6	215	2	I45857	beta-crystallin -
35	53	20.6	238	1	CYCHB1	beta-crystallin B1
36	53	20.6	285	1	IDECRP	replication initia
37	53	20.6	285	2	T00306	replication initia
38	53	20.6	285	2	I64780	replication-assocl
39	53	20.6	705	2	T06682	hypothetical prote
40	52.5	20.4	273	2	B83551	hypothetical prote
41	52.5	20.4	320	2	D84664	probable epoxide h
42	52.5	20.4	321	2	C84664	epoxide hydrolase
43	52.5	20.4	500	2	H96570	hypothetical prote
44	52.5	20.4	1177	2	AG0284	probable pyruvate-
45	52	20.2	118	2	G81992	NADH dehydrogenase

ALIGNMENTS

RESULT 1

CYRTB1

beta-crystallin B1 precursor - rat

N:Contains: beta B1b crystallin

C:Species: Rattus norvegicus (Norway rat)

C>Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 22-Jun-1999

C:Accession: A02925; B02925; S33586

R:den Dunnen, J.T.; Moormann, R.J.M.; Schoenmakers, J.G.G.

Biochim. Biophys. Acta 824, 295-303, 1985

A:Title: Rat lens beta-crystallins are internally duplicated and homologous to gamma-

A:Reference number: A90654; MUID:85175137

A:Accession: A02925

A:Molecule type: DNA

A:Residues: 1-50 <DE1>

A:Cross-references: GB:X06377; NID:g56014; PIDN:CAA29679.1; PID:g56015

A:Accession: B02925

A:Molecule type: mRNA

A:Residues: 34-249 <DE2>

R:David, L.L.; Shearer, T.R.

FEBS Lett. 324, 265-270, 1993

A:Title: beta-crystallins insolubilized by calpain II in vitro contain cleavage sites

A:Reference number: S33586; MUID:94009594

A:Accession: S33586

A:Molecule type: protein

A:Residues: 50-55,233,'X',235-238,'X',240 <DAV>

C:Superfamily: beta-crystallin

C:Keywords: duplication; eye lens

F:12-249/Product: beta-crystallin B1b #status predicted <BBC>

F:56-95/Domain: crystallin repeat <GK1>

F:96-140/Domain: crystallin repeat <GK2>

F:146-187/Domain: crystallin repeat <GK3>

F:188-230/Domain: crystallin repeat <GK4>

Query Match 25.9%; Score 66.5; DB 1; Length 249;

Best Local Similarity 33.3%; Pred. No. 0.38;

Matches 18; Conservative 5; Mismatches 20; Indels 11; Gaps 2;

OY 1 TVSRVPMWTAMAFHGYSYOH-----DLRAGFWRL-----VRRFVRRPHE 43

Db 184 TVSGTGWGYQYDGYRGXYLPEDFRHMWEMGAFQPMQAVRLRDROHNE 237

RESULT 2

T45634

hypothetical protein F13112.30 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000

C:Accession: T45634

R:Choinne, N.; Robert, C.; Brottier, P.; Wincker, P.; Catolico, L.; Attiguenave, F.;

submitted to the Protein Sequence Database, November 1999

A:Reference number: 223010

A:Accession: T45634
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-537 <CHO>
 A:Cross-references: EMBL:AL133292
 A:Experimental source: cultivar Columbia; BAC clone F13112
 C:Genetics:
 A:Map position: 3
 A:introns: 35/2; 153/3; 229/2; 350/3; 399/3; 445/3; 457/1
 A:Note: F13112.30

Query Match 23.9%; Score 61.5; DB 2; Length 537;
 Best Local Similarity 45.5%; Pred. No. 3.6;
 Matches 15; Conservative 3; Mismatches 6; Indels 9; Gaps 2;

OY 3 SRPWTAMAFHGYSYOHDLRAYGFWRLVRR 34
 DB 363 SAVPMSMAFTGTA-----GFMSDLLIRR 387

RESULT 3
 T16187
 hypothetical protein F27D9.5 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 24-Nov-1999
 C:Accession: T16187
 R:Bentley, D.
 submitted to the EMBL Data Library, February 1996
 A:Description: The sequence of C. elegans cosmid F27D9.
 A:Reference number: Z18473
 A:Accession: T16187
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-724 <BEN>
 A:Cross-references: EMBL:U49829; NID:g1203924; PID:g1203927; PIDN:AAA93384.1; CESP:F27D9
 C:Genetics:
 A:Gene: CESP:F27D9.5
 A:introns: 26/2; 58/1; 124/3; 341/3; 437/3; 672/3
 C:Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; lipoy

Query Match 23.7%; Score 61; DB 2; Length 724;
 Best Local Similarity 38.6%; Pred. No. 5.7;
 Matches 17; Conservative 6; Mismatches 19; Indels 2; Gaps 2;

OY 4 RVPWT-AMAFHGYSYOHDLRAYGFWRLVRRFRRPHVESQ 45
 DB 216 RVAMNDKQAREGRLSKQEAASSFGDDRMVKEFDNPHIEHQ 259

RESULT 4
 S07264
 beta-crystallin B1 - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 13-Aug-1999
 C:Accession: S07264; A27898
 R:Quax-Jaeken, Y.; Janssen, C.; Quax, W.; van den Heuvel, R.; Bloemendal, H.
 J. Mol. Biol. 180, 457-472, 1984
 A:Title: Bovine beta-crystallin complementary DNA clones. Alternating proline / alanine
 A:Reference number: S07264; MUID:85134866
 A:Accession: S07264
 A:Molecule type: mRNA
 A:Residues: 1-253 <QUA>
 A:Cross-references: EMBL:X01808; NID:g289; PIDN:CAA25951.1; PID:g290
 R:Berbers, G.A.M.; Hoekman, W.A.; Bloemendal, H.; de Jong, W.W.; Kleinschmidt, T.; Braun
 Eur. J. Biochem. 139, 467-479, 1984
 A:Title: Homology between the primary structures of the major bovine beta-crystallin cha
 A:Reference number: A91135; MUID:84132067
 A:Accession: A27898
 A:Molecule type: protein
 A:Residues: 2'12'4'4'7'9'10'12'50'52'93'103'146'148'253 <BBR>
 A:Experimental source: lens cortex

C:Superfamily: beta-crystallin
 C:Keywords: blocked amino end; duplication; eye lens
 F:26-53/Region: alanine/proline-rich
 F:2/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #st

Query Match 23.5%; Score 60.5; DB 2; Length 253;
 Best Local Similarity 32.1%; Pred. No. 2.3;
 Matches 17; Conservative 5; Mismatches 20; Indels 11; Gaps 2;

OY 2 VSRPWTAMAFHGYSYOH-----DLRAYGFWRL-----VRRFVRRPHVE 43
 DB 189 VSSGTWVGIOYFGRKGYTLLEPGDRHWNKCAFOPOMAVRRLLDRQWHRE 241

RESULT 5
 T42847
 replication protein - Yersinia pestis plasmid pCD1
 C:Species: Yersinia pestis
 C:Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 21-Jul-2000
 C:Accession: T42847
 R:Perry, R.D.; Straley, S.C.; Fetherston, J.D.; Rose, D.J.; Gregor, J.; Blattner, F.R
 Infect. Immun. 66, 4611-4623, 1998
 A:Title: DNA sequencing and analysis of the low-Ca2+-response plasmid pCD1 of Yersini
 A:Reference number: Z22273; MUID:98427122
 A:Accession: T42847
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-288 <PER>
 A:Cross-references: EMBL:AF074612; NID:g3822037; PIDN:AAC69762.1; PID:g3822042
 A:Experimental source: strain KIM5
 C:Genetics:
 A:Genome: plasmid pCD1
 A:Note: repA
 C:Superfamily: repl protein

Query Match 23.2%; Score 59.5; DB 2; Length 288;
 Best Local Similarity 30.8%; Pred. No. 3.5;
 Matches 20; Conservative 6; Mismatches 16; Indels 23; Gaps 3;

OY 3 SRVPW-----TAMAF-HGYSYOHDLRAYGFWRLVRRFVHR-R 39
 DB 174 SRVEMNQREKORLPRLMEDELIAKAMRPVRRFRSTYERKAHGLKRRARRVDYKTR 233

OY 40 PVYES 44
 DB 234 RDIEA 238

RESULT 6
 T43618
 repA protein homolog - Yersinia pestis plasmid pCD1
 C:Species: Yersinia pestis
 C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
 C:Accession: T43618
 R:Hu, P.; Elliott, J.; McCreedy, P.; Skowronski, E.; Garnes, J.; Kobayashi, A.; Bruba
 J. Bacteriol. 180, 5192-5202, 1998
 A:Title: Structural organization of virulence-associated plasmids of Yersinia pestis.
 A:Reference number: Z22578; MUID:98422474
 A:Accession: T43618
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-292 <HUP>
 A:Cross-references: EMBL:AF053946; NID:g2996222; PIDN:AAC62601.1; PID:g2996278
 A:Experimental source: strain KIM
 C:Genetics:
 A:Genome: plasmid pCD1
 A:Note: repA
 C:Superfamily: repl protein

Query Match 23.2%; Score 59.5; DB 2; Length 292;

Best Local Similarity 30.8%; Pred. No. 3.6;
Matches 20; Conservative 6; Mismatches 16; Indels 23; Gaps 3;
OY 3 SRVPM-----TAAAF--HGYSYQHDRLAYGFWRLVRFVIR-R 39
Db 178 SRVEMENQREKORLPRIEMDELAKAMRFVRFERSYQTERKAKHGKRAARRDVRDTR 237
OY 40 PVFES 44
Db 238 RDIFA 242

RESULT 7
C70905
hypothetical protein RV0176 - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: C70905
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holtroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987
A:Accession: C70905
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1322 <COL>
A:Cross-references: GB:297050; GB:AL123456; NID:g3256008; PIDN:CAB09743.1; PID:g2213513
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: RV0176
C:Superfamily: Mycobacterium tuberculosis hypothetical protein RV0176

Query Match 23.0%; Score 59; DB 2; Length 322;
Best Local Similarity 44.1%; Pred. No. 4.6;
Matches 15; Conservative 1; Mismatches 14; Indels 4; Gaps 1;
OY 8 TAW-----AFHGYSYQHDRLAYGFWRLVRFVIR 37
Db 83 TGWSLGRALTGIRVRRDGSALGPRLVRLDLAH 116

RESULT 8
T20346
pyruvate carboxylase (EC 6.4.1.1) D2023.2 [similarity] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Aug-2000
C:Accession: T20346
R:Kershaw, J.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19260
A:Accession: T20346
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1175 <MIT>
A:Cross-references: EMBL:Z81052; PIDN:CAB02872.1; GSPDB:GN00023; CESP:D2023.2
A:Experimental source: clone D2023
C:Genetics:
A:Gene: CESP:D2023.2
A:Map position: 5
A:Introns: 34/3; 103/3; 246/1; 451/3; 567/2; 821/1; 1045/3; 1126/3
C:Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-binding
C:Keywords: ligase
F:1140/Binding site: biotin (lys) (covalent) #status predicted

Query Match 22.6%; Score 58; DB 2; Length 1175;
Best Local Similarity 43.3%; Pred. No. 23;
Matches 13; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

OY 16 RSYQHDRLAYGFWRLVRFVIRRRPHEVSO 45
Db 214 RSYSEQAQAFEDGSLPFVKFERPRHIEVQ 243

RESULT 9
A47255
pyruvate carboxylase (EC 6.4.1.1) precursor [similarity] - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Feb-2002
C:Accession: A47255
R:Zhang, J.; Xia, W.L.; Brew, K.; Ahmad, F.
Proc. Natl. Acad. Sci. U.S.A. 90, 1766-1770, 1993
A:Title: Adipose pyruvate carboxylase: amino acid sequence and domain structure deduced
A:Reference number: A47255; MUID:93189578
A:Accession: A47255
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1178 <ZHA>
A:Cross-references: GB:I09192; NID:g293743; PIDN:AAA39737.1; PID:g293744
A:Experimental source: 3T3-L1 adipocytes
A:Note: sequence extracted from NCBI backbone (NCBIN:126874, NCBI:126875)
C:Superfamily: pyruvate carboxylase; biotin carboxylase homology; lipoyl/biotin-bind
C:Keywords: biotin binding; ligase; mitochondrion
F:1-20/Domain: transit peptide (mitochondrion) #status predicted <TRP>
F:21-1178/Product: pyruvate carboxylase #status predicted <MAT>
F:39-494/Domains: biotin carboxylase homology <BCH>
F:1105-1178/Domain: lipoyl/biotin-binding homology <LPB>
F:1144/Binding site: biotin (lys) (covalent) #status predicted

Query Match 22.6%; Score 58; DB 1; Length 1178;
Best Local Similarity 31.7%; Pred. No. 23;
Matches 13; Conservative 6; Mismatches 14; Indels 8; Gaps 1;
OY 13 HGYSYQHDRLAYGFWRLVRFVIRRRPHEVSO 45
Db 208 HSYELEENYTRAYSEALAFNGALFVEKRIEPRHIEVQ 248

RESULT 10
JC2460
pyruvate carboxylase (EC 6.4.1.1) precursor - human
N:Alternate names: pyruvate:carbon dioxide ligase (ADP-forming)
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 18-Aug-2000 #text_change 01-Feb-2002
C:Accession: G01933; JC2460; B27883; S01469
R:Walker, M.E.; Jitrapakdee, S.; Val, D.L.; Wallace, J.C.
submitted to the EMBL Data Library, July 1995
A:Reference number: H00708
A:Accession: G01933
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1178 <WAL>
A:Cross-references: EMBL:U30891; NID:g1101028; PIDN:AAA82937.1; PID:g1101029
R:MacKay, N.; Rigat, B.; Douglas, C.; Chen, H.S.; Robinson, B.H.
Biochem. Biophys. Res. Commun. 202, 1009-1014, 1994
A:Title: cDNA cloning of human kidney pyruvate carboxylase.
A:Reference number: JC2460; MUID:94324922
A:Accession: JC2460
A:Molecule type: mRNA
A:Residues: 1-224, 'WP', 227-351, 'A', 353-384, 'PT', 387-485, 'DV', 488-637, 'R', 639-728, 'A',
A:Cross-references: GB:S72370; NID:g652807; PIDN:AA31500.1; PID:g652808
R:Lamhonwah, A.M.; Qian, F.; Gravel, R.A.
Arch. Biochem. Biophys. 254, 631-636, 1987
A:Title: Sequence homology around the biotin-binding site of human propionyl-CoA carb
A:Reference number: A27883; MUID:87212051
A:Accession: B27883
A:Molecule type: mRNA
A:Residues: 1083-1178 <LAM>
A:Cross-references: GB:M26122; NID:g189657; PIDN:AAA34423.1; PID:g387003
R:Freytag, S.O.; Collier, K.J.
J. Biol. Chem. 259, 12831-12837, 1984

A>Title: Molecular cloning of a cDNA for human pyruvate carboxylase. Structural relation
A:Reference number: S01469; MUID:85030380

A:Accession: S01469

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1135-1178 <FRED>

A:Cross-references: EMBL:K02282; NID:g189655; PIDN:AAA60033.1; PTD:g189656

C:Genetics:

A:Gene: GDB:PC

A:Cross-references: GDB:119472; OMIM:266150

A:Map position: 11q11-11q13.1

C:Superfamily: pyruvate carboxylase: biotin carboxylase homology; lipoyl/biotin-binding C:Keywords: biotin binding; gluconeogenesis; ligase; mitochondrion F:1-20/Domain: transit peptide (mitochondrion) #status predicted <MNT> F:39-494/Product: pyruvate carboxylase #status predicted <BCH> F:1105-1178/Domain: lipoyl/biotin-binding homology <LPB> F:1144/Binding site: biotin (lys) (covalent) #status predicted

Query Match 22.6%; Score 58; DB 1; Length 1178;
Best Local Similarity 31.7%; Pred. NO. 23;
Matches 13; Conservative 6; Mismatches 14; Indels 8; Gaps 1;

OY 13 HG-----RSQHDLRAGFMRLVRRFYHRRPHEEQ 45
| | | | | | | | | | | | | | |
Db 208 HSYEELENYTRAYSEALAFGNGALFEVEKEFRKHIEVQ 248

RESULT 11

JC4391

Pyruvate carboxylase (EC 6.4.1.1) precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 20-Jan-1996 #sequence_revision 25-Apr-1997 #text_change 11-Jan-2002

C:Accession: S68252; S72393; JC4391; S06440

R:jitrpkdsk, S.: Booker, G.W.; Cassidy, A.I.; Wallace, J.C.

Biochem. J. 316, 631-637, 1996

A>Title: Cloning, sequencing and expression of rat liver pyruvate carboxylase.
A:Reference number: S68252; MUID:96257760

A:Accession: S68252

A:Molecule type: mRNA

A:Residues: 1-1178 <JTTI>

A:Cross-references: EMBL:U36585; NID:g1040973; PIDN:AAC52668.1; PID:g1040974

A:Accession: S72393

A:Molecule type: Protein

A:Residues: 489-505 <JIT2>

A:Experimental source: Liver

R:Lehn, D.A.; Moran, S.M.; MacDonald, M.J.
Gene 165, 331-332, 1995

A>Title: The sequence of the rat pyruvate carboxylase-encoding cDNA.
A:Reference number: JC4391; MUID:96096548

A:Accession: JC4391

A:Molecule type: mRNA

A:Residues: 1-221, 'P', 223-865, 'D', 867-976, 'G', 978-1178 <LBH>

A:Cross-references: GB:U32314; NID:g929987; PIDN:AAA96256.1; PID:g929988

A:Experimental source: Liver

R:Thampy, K.G.; Huang, W.Y.; Wakil, S.J.
Arch. Biochem. Biophys. 266, 270-276, 1988

A>Title: A rapid purification method for rat liver pyruvate carboxylase and amino acid s
A:Reference number: S06440; MUID:89024676

A:Accession: S06440

A:Molecule type: Protein

A:Residues: 'SG', 23-25, 'LV', 28-29, 'LL', 32-34, 'P', 1134, 'A', 1136-1137, 1139-1152, 'T', 1154-1157, 1159-1163, 1165-1167, 1169-1178, 1180-1181, 1183-1184, 1186-1187, 1189-1190, 1192-1193, 1195-1196, 1198-1199, 1201-1202, 1204-1205, 1207-1208, 1210-1211, 1213-1214, 1216-1217, 1219-1220, 1222-1223, 1225-1226, 1228-1229, 1231-1232, 1234-1235, 1237-1238, 1240-1241, 1243-1244, 1246-1247, 1249-1250, 1252-1253, 1255-1256, 1258-1259, 1261-1262, 1264-1265, 1267-1268, 1270-1271, 1273-1274, 1276-1277, 1279-1280, 1282-1283, 1285-1286, 1288-1289, 1291-1292, 1294-1295, 1297-1298, 1299-1300, 1302-1303, 1305-1306, 1308-1309, 1311-1312, 1314-1315, 1317-1318, 1320-1321, 1323-1324, 1326-1327, 1329-1330, 1332-1333, 1335-1336, 1338-1339, 1341-1342, 1344-1345, 1347-1348, 1350-1351, 1353-1354, 1356-1357, 1359-1360, 1362-1363, 1365-1366, 1368-1369, 1371-1372, 1374-1375, 1377-1378, 1380-1381, 1383-1384, 1386-1387, 1389-1390, 1392-1393, 1395-1396, 1398-1399, 1401-1402, 1404-1405, 1407-1408, 1410-1411, 1413-1414, 1416-1417, 1419-1420, 1422-1423, 1425-1426, 1428-1429, 1431-1432, 1434-1435, 1437-1438, 1440-1441, 1443-1444, 1446-1447, 1449-1450, 1452-1453, 1455-1456, 1458-1459, 1461-1462, 1464-1465, 1467-1468, 1470-1471, 1473-1474, 1476-1477, 1479-1480, 1482-1483, 1485-1486, 1488-1489, 1491-1492, 1494-1495, 1497-1498, 1499-1500, 1502-1503, 1505-1506, 1508-1509, 1511-1512, 1514-1515, 1517-1518, 1520-1521, 1523-1524, 1526-1527, 1529-1530, 1532-1533, 1535-1536, 1538-1539, 1541-1542, 1544-1545, 1547-1548, 1550-1551, 1553-1554, 1556-1557, 1559-1560, 1562-1563, 1565-1566, 1568-1569, 1571-1572, 1574-1575, 1577-1578, 1580-1581, 1583-1584, 1586-1587, 1589-1590, 1592-1593, 1595-1596, 1598-1599, 1601-1602, 1604-1605, 1607-1608, 1610-1611, 1613-1614, 1616-1617, 1619-1620, 1622-1623, 1625-1626, 1628-1629, 1631-1632, 1634-1635, 1637-1638, 1640-1641, 1643-1644, 1646-1647, 1649-1650, 1652-1653, 1655-1656, 1658-1659, 1661-1662, 1664-1665, 1667-1668, 1670-1671, 1673-1674, 1676-1677, 1679-1680, 1682-1683, 1685-1686, 1688-1689, 1691-1692, 1694-1695, 1697-1698, 1699-1700, 1702-1703, 1705-1706, 1708-1709, 1711-1712, 1714-1715, 1717-1718, 1720-1721, 1723-1724, 1726-1727, 1729-1730, 1732-1733, 1735-1736, 1738-1739, 1741-1742, 1744-1745, 1747-1748, 1750-1751, 1753-1754, 1756-1757, 1759-1760, 1762-1763, 1765-1766, 1768-1769, 1771-1772, 1774-1775, 1777-1778, 1780-1781, 1783-1784, 1786-1787, 1789-1790, 1792-1793, 1795-1796, 1798-1799, 1801-1802, 1804-1805, 1807-1808, 1810-1811, 1813-1814, 1816-1817, 1819-1820, 1822-1823, 1825-1826, 1828-1829, 1831-1832, 1834-1835, 1837-1838, 1840-1841, 1843-1844, 1846-1847, 1849-1850, 1852-1853, 1855-1856, 1858-1859, 1861-1862, 1864-1865, 1867-1868, 1870-1871, 1873-1874, 1876-1877, 1879-1880, 1882-1883, 1885-1886, 1888-1889, 1891-1892, 1894-1895, 1897-1898, 1899-1

```

F:1105-1178/Domain: lipoyl/biotin-binding homology <LBP>
F:1144/Binding site: biotin (Lys) (covalent) #status experimental

Query Match          22.6%; Score 58; DB 2; Length 1178;
Best Local Similarity 31.7%; Pred. No. 23;
Matches 13; Conservative 6; Mismatches 14; Indels 8; Gaps 1;

QY 13 HG-----RSYOHDRANGFMRLVRRYRHRPHNESQ 45
      | | | | | | | | | | | | | | | | | | |
      | | | | | | | | | | | | | | | | | | |
Db 208 HSYEELEENYTRAYSERALAFNGALFVEKEFEKPRHIEVQ 248

RESULT 12
JC1231
beta-crystallin A3 - chicken
N:Contalins: beta-crystallin A1
C:Species: Gallus gallus (chicken)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C:Accession: JC1231; A25558; JC1232
R:McBermolt, J.B.; Peterson, C.A.; Plattigorsky, J.
Gene 117, 193-200, 1992
A:Title: Structure and lens expression of the gene encoding chicken betaA3/A1-crystal
A:Reference number: JC1231; MUID:92347693
A:Accession: JC1231
A:Molecule type: DNA
A:Residues: 1-215 <MCD>
A:Cross-references: GB:M88460
A:Experimental source: eye lens
R:Peterson, C.A.; Plattigorsky, J.
Gene 45, 139-147, 1986
A:Title: Preferential conservation of the globular domains of the beta A3/A1-crystal
A:Reference number: A25558; MUID:87106807
A:Accession: A25558
A:Molecule type: mRNA
A:Residues: 1-215 <PFR>
A:Cross-references: GB:M15658; NID:g211668; PIDN:AAA48724.1; PID:g211669
C:Genetics:
A:Gene: beta-A3/A1
A:Introns: 11/1; 32/3; 72/2; 119/3; 167/2
C:Superfamily: beta-crystallin
C:Keywords: duplication; eye lens
F:1-215/Product: beta-crystallin A3 #status predicted <MAN>
F:18-215/Product: beta-crystallin A1 #status predicted <MA2>

Query Match          22.4%; Score 57.5; DB 2; Length 215;
Best Local Similarity 34.3%; Pred. No. 4.7;
Matches 12; Conservative 5; Mismatches 9; Indels 9; Gaps 2;

QY 4 RVP---WTAMAFHGIRSYQHDLRA-----YGFWR 29
      | | | | | | | | | | | | | | | | | | |
      | | | | | | | | | | | | | | | | | | |
Db 162 KIPGAWWCYQYRGYQYVLEADHGGDYKHW 196

RESULT 13
A34337
propiolnyl-CoA carboxylase (EC 6.4.1.3) alpha chain precursor - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 11-Jan-2002
C:Accession: A34337; A30871
R:Browner, M.F.; Taroni, F.; Szul, E.; Rosenberg, L.E.
J Biol. Chem. 264, 12680-12685, 1989
A:Title: Sequence analysis, biosynthesis, and mitochondrial import of the alpha-subunit
A:Reference number: A34337; MUID:89308706
A:Accession: A34337
A:Molecule type: mRNA
A:Residues: 'MPYRERCAIRMCRRNSG',1-704 <BRI>
A:Cross-references: GB:M22631
R:Browner, M.F.; Taroni, F.; Szul, E.; Rosenberg, L.E.
submitted to GenBank, February 1989
A:Reference number: A30871
A:Accession: A30871

```

A:Molecule type: mRNA
 A:Residues: 'MYRRRFAIRMCNRNG',1-298,'WP',301-704 <BR2>
 A:Cross-references: GB:M22631; NID:g206049; PIDN:AAA8512.1; PID:g206050
 R:Browner, M.F.; Taroni, F.; Szul, E.; Rosenberg, L.E.
 J. Biol. Chem. 266, 4660, 1991
 A:Reference number: A43040
 A:Contents: annotation; correction
 A:Note: the first 17 residues in the original paper were derived from bacterial DNA as a
 C:Genetics:
 A:Gene: PCCA
 C:Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; lipoyl
 C:Keywords: biotin binding; heterododecamer; ligase; mitochondrial matrix; mitochondrion
 F:1-27/Domain: transit peptide (mitochondrion) (fragment) #status predicted <TNP>
 F:28-704/Product: propionyl-CoA carboxylase alpha chain #status predicted <MAT>
 F:41-493/Domain: biotin carboxylase homology <BCH>
 F:531-704/Domain: lipoyl/biotin-binding homology <LPB>
 F:670/Binding site: biotin (lys) (covalent) #status predicted

Query Match 22.2%; Score 57; DB 2; Length 704;
 Best Local Similarity 34.1%; Pred. No. 18;
 Matches 15; Conservative 8; Mismatches 19; Indels 2; Gaps 2;
 OY 4 RVPW-TAMAFHGY-RSYQHLRAYGFWRLLVRRPHEVSEQ 45
 Db 206 RIPWDEETRDGFRFSOEASFGDDRLLIEKFDNPHIEIQ 249

RESULT 14
 H72410
 hypothetical protein TM0162 - Thermotoga maritima (strain MSB8)
 C:Species: Thermotoga maritima
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
 C:Accession: H72410
 R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
 Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
 C.M.
 Nature 399, 323-329, 1999
 A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
 A:Reference number: A72200; MUID:99287316
 A:Accession: H72410
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-771 <ARN>
 A:Cross-references: GB:AE001701; GB:AE000512; NID:g4980648; PIDN:AND35255.1; PID:g498065
 A:Experimental source: strain MSB8
 C:Genetics:
 A:Gene: TM0162
 C:Superfamily: Thermotoga maritima hypothetical protein TM0162

Query Match 22.2%; Score 57; DB 2; Length 771;
 Best Local Similarity 36.7%; Pred. No. 20;
 Matches 11; Conservative 6; Mismatches 13; Indels 0; Gaps 0;
 OY 15 YRSYQHLRAYGFWRLLVRRPHEVSE 44
 Db 268 YSQYFDLHAGTGGLIVRLMQRRPEVNN 297

RESULT 15
 D81950
 probable transmembrane efflux protein NMA1022 [imported] - Neisseria meningitidis (strain
 C:Species: Neisseria meningitidis
 C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
 C:Accession: D81950
 R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
 ; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream
 Nature 404, 502-506, 2000
 A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
 A:Reference number: A81775; MUID:20222556
 A:Accession: D81950
 A:Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-459 <PAR>
 A:Cross-references: GB:AL162754; GB:AL157959; NID:g7379424; PIDN:CAR84291.1; PID:g737
 A:Experimental source: serogroup A, strain Z2491
 C:Genetics:
 A:Gene: NMA1022
 C:Superfamily: conserved hypothetical protein H11612

Query Match 22.0%; Score 56.5; DB 2; Length 459;
 Best Local Similarity 32.5%; Pred. No. 14;
 Matches 13; Conservative 6; Mismatches 12; Indels 9; Gaps 2;
 OY 2 VSRVP-----WTAMAFHGY-RSYQHLRAYGFWRLLV 32
 Db 392 VTKVPMFIHAAAFNCCGGLPGYLALYRRDMGIGRWTAII 431

Search completed: August 15, 2002, 12:00:14
 Job time: 204 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 11:59:45 ; Search time 16.31 Seconds

(Without alignments)
106.829 Million cell updates/sec

Title: DEVI-613-COMB

Sequence: 1 TVSRVPMWTAMAFHGYSYQH.....GFWRLLVRRFVHRPHEVSEQ 45

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66.5	25.9	248	1	CRB1_RAT
2	63	24.5	257	1	ICEE_MOUSE
3	60.5	23.5	252	1	CRB1_BOVIN
4	58.5	22.8	251	1	CRB1_HUMAN
5	58	22.6	1178	1	PYC_HUMAN
6	58	22.6	1178	1	PYC_MOUSE
7	57.5	22.4	215	1	CRBA_CHICK
8	57	22.2	704	1	PCCA_RAT
9	57	22.2	1178	1	PYC_RAT
10	56.5	22.0	459	1	NORM_NEIMA
11	56	21.8	242	1	ICEE_HUMAN
12	56	21.8	278	1	YH22_YEAST
13	54	21.0	198	1	CH11_RANCA
14	54	21.0	198	1	CH12_RANCA
15	54	21.0	198	1	CRBA_RANTE
16	54	21.0	215	1	CB31_RANCA
17	54	21.0	215	1	CB32_RANCA
18	54	21.0	976	1	XPR6_YARLI
19	53	20.6	177	1	CRBA_RAT
20	53	20.6	196	1	CRBB_BOVIN
21	53	20.6	196	1	CRBB_HUMAN
22	53	20.6	196	1	CRBA_MOUSE
23	53	20.6	215	1	CRBA_BOVIN
24	53	20.6	215	1	CRBA_HUMAN
25	53	20.6	238	1	CRB1_CHICK
26	53	20.6	285	1	REP2_ECOLI
27	51.5	20.0	459	1	NORM_NEIMB
28	51	19.8	422	1	EF1G_PPUAV
29	51	19.8	648	1	BGLR_CERAE
30	51	19.8	651	1	BGLR_CANPA
31	51	19.8	651	1	BGLR_FELCA
32	51	19.8	651	1	BGLR_HOMAN
33	51	19.8	791	1	G6PE_HUMAN

34	51	19.8	990	1	NFRA_ECOLI	p31600 escherichia
35	51	19.8	1203	1	YT41_CAEEL	011069 caenorhabdi
36	50.5	19.6	167	1	ELBS_ADE40	p10543 human adeno
37	50.5	19.6	629	1	HAP1_RAT	p54256 rattus norv
38	50.5	19.6	703	1	PCCA_HUMAN	p5165 homo sapien
39	50	19.5	196	1	CRBB_CHICK	p55164 homo sapien
40	50	19.5	343	1	GUNC_CLOSF	p23340 clostridium
41	50	19.5	343	1	GUNC_CLOTFM	p07985 clostridium
42	50	19.5	513	1	MANE_BACSM	p16699 bacillus sp
43	49.5	19.3	3859	1	RPOA_DELV	004561 lelystad vi
44	49	19.1	361	1	HA1A_RABIT	p01894 oryctolagus
45	49	19.1	361	1	HA1B_RABIT	p06140 oryctolagus

ALIGNMENTS

RESULT	ID	CRB1_RAT	STANDARD	PRT	248 AA.
AC	P02523	CRB1_RAT			
DT	21-JUL-1986	(Rel. 01, Created)			
DT	01-MAR-1989	(Rel. 10, Last sequence update)			
DT	16-OCT-2001	(Rel. 40, Last annotation update)			
DE	Beta crystallin B1 [Contains: Beta B1B crystallin].				
GN	CRYBB1.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OX	NCBI_TaxID=10116;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=85175137; PubMed=3879970;				
RA	den Dunnen J.T., Moormann R.J.M., Schoenmakers J.G.G.;				
RT	"Introm insertions and deletions in the beta/gamma-crystallin gene				
RT	family: the rat beta B1 gene."				
RL	Proc. Natl. Acad. Sci. U.S.A. 83:2855-2859(1986).				
CC	-1- FUNCTION: CRYSTALLINS ARE THE DOMINANT STRUCTURAL COMPONENTS				
CC	OF THE VERTEBRATE EYE LENS.				
CC	-1- SUBUNIT: HOMO/HETERODIMER, OR COMPLEXES OF HIGHER ORDER. THE				
CC	STRUCTURE OF BETA-CRYSTALLIN OLIGOMERS SEEMS TO BE STABILIZED				
CC	THROUGH INTERACTIONS BETWEEN THE N-TERMINAL ARMS.				
CC	-1- DOMAIN: HAS A TWO-DOMAIN BETA-STRUCTURE, FOLDED INTO FOUR				
CC	VERY SIMILAR GREEK KEY MOTIFS.				
CC	-1- PM: SPECIFIC CLEAVAGES IN THE N-TERMINAL ARM OCCUR DURING LENS				
CC	MATURATION AND GIVE RISE TO TRUNCATED FORMS, LEADING TO IMPAIRED				
CC	OLIGOMERIZATION AND PROTEIN INSOLUBILIZATION. THE PROTEASE				
CC	RESPONSIBLE FOR THIS PARTIAL DEGRADATION COULD BE CALPAIN II.				
CC	-1- SIMILARITY: BELONGS TO THE BETA/GAMMA-CRYSTALLIN FAMILY.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation				
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CC	-----				
DR	EMBL; X06377; CAA29679.1; -				
DR	EMBL; X05900; CAA29329.1; -				
DR	EMBL; M13534; AAA40979.1; -				
DR	EMBL; M13527; AAA40979.1; JOINED.				
DR	EMBL; M13528; AAA40979.1; JOINED.				
DR	EMBL; M13530; AAA40979.1; JOINED.				
DR	EMBL; M13532; AAA40979.1; JOINED.				
DR	PIR; A02925; CYRBT1.				

DR HSP: P02522; 1BBL.
 DR InterPro: IPR001064; Crystallin.
 DR Pfam: PF00030; Crystallin; 2.
 DR PRINTS: PR01367; BGCRTALLIN.
 DR SMART: SM00247; XTALBP; 2.
 DR PROSITE: PS00225; CRYSTALLIN_BETAGAMA; 4.
 KM Eye lens protein; Repeat; Acetylation.
 FT INIT_MET 0
 FT CHAIN 1 248
 FT MOD_RES 1 248
 FT DOMAIN 1 54
 FT DOMAIN 55 94
 FT DOMAIN 95 140
 FT DOMAIN 141 144
 FT DOMAIN 145 186
 FT DOMAIN 187 230
 FT DOMAIN 231 248
 FT SEQUENCE 248 AA; 27912 MW; 215D6825D2FD895F CRC64;

Query Match 25.9%; Score 66.5; DB 1; Length 248;
 Best Local Similarity 33.3%; Pred. No. 0.17;
 Matches 18; Conservative 5; Mismatches 20; Indels 11; Gaps 2;

OY 1 TVSRVETAWAFHGYRSGYOH-----DLRAYGEWRL-----VRFVHRPHVE 43
 DB 183 TVSSGTWVGXYQYGRGYQYLLPEGDFRHNWEGAFOPQWAVRRLRQWQHE 236

RESULT 2
 ICEE_MOUSE STANDARD; PRT; 257 AA.
 AC 089094;
 DT 16-OCT-2001 (Rel. 40; Created)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 16-OCT-2001 (Rel. 40; Last annotation update)
 DE Caspase-14 precursor (EC 3.4.22.-) (CASP-14) (Mln1-ICE) (MICE).
 GN CASP14.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=99040667; PubMed=9823333;
 RA Ahmed M., Srinivasula S.M., Hegde R., Mukattash R.,
 RA Fernandes-Alnemri T., Alnemri E.S.;
 RT "Identification and characterization of murine caspase-14, a new
 member of the caspase family";
 RL Cancer Res. 58:5201-5205(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Embryo;
 RX MEDLINE=99222069; PubMed=10203698;
 RA Van de Craen M., Van Loo G., Pye S., Van Griekinge W.,
 RA Van den Brande I., Molemans F., Fiers W., Declercq W.,
 RA Vandenberghe P.;
 RT "Identification of a new caspase homologue: caspase-14.";
 RL Cell Death Differ. 5:838-846(1998).
 RN [3]
 RP CHARACTERIZATION, AND MUTAGENESIS OF CYS-136.
 RX Hu S., Snipas S.J., Vincenz C., Salvesen G., Dixit V.M.;
 RT J. Biol. Chem. 273:29648-29653(1998).
 CC -I- FUNCTION: SEEMS TO BE INVOLVED IN THE DEATH RECEPTOR AND GRANZYME
 B APOPTOTIC PATHWAYS. MAY FUNCTION AS A DOWNSTREAM SIGNAL
 TRANSDUCER OF CELL DEATH. MAY PLAY A ROLE IN ONTOGENESIS AND SKIN
 PHYSIOLOGY.
 CC -I- SUBUNIT: MAY DIMERIZE WITH LARGE PRODOMAIN CASPASES.
 CC -I- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -I- TISSUE SPECIFICITY: EMBRYO, ADULT LIVER AND LESS IN ADULT BRAIN
 CC AND KIDNEY.
 CC -I- PTM: CLEAVAGE BY GRANZYME B, CASPASE-8 AND -10 GENERATES THE
 CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
 CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
 CC PROTEASE.
 CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14, ALSO KNOWN AS THE
 CC CASPASE FAMILY.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: AF092997; AAC63364.1; -;
 DR EMBL: AJ007750; CA07678.1; -;
 DR HSP: P42574; ICP3.
 DR MGD: MGI:1335092; Casp14.
 DR InterPro: IPR003576; Caspase.
 DR InterPro: IPR002138; ICE_p10.
 DR InterPro: IPR001309; ICE_p20.
 DR Pfam: PF00655; ICE_p10; 1.
 DR Pfam: PF00656; ICE_p20; 1.
 DR SMART: SM00115; CASC; 1.
 DR PROSITE: PS01121; CASPASE_HIS; FALSE_NEG.
 DR PROSITE: PS01122; CASPASE_CYS; FALSE_NEG.
 DR PROSITE: PS0207; CASPASE_P10; 1.
 DR PROSITE: PS0208; CASPASE_P20; 1.
 KW Hydrolyase; Thiol protease; Apoptosis; Zymogen.
 FT PROPEP 1 7
 FT CHAIN 1 7
 FT CHAIN 8 2
 FT ACT_SITE 93 93
 FT ACT_SITE 136 136
 FT MUTAGEN 136 136
 FT SEQUENCE 257 AA; 29458 MW; A228D88DFBA0EB84 CRC64;

Query Match 24.5%; Score 63; DB 1; Length 257;
 Best Local Similarity 42.3%; Pred. No. 0.49;
 Matches 11; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

OY 14 GYRSGYOHDLRAYGEWRLVRFVHR 39
 DB 189 GYSTRHDEKSGFTQTLVDVFIHK 214

RESULT 3
 CRBL_BOVIN STANDARD; PRT; 252 AA.
 AC P07318;
 DT 01-APR-1988 (Rel. 07; Created)
 DT 01-NOV-1990 (Rel. 16; Last sequence update)
 DT 01-NOV-1997 (Rel. 35; Last annotation update)
 DE Beta crystallin Bl.
 GN CRYB1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85134866; PubMed=6527379;
 RA Quax-Jeukens Y., Janssen C., Quax W.J., van den Heuvel R.,
 RT Bloemendal H.;
 RT "Bovine beta-crystallin complementary DNA clones. Alternating
 RT proline/alanine sequence of beta B1 subunit originates from a
 RT repetitive DNA sequence.";


```

RL J. Mol. Biol. 180:457-472(1984).
RN [2]
RP SEQUENCE.
RC TISSUE=Iens cortex;
RX MEDLINE=84132067; Pubmed=6696025;
RA Berbers G.A.M., Hoekman W.A., Bloemendaal H., de Jong W.W.,
RA Kleinschmidt T., Braunitzer G.;
RT "Homology between the primary structures of the major bovine beta-
RT crystallin chains.";
RL Eur. J. Biochem. 139:467-479(1984).
CC -1- FUNCTION: CRYSTALLINS ARE THE DOMINANT STRUCTURAL COMPONENTS
CC OF THE VERTEBRATE EYE LENS.
CC -1- SUBUNIT: HOMO/HETERODIMER, OR COMPLEXES OF HIGHER ORDER. THE
CC STRUCTURE OF BETA-CRYSTALLIN OLIGOMERS SEEMS TO BE STABILIZED
CC THROUGH INTERACTIONS BETWEEN THE N-TERMINAL ARMS.
CC -1- DOMAIN: HAS A TWO-DOMAIN BETA-STRUCTURE, FOLDED INTO FOUR
CC VERY SIMILAR GREEK KEY MOTIFS.
CC -1- PTM: SPECIFIC CLEAVAGES IN THE N-TERMINAL ARM OCCUR DURING LENS
CC MATURATION AND GIVE RISE TO TRUNCATED FORMS, LEADING TO IMPAIRED
CC OLIGOMERIZATION AND PROTEIN INSOLUBILIZATION.
CC -1- SIMILARITY: BELONGS TO THE BETA/GAMMA-CRYSTALLIN FAMILY.
CC -----
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CC -----
DR EMBL: X01808; CAA25951.1; -.
DR PIR: A27898; A27898.
DR HSP: P02523; 1B1B.
DR InterPro: IPR001064; Crystallin.
DR Pfam: PF00030; Crystallin_2.
DR PRINTS: PR01367; BGCRCRYSTALLIN.
DR SMART: SM00247; XTALBdg; 2.
DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; 4.
KW Eye lens protein; Repeat; Acetylation.
FT INIT_MET 0
FT MOD_RES 1
FT DOMAIN 1 58 ACETYLATION (PROBABLE).
FT DOMAIN 59 98 N-TERMINAL ARM.
FT DOMAIN 99 144 MOTIF 1.
FT DOMAIN 145 148 MOTIF 2.
FT DOMAIN 149 190 MOTIF 3.
FT DOMAIN 191 234 MOTIF 4.
FT DOMAIN 235 252 C-TERMINAL ARM.
FT CONFLICT 7 10 ASAT -> TSAA (IN REF. 2).
FT CONFLICT 50 50 MISSING (IN REF. 2).
FT CONFLICT 93 101 MISSING (IN REF. 2).
FT CONFLICT 146 146 A -> S (IN REF. 2).
SQ SEQUENCE 252 AA; 28012 MW; 7E508660EE477D20 CRC64;

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Query Match 23.5%; Score 60.5; DB 1; Length 252;
Best Local Similarity 32.1%; Pred. No. 1;
Matches 17; Conservative 5; Mismatches 20; Indels 11; Gaps 2;

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QY 2 VSRVPTWAMAFHGYSYOH-----DLRAYGFWRLL-----VRRFVHRPPHVE 43
Db 188 VSSSTWGYGYPGYRGYQYLLEPDGFRHMNMWGAFOQMGAVRRLRDRQWIRE 240

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RESULT 4
ID CRB1_HUMAN STANDARD; PRT; 251 AA.
AC P53674;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Beta crystallin B1.

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GN CRB1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
ON NCBI_TaxId=9606;
RX MEDLINE=66224006; Pubmed=8626774;
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-21 AND 24-251.
RC TISSUE=Iens;
RX MEDLINE=20057165; Pubmed=10591208;
RA Dunham I., Hunt A.R., Collins J.E., Bruskiewicz R., Beare D.M.,
RA Clump M., Smink L.J., Alnscoough R., Almeida J.P., Babbage A.,
RA Baguley C., Bailey J., Barlow K., Bates K.N., Beasley O., Bird C.P.,
RA Blakey S., Bridgman A.M., Buck D., Burgess J., Burrill W.D.,
RA Burton J., Carder C., Carter N.P., Chen Y., Clark G., Clegg S.M.,
RA Cobley V., Cole C.G., Collier R.E., Connor R.E., Conroy D., Corby N.,
RA Coville G.J., Cox A.V., Davis J., Dawson E., Dhami P.D., Dockree C.,
RA Dodsworth S.J., Durbin R.M., Ellington A., Evans K.L., Fey J.M.,
RA Fleming K., French L., Garner A.A., Gilbert J.G.R., Goward M.E.,
RA Grafham D., Griffiths M.N., Hall C., Hall R., Hall-Tamlyn G.,
RA Heathcote R.W., Ho S., Holmes S., Hunt S.E., Jones M.C., Kershaw J.,
RA Kimberley A., King A., Laird G.K., Langford C.F., Laversha M.A.,
RA Lloyd C., Lloyd D.M., Martyn I.D., Mashreghi-Mohammadi M.,
RA Matthews L., Mccann O.T., Mcclay J., McLaren S., Mcmurtry A.A.,
RA Malne S.A., Mortimore B.J., Odell C.N., Pavitt R., Pearce A.V.,
RA Pearson D., Phillimore B.J., Phillips S.H., Plumb R.W., Ramsay H.,
RA Ramsey Y., Rogers L., Ross M.T., Scott C.E., Sena H.K., Skuce C.D.,
RA Smalley S., Smith M.L., Soderlund C., Spurgeon L., Steward A.,
RA Sulston J.E., Swan R.M., Vaudin M., Walli M., Wallis J.M.,
RA Whiteley M.N., Willey D., Williams L., Williams S., Williamson H.,
RA Wilmer T.E., Wilming L., Wright C.L., Hubbard T., Bentley D.R.,
RA Beck S., Rogers J., Shimizu N., Minoshima S., Kawasaki K., Sasaki T.,
RA Asakawa S., Kudoh J., Shintani A., Shibuya K., Yoshizaki Y., Aoki N.,
RA Mitsuyama S., Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S.,
RA Do A., Do T., Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S.,
RA Lai H., Lao H.I., Lewis J., Lewis S., Lin S.-P., Loh P., Malay E.,
RA Nguyen T., Pan H., Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S.,
RA Sloan D., Song L., Wang Q., Wang Y., Wang Z., White J., Williamson D.,
RA Wu H., Yao Z., Zhan M., Zhang G., Chissoe S., Murray J., Miller N.,
RA Minx P., Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H.,
RA Bourne S., Cordes M., Du Z., Fulton L., Goela D., Graves T.,
RA Hawkins J., Hinds K., Kemp K., Latreille P., Layman D., Ozeresky P.,
RA Rohlfing T., Scheet P., Walker C., Wamsley A., Wohlmann P., Pepin K.,
RA Nelson J., Korf I., Bedell J.A., Hillier L., Maris E., Waterston R.,
RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Salta S.,
RA Budart M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
RA Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,
RA Peyraud M., Kedra D., Serousi E., Fransson I., Tapia I., Bruder C.E.,
RA O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
RA Khan A.S., Lane L., Tiliahun Y., Wright H.;
RT "The DNA sequence of human chromosome 22.";
RL Nature 402:489-495(1999).
RN [3]
RP SEQUENCE OF 199-245 FROM N.A.
RX MEDLINE=96121383; Pubmed=8575764;
RA Hulsebos T.J.M., Gilbert D.J., Delattre O., Smink L.J., Dunham I.,
RA Westerveld A., Thomas G., Jenkins N.A., Copeland N.G.;
RT "Assignment of the beta B1 crystallin gene (CRYB1) to human
RT chromosome 22 and mouse chromosome 5.";
RL Genomics 29:712-718(1995).
CC -1- FUNCTION: CRYSTALLINS ARE THE DOMINANT STRUCTURAL COMPONENTS
CC OF THE VERTEBRATE EYE LENS.
CC -1- SUBUNIT: HOMO/HETERODIMER, OR COMPLEXES OF HIGHER ORDER. THE
CC STRUCTURE OF BETA-CRYSTALLIN OLIGOMERS SEEMS TO BE STABILIZED
CC THROUGH INTERACTIONS BETWEEN THE N-TERMINAL ARMS.
CC -1- DOMAIN: HAS A TWO-DOMAIN BETA-STRUCTURE, FOLDED INTO FOUR

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CC      VERY SIMILAR GREEK KEY MOTIFS.
CC      -1- PTH- SPECIFIC CLEAVAGES IN THE N-TERMINAL ARM OCCUR DURING LENS
CC      MATURATION AND GIVE RISE TO TRUNCATED FORMS, LEADING TO IMPAIRED
CC      OLIGOMERIZATION AND PROTEIN INSOLUBILIZATION.
CC      -1- MASS SPECTROMETRY: MW=27941; MW_ERR=6; METHOD=Electrospray.
CC      -1- SIMILARITY: BELONGS TO THE BETA/GAMMA-CRISTALLIN FAMILY.
CC      -----
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CC      -----
DR      EMBL; U35340; AAC50383.1; -
DR      EMBL; 295115; CAB08268.1; -
DR      EMBL; X86398; CAB60150.1; -
DR      HSSP; P02522; 1BLB.
DR      MIM; 600929; -.
DR      InterPro; IPR001064; Crystallin.
DR      Pfam; PF00030; Crystall1; 2.
DR      PRINTS; PR01367; BGCYSTALLIN.
DR      SMART; SM00247; XTALBq; 2.
DR      PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 4.
KM      Eye lens protein; Repeat: Acetylation.
FT      INIT_MET 0
FT      MOD_RES 1 1 ACETYLATION.
FT      DOMAIN 1 57 N-TERMINAL ARM.
FT      DOMAIN 58 97 MOTIF 1.
FT      DOMAIN 98 143 MOTIF 2.
FT      DOMAIN 144 147 CONNECTING PEPTIDE.
FT      DOMAIN 148 189 MOTIF 3.
FT      DOMAIN 190 233 MOTIF 4.
FT      DOMAIN 234 251 C-TERMINAL ARM.
SQ      SEQUENCE 251 AA; 27892 MW; 0AD81A8EACA86F54 CRC64;
QY      2 VSRVPTAAAFHGRSYOH-----DLRAYGFMTLL-----VRRFNRHPRHYE 43
Db      187 VSSGTVWGIGYRGRGYTLLEPGDERHNMWNGAFOPOMOSERLKDKNHLE 239

Query Match 22.8%; Score 58.5; DB 1; Length 251;
Best Local Similarity 28.3%; Pred. No. 1.8;
Matches 15; Conservative 8; Mismatches 19; Indels 11; Gaps 2;

RESULT 5
PYC_HUMAN
ID      PYC_HUMAN STANDARD: PRT; 1178 AA.
AC      P1198; Q16705;
DT      01-OCT-1989 (Rel. 12, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)
DT      01-MAR-2002 (Rel. 41, Last annotation update)
DE      Pyruvate carboxylase, mitochondrial precursor (EC 6.4.1.1) (Pyruvic
DE      carboxylase) (PCB).
GN      PC.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Liver, and Kidney;
RX      MEDLINE=95002302; PubMed=7918683;
RA      Wexler I.D., Du Y., Lisgaris M.V., Mandal S.K., Freytag S.O.,
RA      Yang B.-S., Liu T.-C., Kwon M., Patel M.S., Kerr D.S.;
RT      "Primary amino acid sequence and structure of human pyruvate
RT      carboxylase.";
RL      Biochim. Biophys. Acta 1227:46-52(1994).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Kidney;

```

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RX      MEDLINE=94324922; PubMed=8048912;
RA      Mackay N., Rigat B., Douglas C., Chen H.S., Robinson B.H.;
RT      "cDNA cloning of human kidney pyruvate carboxylase.";
RL      Biochem. Biophys. Res. Commun. 202:1009-1014(1994).
RN      [3]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Liver, and Kidney;
RA      Walker M.E., Jitrapakdee S., Val D.L., Wallace J.C.;
RL      Submitted (Jul-1995) to the EMBL/GenBank/DBJ databases.
RN      [4]
RP      SEQUENCE OF 1083-1178 FROM N.A.
RX      MEDLINE=87212051; PubMed=3555348;
RA      Lamnonwan A.-W., Quan F., Gravel R.A.;
RT      "Sequence homology around the biotin-binding site of human
RT      propionyl-CoA carboxylase and pyruvate carboxylase.";
RL      Arch. Biochem. Biophys. 254:631-636(1987).
RN      [5]
RP      SEQUENCE OF 1135-1178 FROM N.A.
RX      MEDLINE=85030380; PubMed=6548474;
RA      Freytag S.O., Collier K.J.;
RT      "Molecular cloning of a cDNA for human pyruvate carboxylase.
RT      Structural relationship to other biotin-containing carboxylases and
RT      regulation of mRNA content in differentiating preadipocytes.";
RL      J. Biol. Chem. 259:12831-12837(1984).
RN      [6]
RP      VARIANTS PC DEFICIENCY THR-610 AND ILE-743.
RX      MEDLINE=98254451; PubMed=9585612;
RA      Carbone M.A., Mackay N., Ling M., Cole D.E.C., Douglas C., Rigat B.,
RA      Feigenbaum A., Clarke J.T.R., Haworth J.C., Greenberg C.R.,
RA      Seargeant L., Robinson B.H.;
RT      "Amerindian pyruvate carboxylase deficiency is associated with two
RT      distinct missense mutations.";
RL      Am. J. Hum. Genet. 62:1312-1319(1998).
CC      -1- FUNCTION: PYRUVATE CARBOXYLASE CATALYZES A 2-STEP REACTION,
CC      INVOLVING THE ATP-DEPENDENT CARBOXYLATION OF THE COVALENTLY
CC      ATTACHED BIOTIN IN THE FIRST STEP AND THE TRANSFER OF THE
CC      CARBOXYL GROUP TO PYRUVATE IN THE SECOND. CATALYZES IN A TISSUE
CC      SPECIFIC MANNER, THE INITIAL REACTIONS OF GLUCOSE (LIVER, KIDNEY)
CC      AND LIPID (ADIPOSE TISSUE, LIVER, BRAIN) SYNTHESIS FROM PYRUVATE.
CC      -1- CATALYTIC ACTIVITY: ATP + pyruvate + Hco(3)(-) = ADP + phosphate +
CC      oxaloacetate.
CC      -1- COFACTOR: BIOTIN AND MANGANESE.
CC      -1- PATHWAY: GLUCONEOGENESIS AND LIPONEOGENESIS.
CC      -1- SUBUNIT: HOMOTETRAMER.
CC      -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC      -1- DISEASE: DEFICIENCY IN PC CAUSES LACTIC ACIDOSIS, MENTAL
CC      RETARDATION AND DEATH. OCCURS IN THREE FORMS: TYPE A (MILD); TYPE
CC      B (SEVERE NEONATAL) AND A VERY MILD LACTICACIDEMIA.
CC      -1- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPOAMIDE TRANSFERASES
CC      AND CARBAMYL PHOSPHATE SYNTHETASES.
CC      -----
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CC      -----
DR      EMBL; U04641; AAA99537.1; -
DR      EMBL; 572370; AAB31500.1; -
DR      EMBL; U30891; AAA82937.1; -
DR      EMBL; M26122; AAA36423.1; -
DR      EMBL; K02282; AAA60033.1; -
DR      PIR; B27883; B27883.
DR      PIR; S01469; S01469.
DR      HSSP; P24182; 1BNC.
DR      MIM; 266150; -.
DR      InterPro; IPR001882; Biotin.
DR      InterPro; IPR000089; Biotin_1lpoyl.
DR      InterPro; IPR000901; CPSase.
DR      InterPro; IPR000891; HMGCL-like.
DR      InterPro; IPR003379; PYC_OMDA.

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DR Pfam; PF02785; Biotin_carb_C; 1.
 DR Pfam; PF00364; biotin_lipoyl; 1.
 DR Pfam; PF00289; CPSase_L_chain; 1.
 DR Pfam; PF02786; CPSase_L_D2; 1.
 DR Pfam; PF00682; HMGCL-like; 1.
 DR Pfam; PF02436; PYC_OADA; 1.
 DR PROSITE; PS00188; BIOTIN; 1.
 KM Ligase; Multifunctional enzyme; Biotin; Manganese; Gluconeogenesis;
 KM ATP-binding; Mitochondrion; Lipid synthesis; Transl. peptide;
 KM Disease mutation.
 FT TRANSIT 1 20 MITOCHONDRION (POTENTIAL).
 FT CHAIN 21 1178 PYRUVATE CARBOXYLASE.
 FT DOMAIN 21 549 BIOTIN CARBOXYLASE (BY SIMILARITY).
 FT DOMAIN 550 1000 CARBOXYLTRANSFERASE (BY SIMILARITY).
 FT DOMAIN 1096 1178 BIOTIN CARBOXYL CARRIER PROTEIN
 (BY SIMILARITY).
 FT NP_BIND 198 203 ATP (BY SIMILARITY).
 FT ACT_SITE 328 328 BY SIMILARITY.
 FT BINDING 1144 1144 BIOTIN (BY SIMILARITY).
 FT VARIANT 610 610 A -> T (IN PC DEFICIENCY TYPE A).
 FT VARIANT 610 610 /FTid=VAR.008095.
 FT VARIANT 743 743 M -> I (IN PC DEFICIENCY TYPE A).
 FT VARIANT 743 743 /FTid=VAR.008096.
 FT CONFLICT 225 226 LA -> WP (IN REF. 2).
 FT CONFLICT 352 352 A -> S (IN REF. 3).
 FT CONFLICT 385 386 RS -> PT (IN REF. 2).
 FT CONFLICT 486 487 EL -> DV (IN REF. 2).
 FT CONFLICT 638 638 P -> R (IN REF. 2).
 FT CONFLICT 729 729 E -> A (IN REF. 2).
 FT CONFLICT 774 775 DT -> AP (IN REF. 2).
 SQ SEQUENCE 1178 AA; 129633 MW; 381F52753A20095 CRC64;

Query Match 22.6%; Score 58; DB 1; Length 1178;
 Best Local Similarity 31.7%; Pred. No. 9.2;
 Matches 13; Conservative 6; Mismatches 14; Indels 8; Gaps 1;

QY 13 HG-----RSYOHDLRAGFRLVRRFVHRPHVESQ 45
 Db 208 HSYEELEENYTRAYSEALAFNGALFVEKIEKPRHIEVQ 248

RESULT 6
 PYC_MOUSE STANDARD; PRT; 1178 AA.
 AC 005920;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Pyruvate carboxylase, mitochondrial precursor (EC 6.4.1.1) (Pyruvic
 carboxylase) (PCB).
 DE PC OR PCX.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Adipocyte;
 RX MEDLINE=93189578; PubMed=8446588;
 RA Zhang J., Xia W.L., Brew K., Ahmad F.;
 RT "Adipose pyruvate carboxylase: amino acid sequence and domain
 structure deduced from cDNA sequencing.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:1766-1770(1993).
 CC -1- FUNCTION: PYRUVATE CARBOXYLASE CATALYZES A 2-STEP REACTION,
 INVOLVING THE ATP-DEPENDENT CARBOXYLATION OF THE COVALENTLY
 ATTACHED BIOTIN IN THE FIRST STEP AND THE TRANSFER OF THE
 CARBOXYL GROUP TO PYRUVATE IN THE SECOND. CATALYZES IN A TISSUE
 SPECIFIC MANNER, THE INITIAL REACTIONS OF GLUCOSE (LIVER, KIDNEY)
 AND LIPID (ADIPOSE TISSUE, LIVER, BRAIN) SYNTHESIS FROM PYRUVATE
 -1- CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3)(-) = ADP + phosphate +
 oxaloacetate.
 CC -1- COFACTOR: BIOTIN AND MANGANESE.

CC -1- PATHWAY: GLUCONEOGENESIS AND LIPOGENESIS.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
 CC -1- TISSUE SPECIFICITY: LIVER, KIDNEY, ADIPOSE TISSUE, LIVER
 AND BRAIN.
 CC -1- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPAMIDE TRANSFERASES
 AND CARBAMYL PHOSPHATE SYNTHETASES.
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 CC EMBL; L09192; AAA39737.1; -.
 DR PIR; A47255; A47255.
 DR HSSP; P24182; IBNC.
 DR SWISS-2DPAGE; 005920; MOUSE.
 DR MGI; 97520; PCX.
 DR InterPro; IPR001882; Biotin.
 DR InterPro; IPR000089; Biotin_lipoyl.
 DR InterPro; IPR000901; CPSase.
 DR InterPro; IPR000891; HMGCL-like.
 DR InterPro; IPR003379; PYC_OADA.
 DR Pfam; PF02785; Biotin_carb_C; 1.
 DR Pfam; PF00364; biotin_lipoyl; 1.
 DR Pfam; PF00289; CPSase_L_chain; 1.
 DR Pfam; PF02786; CPSase_L_D2; 1.
 DR Pfam; PF00682; HMGCL-like; 1.
 DR Pfam; PF02436; PYC_OADA; 1.
 DR PROSITE; PS00188; BIOTIN; 1.
 KM Ligase; Multifunctional enzyme; Biotin; Manganese; Gluconeogenesis;
 KM ATP-binding; Mitochondrion; Lipid synthesis; Transl. peptide.
 KM ATP-binding; Mitochondrion; Lipid synthesis; Transl. peptide.
 FT TRANSIT 1 20 MITOCHONDRION (POTENTIAL).
 FT CHAIN 21 1178 PYRUVATE CARBOXYLASE.
 FT DOMAIN 21 549 BIOTIN CARBOXYLASE (BY SIMILARITY).
 FT DOMAIN 550 1000 CARBOXYLTRANSFERASE (BY SIMILARITY).
 FT DOMAIN 1096 1178 BIOTIN CARBOXYL CARRIER PROTEIN
 (BY SIMILARITY).
 FT NP_BIND 198 203 ATP (BY SIMILARITY).
 FT ACT_SITE 328 328 BY SIMILARITY.
 FT BINDING 1144 1144 BIOTIN (BY SIMILARITY).
 SQ SEQUENCE 1178 AA; 129684 MW; 14CEA0F9DA8B8127 CRC64;

Query Match 22.6%; Score 58; DB 1; Length 1178;
 Best Local Similarity 31.7%; Pred. No. 9.2;
 Matches 13; Conservative 6; Mismatches 14; Indels 8; Gaps 1;

QY 13 HG-----RSYOHDLRAGFRLVRRFVHRPHVESQ 45
 Db 208 HSYEELEENYTRAYSEALAFNGALFVEKIEKPRHIEVQ 248

RESULT 7
 CRBA_CHICK STANDARD; PRT; 215 AA.
 AC P10042;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Beta crystallin A3 [Contains: Beta crystallin A1].
 CN CRIBAL.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87106807; PubMed=3803920;

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RA Peterson C.A., Platiorsky J.;
RT "Preferential conservation of the globular domains of the beta A3/A1-
RL crystallin polypeptide of the chicken eye lens.";
RN Gene 45:139-147(1986).
RP SEQUENCE FROM N.A.
RX MEDLINE-92347693; PubMed1353472;
RA McDermott J.B., Peterson C.A., Platiorsky J.;
RT "Structure and lens expression of the gene encoding chicken beta
RT A3/A1-crystallin.";
RL Gene 117:193-200(1992).
CC -!- FUNCTION: CRYSTALLINS ARE THE DOMINANT STRUCTURAL COMPONENTS
CC OF THE VERTEBRATE EYE LENS.
CC -!- SUBUNIT: HOMO/ETERODIMER, OR COMPLEXES OF HIGHER ORDER. THE
CC STRUCTURE OF BETA-CRYSTALLIN OLIGOMERS SEEMS TO BE STABILIZED
CC THROUGH INTERACTIONS BETWEEN THE N-TERMINAL ARMS (BY SIMILARITY).
CC -!- DOMAIN: HAS A TWO-DOMAIN BETA-STRUCTURE, FOLDED INTO FOUR
CC VERY SIMILAR GREEK KEY MOTIFS.
CC -!- SIMILARITY: BELONGS TO THE BETA/GAMMA-CRYSTALLIN FAMILY.
CC -----
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CC -----
DR EMBL: M15658; AAA48724.1; -.
DR EMBL: M15658; AAA48725.1; ALT_INIT.
DR EMBL: M84460; AAA48612.1; ALT_INIT.
DR EMBL: M84460; AAA48611.1; ALT_SEQ.
DR PIR: A25358; A25358.
DR PIR: JCI231; JCI231.
DR HSSP: P02522; 1BLB.
DR InterPro: IPR001064; Crystallin.
DR pfam: PF00030; crystall. 2.
DR PRINTS: PR01367; BGCRCRYSTALLIN.
DR SMART: SM00247; XTALDg; 2.
DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; 4.
KW Eye lens protein; Repeat; Alternative initiation.
FT CHAIN 1 215 BETA CRYSTALLIN A3.
FT INIT_MET 19 215 FOR BETA CRYSTALLIN A1.
FT DOMAIN 1 18 N-TERMINAL ARM.
FT DOMAIN 1 30 FOR BETA CRYSTALLIN A1.
FT DOMAIN 31 70 MOTIF 1.
FT DOMAIN 71 118 MOTIF 2.
FT DOMAIN 119 123 CONNECTING PEPTIDE.
FT DOMAIN 124 165 MOTIF 3.
FT DOMAIN 166 215 MOTIF 4.
SQ SEQUENCE 215 AA; 24749 MW; 69518AE6826B2921 CRC64;

Query Match 22.4%; Score 57.5; DB 1; Length 215;
Best Local Similarity 34.3%; Pred. No. 2.1;
Matches 12; Conservative 5; Mismatches 9; Indels 9; Gaps 2;

OY 4 RVP---WTAMAFHGYSRYOHLRA-----YGFWR 29
DB 162 KIPGAMVCYGYRGYGVLEADHNGDYKHM 196

RESULT 8
PCCA_RAT STANDARD; PRT; 704 AA.
AC P14882;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Propionyl-CoA carboxylase alpha chain, mitochondrial precursor
DE (EC 6.4.1.3) (PCCAase alpha subunit) (Propanoyl-CoA:carbon dioxide
DE ligase alpha subunit) (Fragment).
GN PCCA.

```

```

OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-89308706; PubMed2745462;
RA Browner M.F., Taroni F., Szul E., Rosenberg L.E.;
RT "Sequence analysis, biogenesis, and mitochondrial import of the
RT alpha-subunit of rat liver propionyl-CoA carboxylase.";
RL J. Biol. Chem. 264:12680-12685(1989).
RN [2]
RP REVISIONS.
RA Browner M.F., Taroni F., Szul E., Rosenberg L.E.;
RL Submitted (FEB-1989) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ATP + propanoyl-CoA + HCO(3)(-) = ADP +
CC phosphate + (S)-methylmalonyl-CoA.
CC -!- COFACTOR: BIOTIN.
CC -!- PATHWAY: KEY ENZYME IN THE CATABOLIC PATHWAY OF ODD-CHAIN
CC FATTY ACIDS, ISOLEUCINE, THREONINE, METHIONINE, AND VALINE.
CC -!- SUBUNIT: PROBABLY A DODECAMER COMPOSED OF SIX BIOTIN-CONTAINING
CC ALPHA SUBUNITS AND SIX BETA SUBUNITS.
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -!- DISEASE: PROPIONIC ACIDEMIA DUE TO RECESSIVELY INHERITED
CC DEFICIENCY OF PCCAASE ACTIVITY OFTEN CAUSES LIFE-THREATENING
CC KETOSIS AND ACIDOSIS.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: M22631; AAA88512.1; ALT_SEQ.
DR PIR: A34337; A34337.
DR HSSP: P24182; 1DVL.
DR InterPro: IPR001882; Biotin.
DR InterPro: IPR000089; Biotin_1lpoy1.
DR InterPro: IPR000901; CPSase.
DR pfam: PF02785; Biotin_carb_C; 1.
DR pfam: PF00364; biotin_1lpoy1; 1.
DR pfam: PF00289; CPSase_L_chain; 1.
DR pfam: PF02786; CPSase_L_D2; 1.
DR PROSITE: PS00188; BIOTIN; 1.
DR PROSITE: PS00866; CPSASE_1; 1.
DR PROSITE: PS00867; CPSASE_2; 1.
KW Mitochondrion; Ligase; Biotin; ATP-binding; Transit peptide.
FT NON_TER 1 1
FT TRANSIT 1 21
FT CHAIN 22 704 MITOCHONDRION.
FT NP_BIND 199 204 ATP (POTENTIAL).
FT ACT_SITE 329 329 BY SIMILARITY.
FT BINDING 670 670 BIOTIN (BY SIMILARITY).
SQ SEQUENCE 704 AA; 77711 MW; 36CEEC52DE2D2A8A CRC64;

Query Match 22.2%; Score 57; DB 1; Length 704;
Best Local Similarity 34.1%; Pred. No. 7.5;
Matches 15; Conservative 8; Mismatches 19; Indels 2; Gaps 2;

OY 4 RVPW-TAMAFHGYSRYOHLRAYGFWRLVRRFVRRHPVESQ 45
DB 206 RLPWDEETRDGRFSSQEAASFQDRLLEKFIQDPHIEIQ 249

RESULT 9
PVC_RAT STANDARD; PRT; 1178 AA.
AC P52873; Q64555;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
GN PVC.

```

DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Pyruvate carboxylase, mitochondrial precursor (EC 6.4.1.1) (Pyruvic
 DE carboxylase) (PCB).
 GN PC.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=96096548; PubMed=8522203;
 RA Lehn D.A., Moran S.M., Macdonald M.J.;
 RT "The sequence of the rat pyruvate carboxylase-encoding cDNA."
 RL Gene 165:331-332(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Liver;
 RX MEDLINE=96257760; PubMed=8687410;
 RA Jitrapakdee S., Booker G.W., Cassidy A.I., Wallace J.C.;
 RT "Cloning, sequencing and expression of rat liver pyruvate
 RT carboxylase."
 RL Biochem. J. 316:631-637(1996).
 CC -1- FUNCTION: PYRUVATE CARBOXYLASE CATALYZES A 2-STEP REACTION,
 CC INVOLVING THE ATP-DEPENDENT CARBOXYLATION OF THE COVALENTLY
 CC ATTACHED BIOTIN IN THE FIRST STEP AND THE TRANSFER OF THE
 CC CARBOXYL GROUP TO PYRUVATE IN THE SECOND. CATALYZES IN A TISSUE
 CC SPECIFIC MANNER, THE INITIAL REACTIONS OF GLUCOSE (LIVER, KIDNEY)
 CC AND LIPID (ADIPOSE TISSUE, LIVER, BRAIN) SYNTHESIS FROM PYRUVATE.
 CC -1- CATALYTIC ACTIVITY: ATP + pyruvate + HCO(3)(-) = ADP + phosphate +
 CC oxalacetate.
 CC -1- COFACTOR: BIOTIN AND MANGANESE (BY SIMILARITY).
 CC -1- PATHWAY: GLUCONEOGENESIS AND LIPOGENESIS.
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
 CC -1- SIMILARITY: WITH OTHER BIOTIN CARBOXYLASES, LIPAMIDE TRANSFERASES
 CC AND CARBAMYL PHOSPHATE SYNTHETASES.
 CC -----
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 CC -----
 CC EMBL: U32314; AAA96256.1; -;
 DR EMBL: U36585; AAC52668.1; -;
 DR HSSP: P24182; IBNC.
 DR InterPro: IPR001882; Biotin.
 DR InterPro: IPR000089; Biotin_lipoyl.
 DR InterPro: IPR000901; CPSase.
 DR InterPro: IPR00379; HMG-L-like.
 DR InterPro: IPR00379; HMG-L-like.
 DR Pfam: PF02785; Biotin_card_C; 1.
 DR Pfam: PF00364; Biotin_lipoyl; 1.
 DR Pfam: PF00289; CPSase_L_chain; 1.
 DR Pfam: PF02786; CPSase_L_D2; 1.
 DR Pfam: PF00682; HMG-L-like; 1.
 DR Pfam: PF02436; PYC_OADA; 1.
 DR PROSITE: PS00188; BIOTIN; 1.
 KW Ligase: Multifunctional enzyme: Biotin; Manganese; Gluconeogenesis;
 KW AMP-binding; Mitochondrion; Lipid synthesis; Transist peptide.
 FT TRANST 1 20
 FT CHAIN 1 20
 FT DOMAIN 21 1178
 FT DOMAIN 21 549
 FT DOMAIN 550 1000
 FT DOMAIN 1096 1178
 FT DOMAIN 1096 1178
 FT NP_BIND 198 203
 FT ACT_SITE 328 328
 FT BINDING 1144 1144
 FT CONFLICT 222 222
 P -> S (IN REF. 2).

FT CONFLICT 866 866 D -> I (IN REF. 2).
 FT CONFLICT 977 977 G -> R (IN REF. 2).
 SQ SEQUENCE 1178 AA; 129689 MW; 8E5FA19BC132A8DD CRC64;
 Query Match 22.2%; Score 57; DB 1; Length 1178;
 Best Local Similarity 31.7%; Pred. No. 12;
 Matches 13; Conservative 6; Mismatches 14; Indels 8; Gaps 1;
 OY 13 HG-----RSTQNDLRAGFWRLVRFVRRPVSQ 45
 Db 208 HSYEELEENYRAYPALAFAFGALFVEKIEKPRHIEVQ 248
 RESULT 10
 NORM_NEIMA STANDARD; PRT; 459 AA.
 AC 09JVT7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Probable multidrug resistance protein norm (Na(+)/drug antiporter)
 DE (multidrug-efflux transporter).
 GN NORM OR NMA1022.
 OS Neisseria meningitidis (serogroup A).
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=65699;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=22491 / SEROTYPE 4A;
 RX MEDLINE=20222556; PubMed=10761919;
 RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
 RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
 RA Davies R.M., Davis P., Devlin K., Feltywell T., Hamlin N., Holtroyd S.,
 RA Jagers K., Leather S., Moule S., Mungall K., Quail M.A.,
 RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
 RA Whitehead S., Spratt B.G., Barrell B.G.;
 RT "complete DNA sequence of a serogroup A strain of Neisseria
 RT meningitidis 22491".
 RL Nature 404:502-506(2000).
 CC -1- FUNCTION: FUNCTIONS AS A NA(+)/DRUG ANTIporter (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
 CC (Potential).
 CC -1- SIMILARITY: BELONGS TO THE MULTI ANTIMICROBIAL EXTRUSION (MATE)
 CC FAMILY. NORM (TC 2.A.66.1.1) SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL: AL162754; CAB84291.1; -;
 DR InterPro: IPR002528; UPF0013.
 DR Pfam: PF01554; UPF0013; 2.
 KW Transport; Sodium transport; Transmembrane; Inner membrane;
 KW Complete proteome.
 FT TRANSMEM 20 40
 FT TRANSMEM 53 73
 FT TRANSMEM 100 120
 FT TRANSMEM 132 152
 FT TRANSMEM 168 188
 FT TRANSMEM 202 222
 FT TRANSMEM 252 272
 FT TRANSMEM 285 305
 FT TRANSMEM 325 345
 FT TRANSMEM 358 378
 FT TRANSMEM 395 415
 FT TRANSMEM 423 443
 FT TRANSMEM 459 AA; 49941 MW; B2EPD115C8EA94E CRC64;
 SQ SEQUENCE

Query Match 22.0%; Score 56.5; DB 1; Length 459;
 Best Local Similarity 32.5%; Pred. No. 5.7;
 Matches 13; Conservative 6; Mismatches 12; Indels 9; Gaps 2;

OY 2 VSRVP-----WTAMAFHGYSRYOHLRAFGFRLIV 32
 DB 392 VTRKVPMTIHAAAFWCGCLLPGLLAYRFDWGTGFWTALII 431

RESULT 11
 ICEE_HUMAN ID ICEE_HUMAN STANDARD; PRT; 242 AA.

AC P31944; 095823; 26, Created)
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Caspase-14 precursor (EC 3.4.22.-) (CASP-14).
 GN CASP14.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Poyet J.-L., Srinivasula S.M., Fernandes-Alnemri T., Alnemri E.S.;
 RT "Identification and characterization of human caspase 14.";
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE OF 68-74; 137-147 AND 154-162.
 RC TISSUE=keratinocytes;
 RA MEDLINE=93162043; PubMed=1286667;
 RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
 RA Vandekekerckhove J.;
 RT "Microsequences of 145 proteins recorded in the two-dimensional gel
 RT protein database of normal human epidermal keratinocytes.";
 RL Electrophoresis 13:960-969(1992).
 CC -1- FUNCTION: MAY BE INVOLVED IN THE DEATH RECEPTOR AND GRANZYME B
 CC APOPTOTIC PATHWAYS. MAY FUNCTION AS A DOWNSTREAM SIGNAL TRANSDUCER
 CC OF CELL DEATH.
 CC -1- SUBUNIT: MAY DIMERIZE WITH LARGE PRODOMAIN CASPASES.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity)
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14, ALSO KNOWN AS THE
 CC CASPASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: AF097874; AAD16173.1; -.
 DR HSSP: P42574; 1CP3.
 DR Aarhus/Chent-2DPAGE; 6109; IEF.
 DR MIM: 605848; -.
 DR InterPro: IPR003576; Caspase.
 DR InterPro: IPR002138; ICE_P10.
 DR InterPro: IPR001309; ICE_P20.
 DR InterPro: IPR002398; ILBconv-enz.
 DR Pfam: PF00655; ICE_P10; 1.
 DR Pfam: PF00656; ICE_P20; 1.
 DR PRINTS: PR00376; ILBCEZYME.
 DR SMART: SM00115; CASC; 1.
 DR PROSITE: PS01121; CASPASE_HIS; FALSE_NEG.
 DR PROSITE: PS01122; CASPASE_CYS; FALSE_NEG.
 DR PROSITE: PS0207; CASPASE_P10; 1.
 DR PROSITE: PS50208; CASPASE_P20; 1.
 KW Hydrolyase; Thiol protease; Apoptosis; Zymogen.
 FT PROPEP 1 ?
 FT CHAIN ? 146 CASPASE-14 SUBUNIT 1 (POTENTIAL).

FT CHAIN 147 242 CASPASE-14 SUBUNIT 2 (POTENTIAL).
 FT ACT_SITE 89
 FT ACT_SITE 132
 SQ SEQUENCE 242 AA; 27679 MW; E539F87EB8D808A2 CRC64;

Query Match 21.8%; Score 56; DB 1; Length 242;
 Best Local Similarity 31.8%; Pred. No. 3.6;
 Matches 14; Conservative 7; Mismatches 17; Indels 6; Gaps 1;

OY 5 VPTWAFPH-----GYSYOHDLRAFGFRLIVREFVRPPV 42
 DB 159 IPPTDALHVSIVSEGTIAYRHDQKSCFTQILVDFVTRKKHI 202

RESULT 12
 YH2_YEAST ID YH2_YEAST STANDARD; PRT; 278 AA.

AC P38878; 31, Created)
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Hypothetical 32.1 kDa protein in CTF8-EGD2 intergenic region.
 GN YHR192W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / AB972;
 RA MEDLINE=94378003; PubMed=8091229;
 RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
 RA Du Z., Favell A., Fulton L., Gatlung S., Geisel C., Kirsten J.,
 RA Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
 RA Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
 RA Nham M., Rifkin L., Riles L., St Peter H., Trevisan E., Vaughan K.,
 RA Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,
 RA Vaudin M.;
 RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
 RT VIII.";
 RL Science 265:2077-2082(1994).
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 CC -----
 DR EMBL: U00030; AAB68359.1; -.
 DR PIR: S46681; S46681.
 DR SCD: S0001235; YHR192W.
 KW Hypothetical protein; Transmembrane.
 FT TRANSMEM 46 66
 FT TRANSMEM 78 98 POTENTIAL.
 FT SEQUENCE 278 AA; 32062 MW; D896557EE805C89 CRC64;

Query Match 21.8%; Score 56; DB 1; Length 278;
 Best Local Similarity 50.0%; Pred. No. 4.1;
 Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 1 TVSRVPMTAMAFHGYSRY 18
 DB 62 TVLALSTYWEYHGYPY 79

RESULT 13
 CB11_RANCA ID CB11_RANCA STANDARD; PRT; 198 AA.
 AC Q91315;

```

DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Beta crystallin A1-1.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OC NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lens;
RX MEDLINE=96192032; PubMed=8619837;
RA Lu S.-F., Pan F.-M., Chiu S.-H.;
RT "Sequence analysis of four acidic beta-crystallin subunits of
RT amphibian lenses: phylogenetic comparison between beta- and
RT gamma-crystallins."
RT Biochem. Biophys. Res. Commun. 221:219-228(1996).
RL
CC -1- FUNCTION: CRYSTALLINS ARE THE DOMINANT STRUCTURAL COMPONENTS
CC OF THE VERTEBRATE EYE LENS.
CC -1- SUBUNIT: HOMO/HETERODIMER, OR COMPLEXES OF HIGHER ORDER. THE
CC STRUCTURE OF BETA-CRYSTALLIN OLIGOMERS SEEMS TO BE STABILIZED
CC THROUGH INTERACTIONS BETWEEN THE N-TERMINAL ARMS (BY SIMILARITY).
CC -1- DOMAIN: HAS A TWO-DOMAIN BETA-STRUCTURE, FOLDED INTO FOUR
CC VERY SIMILAR GREEK KEY MOTIFS.
CC -1- SIMILARITY: BELONGS TO THE BETA/GAMMA-CRYSTALLIN FAMILY.
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CC -----
CC EMBL; X87759; CA61033.1; -.
CC HSSP; P02522; IBLB.
CC InterPro; IPR001064; Crystallin.
CC Pfam; PF00030; crystall; 2.
CC PRINTS; PR01367; BGCRCRYSTALLIN.
CC SMART; SM00247; XTALBdg; 2.
CC PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 4.
CC Eye lens protein; Repeat.
CC KW DOMAIN 1 13 N-TERMINAL ARM.
CC FT DOMAIN 14 53 MOTIF 1.
CC FT DOMAIN 54 101 MOTIF 2.
CC FT DOMAIN 102 106 CONNECTING PEPTIDE.
CC FT DOMAIN 107 148 MOTIF 3.
CC FT DOMAIN 149 198 MOTIF 4.
CC SQ SEQUENCE 198 AA; 23236 MW; 327BAFD1461F20E7 CRC64;

Query Match 21.0%; Score 54; DB 1; Length 198;
Best Local Similarity 34.5%; Pred. No. 5.3;
Matches 10; Conservative 4; Mismatches 9; Indels 6; Gaps 1;

OY 7 WTAAAFHGYSYQHDLA-----YGFWR 29
Db 151 WVCYQPGYRGYXILSDHHGGEYKHWR 179

RESULT 14
CB12_RANCA STANDARD; PRT; 198 AA.
AC 091316;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Beta crystallin A1-2.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OC NCBI_TaxID=8400;

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RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lens;
RX MEDLINE=96192032; PubMed=8619837;
RA Lu S.-F., Pan F.-M., Chiu S.-H.;
RT "Sequence analysis of four acidic beta-crystallin subunits of
RT amphibian lenses: phylogenetic comparison between beta- and
RT gamma-crystallins."
RT Biochem. Biophys. Res. Commun. 221:219-228(1996).
RL
CC -1- FUNCTION: CRYSTALLINS ARE THE DOMINANT STRUCTURAL COMPONENTS
CC OF THE VERTEBRATE EYE LENS.
CC -1- SUBUNIT: HOMO/HETERODIMER, OR COMPLEXES OF HIGHER ORDER. THE
CC STRUCTURE OF BETA-CRYSTALLIN OLIGOMERS SEEMS TO BE STABILIZED
CC THROUGH INTERACTIONS BETWEEN THE N-TERMINAL ARMS (BY SIMILARITY).
CC -1- DOMAIN: HAS A TWO-DOMAIN BETA-STRUCTURE, FOLDED INTO FOUR
CC VERY SIMILAR GREEK KEY MOTIFS.
CC -1- PTM: THE N-TERMINUS IS BLOCKED.
CC -1- SIMILARITY: BELONGS TO THE BETA/GAMMA-CRYSTALLIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X87760; CA61034.1; -.
CC HSSP; P02522; IBLB.
CC InterPro; IPR001064; Crystallin.
CC Pfam; PF00030; crystall; 2.
CC PRINTS; PR01367; BGCRCRYSTALLIN.
CC SMART; SM00247; XTALBdg; 2.
CC PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 4.
CC Eye lens protein; Repeat.
CC KW DOMAIN 1 13 N-TERMINAL ARM.
CC FT DOMAIN 14 53 MOTIF 1.
CC FT DOMAIN 54 101 MOTIF 2.
CC FT DOMAIN 102 106 CONNECTING PEPTIDE.
CC FT DOMAIN 107 148 MOTIF 3.
CC FT DOMAIN 149 198 MOTIF 4.
CC SQ SEQUENCE 198 AA; 23096 MW; 52A09C6422C0C775 CRC64;

Query Match 21.0%; Score 54; DB 1; Length 198;
Best Local Similarity 34.5%; Pred. No. 5.3;
Matches 10; Conservative 4; Mismatches 9; Indels 6; Gaps 1;

OY 7 WTAAAFHGYSYQHDLA-----YGFWR 29
Db 151 WVCYQPGYRGYXILSDHHGGEYKHWR 179

RESULT 15
CRBA_RANTE STANDARD; PRT; 198 AA.
ID CRBA_RANTE
AC P07317;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Beta crystallin A1.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OC NCBI_TaxID=8407;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lens;
RX MEDLINE=88050966; PubMed=3499937;
RA Luchin S.V., Zinovleva R.D., Tomarev S.I., Dolgilevich S.M.,
RA Gause G.G. Jr., Bax J.B., Driessen H.P.C., Blundell T.L.;
RT "Frog lens beta A1-crystallin: the nucleotide sequence of the cloned
RT cDNA and computer graphics modelling of the three-dimensional

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 15, 2002, 11:59:20 ; Search time 41.42 Seconds
(without alignments)
187.947 Million cell updates/sec

Title: DEVI-613-COMB
Perfect score: 257
Sequence: 1 TVSRVPTWMAFHGYSYQH.....GFNRLVRFVHRPRHVESQ 45

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP.TREMBL_19:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvrius:*
16: sp_bacteriapi:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	66.5	25.9	245	11	Q9JHV9
2	65.5	25.5	250	11	Q9WVJ5
3	61.5	23.9	537	10	Q9SD75
4	61	23.7	724	5	Q19842
5	59.5	23.2	288	2	Q52214
6	59.5	23.2	288	2	Q9R3G9
7	59.5	23.2	292	2	Q68716
8	59	23.0	322	16	Q07420
9	58.5	22.8	336	4	Q9H495
10	58.5	22.8	397	4	Q9H497
11	58.5	22.8	397	4	Q9H6E7
12	58	22.6	1175	5	Q17732
13	57	22.2	290	2	Q52218
14	57	22.2	771	16	Q9WV09
15	57	22.2	1180	13	Q9DDT1
16	56.5	22.0	77	4	Q9BX23

17	56	21.8	285	2	Q9S121	09s121 escherichia	
18	55.5	21.6	232	13	Q90WT1	090wt1 brachydanio	
19	55.5	21.6	300	3	Q94457	094457 schizosacch	
20	55	21.4	285	2	Q9AJU6	09aj16 shigella fl	
21	55	21.4	285	2	Q47618	047618 escherichia	
22	55	21.4	289	2	Q9AFJ7	09afj7 shigella fl	
23	54.5	21.2	271	2	Q9FCG3	09fcg3 streptomyce	
24	54.5	21.2	1929	5	Q95Y09	095y09 leishmania	
25	54	21.0	339	2	Q9KWB6	09kwb6 agrobacteri	
26	54	21.0	398	16	Q9P084	09p084 ureaplasma	
27	54	21.0	441	16	Q920A4	0920a4 rhizobium m	
28	54	21.0	631	5	Q9VEG1	09veg1 drosophila	
29	54	21.0	1583	10	Q9S7A7	09s7a7 oryza sativ	
30	53.5	20.8	227	13	Q9W6T4	09w6t4 xenopus lae	
31	53.5	20.8	287	2	Q9ZBW5	09zwb5 klebsiella	
32	53.5	20.8	291	10	Q80435	080435 arabidopsis	
33	53.5	20.8	1359	4	Q96U65	096u65 homo sapien	
34	53	20.6	32	6	Q28257	028257 canis famli	
35	53	20.6	108	10	Q9AX84	09ax84 oryza sativ	
36	53	20.6	198	6	Q95KK5	095kk5 oryctolagus	
37	53	20.6	37	198	11	Q91XW3	091xw3 canis porce
38	53	20.6	215	6	Q95KK6	095kk6 oryctolagus	
39	53	20.6	215	11	Q91XW4	091xw4 canis porce	
40	53	20.6	285	2	Q82926	082926 escherichia	
41	53	20.6	285	2	Q930L1	093q11 escherichia	
42	53	20.6	326	2	Q9KZK7	09kzk7 streptomyce	
43	53	20.6	705	10	Q9SU64	09s64 arabidopsis	
44	53	20.6	966	16	Q92K03	092kq3 rhizobium m	
45	52.5	20.4	211	10	Q94419	094419 arabidopsis	

ALIGNMENTS

RESULT 1
ID Q9JHV9 PRELIMINARY; PRT; 245 AA.
AC Q9JHV9:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE BETAB1-CRYSTALLIN (FRAGMENT).
GN CRYBB1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN-SPRAGUE-DAWLEY; TISSUE=LENS;
RA Lampi K.J., Shih M., Shearer T.R., David L.L.;
RT "Lens proteomics: Analysis of rat crystallin sequences and two-dimensional electrophoresis map."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CRYSTALLINS ARE THE DOMINANT STRUCTURAL COMPONENTS OF THE VERTEBRATE EYE LENS (BY SIMILARITY).
CC -!- DOMAIN: HAS A TWO-DOMAIN BETA-STRUCTURE, FOLDED INTO FOUR VERY SIMILAR GREEK KEY MOTIFS (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE BETA/GAMMA-CRYSTALLIN FAMILY.
DR EMBL; AF286652; AAF97950.1; -.
DR HSSP; P02522; 2BB2.
DR InterPro; IPR001064; Crystallin.
DR PRINTS; PR01367; BGC-CRYSTALLIN.
DR SMART; SM00247; XTB1bf.2.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 4.
KW duplication; Eye lens protein.
FT NON_TER 1
SQ SEQUENCE 245 AA; 27576 MW; E1565A564FCDD147 CRC64;

Query Match 25.98; Score 66.5; DB 11; Length 245;
Best Local Similarity 33.3%; Pred. No. 0.6;
Matches 18; Conservative 5; Mismatches 20; Indels 11; Gaps 2;

RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Bentley D.;
 RT "the sequence of *C. elegans* cosmid F27D9."
 RL Submitted (Feb-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RT "Direct Submission";
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U49829; AAA93384.1; -.
 DR HSSP; P24182; 1BNC.
 DR InterPro; IPR001249; AcCoA biotinCC.
 DR InterPro; IPR001882; Biotin_1lipoyl.
 DR InterPro; IPR000089; Biotin_1lipoyl.
 DR InterPro; IPR000901; CPsase.
 DR Pfam; PF02785; Biotin_carb_C; 1.
 DR Pfam; PF00364; biotin_1lipoyl; 1.
 DR Pfam; PF00289; CPsase_L_chain; 1.
 DR Pfam; PF02786; CPsase_L_D2; 1.
 DR PROSITE; PS00188; BIOTIN; UNKNOWN_1.
 DR PROSITE; PS00866; CPsase_1; 1.
 DR PROSITE; PS00867; CPsase_2; UNKNOWN_1.
 KW Hypothetical protein.
 SO SEQUENCE 724 AA; 79762 MW; E09832FB65AABA45 CRC64;

Query Match 23.7%; Score 61; DB 5; Length 724;
 Best Local Similarity 38.6%; Pred. No. 10;
 Matches 17; Conservative 6; Mismatches 19; Indels 2; Gaps 2;

Oy 4 RVPWT-AMAFHGYR-STQHDLRATGFWRLVRRFVHRPHVRSQ 45
 Db 216 RVAMNDKQAREGYRLSKQEAASFGDDRMVLEKFDNPRHTEMQ 259

RESULT 5
 ID 052214 PRELIMINARY; PRT; 288 AA.
 AC 052214;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE REPLICATION PROTEIN.
 GN REPA.
 OS *Yersinia enterocolitica*.
 OG Plasmid pY6227.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC *Yersinia*.
 OX NCBI_TaxID=630;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=90299777; Pubmed=1694522;
 RA Vanocoghehem J.C., Cornelis G.R.;
 RT "Structural and functional similarities between the replication region
 of the *Yersinia* virulence plasmid and the RepT1A replicons."
 RL J. Bacteriol. 172:3600-3608(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=M22703;
 RA Irlarte M., Lambersmont I., Kerbouch C., Cornelis G.R.;
 RT "Detailed genetic map of the pY6227 plasmid of *Yersinia*
enterocolitica serotype O:3."
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; M55182; AAA98437.1; -.
 DR EMBL; AF102990; AAD16866.1; -.
 DR InterPro; IPR003446; IncFII_repa.
 DR Pfam; PF02387; IncFII_repa; 1.
 KW plasmid
 SO SEQUENCE 288 AA; 33548 MW; ABBFBA5FC74AAB45 CRC64;

Query Match 23.2%; Score 59.5; DB 2; Length 288;
 Best Local Similarity 30.8%; Pred. No. 5.8;
 Matches 20; Conservative 6; Mismatches 16; Indels 23; Gaps 3;

Oy 3 SRVFW-----TAMAF--HGYSYQHDLRATGFWRLVRRFVHR-R 39
 Db 174 SRVEMNQREKQRLPRLEMDLAKAMRFVRRFRSRYTERKAHGKLRARARRDVRT 233
 Oy 40 PHVES 44
 Db 234 RDIEA 238

RESULT 6
 ID 09R3G9 PRELIMINARY; PRT; 288 AA.
 AC 09R3G9;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE PUTATIVE REPLICATION INITIATION PROTEIN.
 GN YPCD1.77C OR REPA.
 OS *Yersinia pestis*.
 OG Plasmid pCD1.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC *Yersinia*.
 OX NCBI_TaxID=632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CO-92 BIOVAR ORIENTALIS;
 RA Baker S.G., Mungall K.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CO-92 BIOVAR ORIENTALIS;
 RA James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CO-92 BIOVAR ORIENTALIS;
 RA Karlyshev A.V., Wren B.W.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KIM5;
 RX MEDLINE=98427122; Pubmed=9746557;
 RA Perry R.D., Straley S.C., Featherston J.D., Rose D.J., Gregor J.,
 RA Blatner F.R.;
 RT "DNA sequencing and analysis of the low-Ca2+-response plasmid pCD1 of
Yersinia pestis KIM5."
 RL Infect. Immun. 66:4611-4623(1998).
 DR EMBL; AL117189; CAB54954.1; -.
 DR EMBL; AF074612; AAC69762.1; -.
 DR InterPro; IPR003446; IncFII_repa.
 DR Pfam; PF02387; IncFII_repa; 1.
 KW plasmid
 SO SEQUENCE 288 AA; 33547 MW; 75D99C1DA548264D CRC64;

Query Match 23.2%; Score 59.5; DB 2; Length 288;
 Best Local Similarity 30.8%; Pred. No. 5.8;
 Matches 20; Conservative 6; Mismatches 16; Indels 23; Gaps 3;

Oy 3 SRVFW-----TAMAF--HGYSYQHDLRATGFWRLVRRFVHR-R 39
 Db 174 SRVEMNQREKQRLPRLEMDLAKAMRFVRRFRSRYTERKAHGKLRARARRDVRT 233
 Oy 40 PHVES 44
 Db 234 RDIEA 238

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RESULT 7
068716 PRELIMINARY; PRT; 292 AA.
AC 068716;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
REPLICATION PROTEIN REPA HOMOLOG.
GN Yersinia pestis.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-KIM.
RX MEDLINE=98422474; PubMed=9748454;
RA Hu P., Elliott J., McCreedy P., Skowronski E., Garnes J.,
RA Kobayashi A., Brubaker R.R., Garcia E.;
RT "Structural organization of virulence-associated plasmids of Yersinia
RT pestis."
RT J. Bacteriol. 180:5192-5202(1998).
DR EMBL: AF053946; AAC62601.1;
DR InterPro: IPR003446; IncePII_repa.
DR Pfam: PF02387; IncePII_repa; 1.
KW Plasmid.
SQ SEQUENCE 292 AA; 33989 MW; 1CE0B2E22C8EC074 CRC64;

Query Match
Best Local Similarity 23.2%; Score 59.5; DB 2; Length 292;
Matches 20; Conservative 6; Mismatches 16; Indels 23; Gaps 3;

QY 3 SHVPM-----TANAF--HGYSYOHDLRAYGFRLVRFVHR-R 39
DB 178 SVEMENQOREKORLRLMDLIAMKAFVRFVRSYOTERKAKSLKARARVDYDTR 237
QY 40 PVES 44
DB 238 RDIEA 242

RESULT 8
007420 PRELIMINARY; PRT; 322 AA.
AC 007420;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
GN HYPOTHETICAL 35.4 KDA PROTEIN.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Dayes R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544(1998).
DR EMBL: 297050; CAB09743.1; -.
DR TubercuList; RV0176; -.

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KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 322 AA; 35437 MW; 1E32C3005970BED5 CRC64;

Query Match
Best Local Similarity 23.0%; Score 59; DB 16; Length 322;
Matches 15; Conservative 1; Mismatches 14; Indels 4; Gaps 1;

QY 8 TAW----AFHGYSYOHDLRAYGFRLVRFVH 37
DB 83 TGMSLGRALTLGRVVRDSDSALGPWRLVRLDLAH 116

RESULT 9
09H495 PRELIMINARY; PRT; 336 AA.
AC 09H495;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE ADIR2.
GN ADIR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Dron M., Merlet J.F., Tovey M.G.;
RT "Characterization of ADIR a novel Interferon responsive gene."
RT Submitted (Oct-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ299441; CAC14461.1; -.
SQ SEQUENCE 336 AA; 38806 MW; 0053B78AF4FE967C CRC64;

Query Match
Best Local Similarity 22.8%; Score 58.5; DB 4; Length 336;
Matches 12; Conservative 5; Mismatches 8; Indels 5; Gaps 1;

QY 6 PWTANAFHGYSYOHDLRAYG-----FWRL 30
DB 36 PGSAMWPGFORLQEOQLRAAGALSKRYWTL 65

RESULT 10
09H497 PRELIMINARY; PRT; 397 AA.
AC 09H497;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ADIR1.
GN ADIR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Dron M., Merlet J.F., Tovey M.G.;
RT "Characterization of ADIR1 a novel Interferon responsive gene."
RT Submitted (Oct-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ299403; CAC13973.1; -.
DR InterPro: IPR001109; HuPF_HypC.
SQ SEQUENCE 397 AA; 46139 MW; 459CD18EA22709FE CRC64;

Query Match
Best Local Similarity 22.8%; Score 58.5; DB 4; Length 397;
Matches 12; Conservative 5; Mismatches 8; Indels 5; Gaps 1;

QY 6 PWTANAFHGYSYOHDLRAYG-----FWRL 30

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Db      36 PGSAMWPGFORLQEQRLAAGALSKRYWTL 65

RESULT 11
O9H6E7 PRELIMINARY; PRT; 397 AA.
AC O9H6E7;
DT 01-MAR-2001 (TEMBLrel. 16, Created)
DT 01-MAR-2001 (TEMBLrel. 16, last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, last annotation update)
DE CDNA: FLJ22345 FIS, CLONE HRC06114 (ATP-DEPENDANT INTERFERON RESPONSE
DE PROTEIN 1).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,
RA Suzuki Y., Ohtsuyoshi M., Nishi T., Shibahara T., Tanaka T.,
RA Nakamura Y., Isigaki T., Sugano S.;
RT "NEO human cDNA sequencing project.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-RHABDOMYOSARCOMA;
RA Strausberg R.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-EYE, RETINOBLASTOMA;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE-MUSCLE, RHABDOMYOSARCOMA;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK025998; BAB15312.1; -.
DR EMBL: BC001085; AAH01085.1; -.
DR EMBL: BC011746; AAH11746.1; -.
DR EMBL: BC007571; AAH07571.1; -.
DR InterPro: IPR001109; HupE_HyPC.
SQ SEQUENCE 397 AA; 46165 MW; 1E131DCCALAA6C31 CRC64;

Query Match 22.8%; Score 58.5; DB 4; Length 397;
Best Local Similarity 40.0%; Pred. No. 11;
Matches 12; Conservative 5; Mismatches 8; Indels 5; Gaps 1;

Qy      6 PMTAMAFHGRSYOHDLRAYG-----FWRL 30
Db      36 PGSAMWPGFORLQEQRLAAGALSKRYWTL 65

RESULT 12
O17732 PRELIMINARY; PRT; 1175 AA.
AC O17732;
DT 01-JAN-1998 (TEMBLrel. 05, Created)
DT 01-JAN-1998 (TEMBLrel. 05, last sequence update)
DT 01-OCT-2001 (TEMBLrel. 18, last annotation update)
DE PYRUVATE CARBOXYLASE.
GN PYC-1 OR D2023.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida; Rhabdilitoidea;
OC Rhabdilitidae; Pelodieridae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Freedman J.H., Liao V.H.-C.;
RT "Characterization of a cadmium-inducible form of pyruvate carboxylase
RT from Caenorhabditis elegansl.";

RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Kershaw J.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF237467; AAF60326.1; -.
DR EMBL: Z81052; CAB02872.1; -.
DR HSSP: P24182; 1BNC.
DR InterPro: IPR000089; Biotin_lipoyl.
DR InterPro: IPR000901; CPSase.
DR InterPro: IPR000891; HMG-Like.
DR InterPro: IPR003379; PYC_OADA.
DR Pfam: PF02785; Biotin_carb_C; 1.
DR Pfam: PF00364; Biotin_lipoyl; 1.
DR Pfam: PF00289; CPSase_L_chain; 1.
DR Pfam: PF02786; CPSase_L_D2; 1.
DR Pfam: PF00682; HMG-Like; 1.
DR Pfam: PF02436; PYC_OADA; 1.
DR PROSITE: PS00867; CPSASE_2; UNKNOWN_1.
SQ SEQUENCE 1175 AA; 129284 MW; DE3D21194C21E6AF CRC64;

Query Match 22.6%; Score 58; DB 5; Length 1175;
Best Local Similarity 43.3%; Pred. No. 42;
Matches 13; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

Qy      16 RSYOHDLRAYGFWRLRYRFRVRRPHVESQ 45
Db      214 RSYSEAQAFFGDSLFVEKFEVERPRHIEVQ 243

RESULT 13
O52218 PRELIMINARY; PRT; 290 AA.
AC O52218;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, last annotation update)
DE REPLICATION-ASSOCIATED PROTEIN.
GN REPA.
OS Klebsiella pneumoniae.
OG Plasmid pIE545.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91177831; Pubmed=1706708;
RA Praszkier J., Wei T., Siemering K., Pittard J.;
RT "Comparative analysis of the replication regions of IncB, IncK, and
RT IncJ plasmids.";
RL J. Bacteriol. 173:2393-2397(1991).
DR EMBL: M93064; AAA98134.1; -.
DR InterPro: IPR003446; IncFII_repa.
DR Pfam: PF02387; IncFII_repa; 1.
KW Plasmid.
SQ SEQUENCE 290 AA; 33143 MW; 58C003F7E84A0571 CRC64;

Query Match 22.2%; Score 57; DB 2; Length 290;
Best Local Similarity 29.6%; Pred. No. 12;
Matches 16; Conservative 5; Mismatches 11; Indels 22; Gaps 2;

Qy      3 SRPWF-----TMAF--HGRSYOHDLRAYGFWRLIVR 34
Db      176 SRVEMENKLRKKGGLDAGMDELIRAMRFVRRFRSYQALKSHGMKRRARR 229

RESULT 14
O9WY09 PRELIMINARY; PRT; 771 AA.
AC O9WY09;
DT 01-NOV-1999 (TEMBLrel. 12, Created)

```

```

DT 01-NOV-1999 (TREMBLrel. 12, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE HYPOTHETICAL 87.5 KDA PROTEIN.
GN TM0162.
OS Thermotoga maritima.
OC Bacteria; Thermotogales; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB8 / DSM 3109;
RX MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwynn M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of Thermotoga maritima.";
RL Nature 399:323-329(1999).
DR EMBL; AE001701; AAD35255.1; -.
DR TIGR; TM0162; -.
DR InterPro: IPR000379; Est_lip_thioest_actsite.
DR Hypothetical protein; Complete proteome.
SQ SEQUENCE 771 AA; 87498 MW; EBB5D3781852A1D CRC64;

```

```

Query Match 22.2%; Score 57; DB 16; Length 771;
Best Local Similarity 36.7%; Pred. No. 36;
Matches 11; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

```

```

QY 15 YNSYQHDLRAYGFWRLLVRRFVRRPHEVSQ 44
DB 268 YSQYEPDILAHGTGLIVLRMLQRHPEVNN 297

```

```

RESULT 15
Q9DDT1 PRELIMINARY; PRT; 1180 AA.
AC Q9DDT1;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DE 01-PEC-2001 (TREMBLrel. 19, last annotation update)
DE PYRUVATE CARBOXYLASE.
GN PC.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21100417; PubMed=11167010;
RA Yoder J.A., Litman G.W.;
RT "The zebrafish fchl, slc3a2, men1, pc, fgf3 and cycd1 genes define two
RT regions of conserved synteny between linkage group 7 and human
RT chromosome 11q13.";
RL Gene 261:235-242(2000).
CC -1 COFACTOR: BIOTIN (BY SIMILARITY).
DR EMBL; AF295372; AAG37836.1; -.
DR HSSP; P24182; 1BNC.
DR InterPro: IPR001882; Biotin.
DR InterPro: IPR000089; Biotin_lipoyl.
DR InterPro: IPR000901; CPSase.
DR InterPro: IPR000891; HMGL-like.
DR InterPro: IPR003379; PYC_OADA.
DR Pfam; PF02785; Biotin_carb_C; 1.
DR Pfam; PF00364; Biotin_lipoyl; 1.
DR Pfam; PF00289; CPSase_L_chain; 1.
DR Pfam; PF02786; CPSase_L_D2; 1.
DR Pfam; PF00682; HMGL-like; 1.
DR Pfam; PF02436; PYC_OADA; 1.
DR PROSITE; PS0188; BIOTIN; 1.

```

```

KW Biotin.
SQ SEQUENCE 1180 AA; 129884 MW; 26118F2691400E24 CRC64;
Query Match 22.2%; Score 57; DB 13; Length 1180;
Best Local Similarity 36.7%; Pred. No. 56;
Matches 11; Conservative 6; Mismatches 13; Indels 0; Gaps 0;
QY 16 RSYQHDLRAYGFWRLLVRRFVRRPHEVSQ 45
DB 221 RAYSEALAFNGALFVEKFIKPRHIEVQ 250

```

```

Search completed: August 15, 2002, 12:05:33
Job time: 373 sec

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Fri Aug 16 10:36:46 2002

Seq. 105 (3-10) + 6 (3-10) + 7 (3-10)
Residue residue residue

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 15, 2002, 11:59:15 ; Search time 51.96 Seconds
(Without alignments)
51.304 Million cell updates/sec

Title: DEVI-613-COMBFrag
Perfect score: 142
Sequence: 1 SRPWTAWYQHDLRAYRRFVHRRP 24

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: A.Geneseq_032802.*
2: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
3: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
4: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
5: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
6: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.*
7: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.*
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20: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	39.4	117	20	AAV45237 Mature KB5-C20 TCR
2	54	38.0	15	20	AAV30351 Eptiotope derived fr
3	53.5	37.7	96	22	AAU0302 Propionibacterium
4	51	35.9	512	22	AB869433 Drosophila melanog
5	51	35.9	833	19	AAW42636 Protein sequence t
6	51	35.9	833	19	AAW42637 Protein sequence t
7	50	35.2	50	13	AAAR21683 HSV-1 VP16 - prote
8	49	34.5	84	22	AAAG77743 Human colon cancer
9	48.5	34.2	63	22	ABG22898 Novel human diagno
10	48.5	34.2	233	22	AAW39708 Human polypeptide
11	48.5	34.2	235	22	AAW41494 Human polypeptide

12	48	33.8	63	22	AAU49192 Propionibacterium
13	48	33.8	150	22	AAU42419 Propionibacterium
14	48	33.8	151	22	AAU41400 Propionibacterium
15	48	33.8	269	19	AAW70262 Amino acid sequenc
16	48	33.8	280	19	AAW86079 S. pneumoniae deri
17	48	33.8	280	19	AAW80697 S. pneumoniae ilic-
18	48	33.8	402	22	AAU45694 Propionibacterium
19	46.5	32.7	155	18	AAW10569 Mablin II prepro
20	46.5	32.7	155	18	AAW10569 Mablin II prepro
21	46	32.4	15	20	AAW30352 Eptiotope derived fr
22	46	32.4	43	20	AAW25799 Human secreted pro
23	46	32.4	62	22	ABG16003 Novel human diagno
24	46	32.4	247	22	AAU50023 Propionibacterium
25	46	32.4	396	20	AAV25793 Human secreted pro
26	46	32.4	460	22	ABG06687 Novel human diagno
27	46	32.4	781	22	ABG14190 Novel human diagno
28	45.5	32.0	282	22	AB866530 Drosophila melanog
29	45.5	32.0	378	22	AB866530 Drosophila melanog
30	45	31.7	15	20	AAV30353 Eptiotope derived fr
31	45	31.7	50	22	AAU42356 Propionibacterium
32	45	31.7	182	21	AAG33129 Zea mays protein f
33	45	31.7	451	16	AAW79909 N. crassa mtr gene
34	45	31.7	470	15	AAW7118 Mtr protein of Neu
35	45	31.7	488	20	AAV05830 Human altered sphl
36	45	31.7	568	20	AAV15211 Sphingosine-1-phos
37	45	31.7	568	20	AAV05827 Human sphingosine-
38	45	31.7	568	22	AAW78461 Human protein SEQ
39	45	31.7	580	22	AAW79445 Human protein SEQ
40	45	31.7	754	21	AAW11529 SEN virus protein
41	44	31.0	62	22	AAW80330 Human haematologic
42	44	31.0	124	22	ABW11127 Human gal-1-P urid
43	44	31.0	158	22	AAU48192 Propionibacterium
44	44	31.0	431	22	ABW11406 Human N-copine hom
45	44	31.0	461	22	AAU35244 Enterococcus faeca

ALIGNMENTS

RESULT 1
AAV45237 standard; peptide: 117 AA.
XX
XX
AC AAV45237:
XX
XX 06-JAN-2000 (first entry)
XX
XX
DE Mature KB5-C20 TCR scfv:Valpha-linker-Vbeta Vbeta peptide.
XX
XX scfv: TCR: V domain: T cell receptor; Immune system; Infection;
KW tumour; Immune response; linker.
XX
XX OS Synthetic.
XX
XX CA2205881-A.
XX
XX 09-JAN-1999.
XX
XX 09-JUL-1997; 97CA-2205881.
XX
XX 09-JUL-1997; 97CA-2205881.
XX
XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX
XX Mazza G, Malissen B, Gregoire C;
XX
XX WPI: 1999-580982/50.
XX
XX New T cell receptor peptides, useful for treating and/or preventing
XX myelomas and bacterial, viral and fungal infections -
XX
XX Example 1; Fig 1B; 84pp; English.
XX

Query Match Similarity	39.48;	Score 56;	DB 20;	Length 117;
Best Local Similarity	57.18;	Pred. No. 1,2;		
Matches	8;	Conservative	3;	Mismatches
				Indels
				Gaps
OY	1	SRVPTAWYQHDLR	14	
	1:	1: 1: 1: 1: 1:		
Db	28	sgypwmswygqdlq	41	

Query Match	38.0%;	Score 54;	DB 20;	Length 15;
Best Local Similarity	81.8%;	Pred. No. 0.26;		
Matches 9;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY 1 SRVPMWAWQH 11				
Db 3 srvpwtawafh 13				
RESULT 3				
AAU40302				
ID AAU40302 standard; Protein: 96 AA.				
XX AAU40302;				
XX AC				
XX DT				
XX 13-FEB-2002 (first entry)				
DE Propionibacterium acnes immunogenic protein #1198.				
XX KW				
XX KW SAPHO syndrome; synovitis; acne; pustulosis; hyperotosis; osteomyelitis;				
XX KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;				
XX KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;				
XX KW dermatological; osteopathic; neuroprotectant.				
XX OS				
OS Propionibacterium acnes.				
PN WO200181581-A2.				
PD 01-NOV-2001.				
XX 20-APR-2001; 2001WO-US12865.				
PF 21-APR-2000; 2000US-199047P.				
PR 02-JUN-2000; 2000US-208841P.				
PR 07-JUL-2000; 2000US-216747P.				
XX (CORI-) CORIXA CORP.				
PA Skelky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;				
XX L'maisonneuve J, Zhang Y, Jen S, Carter D;				
PI WPI: 2001-616774/71.				
DR N-PSDB: AAS59511.				
XX Propionibacterium acnes polypeptides and nucleic acids useful for				
PT vaccinating against and diagnosing infections, especially useful for				
PT treating acne vulgaris -				
XX Example 1; SEQ ID NO 1497; 10699p; English.				
PS Sequences AAU39105-AAU6017 represent Propionibacterium acnes immunogenic				
XX polypeptides. The proteins and their associated DNA sequences are used in				
CC the treatment, prevention and diagnosis of medical conditions caused by				
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,				
CC pustulosis, hyperotosis and osteomyelitis), uveitis and endophthalmitis.				
CC P. acnes is also involved in infections of bone, joints and the central				
CC nervous system, however it is particularly involved in the inflammatory				
CC lesions associated with acne vulgaris. A method for detecting the				
CC presence or absence of P. acnes in a patient compises contacting a				
CC sample with a binding agent that binds to the proteins of the invention				
CC and determining the amount of bound protein in the sample. The				
CC polypeptides may be used as antigens in the production of antibodies				
CC specific for P. acnes proteins. These antibodies can be used to				
CC downregulate expression and activity of P. acnes polypeptides and				
CC therefore treat P. acnes infections. The antibodies may also be used as				
CC diagnostic agents for determining P. acnes presence, for example, by				

CC enzyme linked immunosorbent assay (ELISA).
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.

SQ Sequence 96 AA;

Query Match 37.7%; Score 53.5; DB 22; Length 96;
 Best Local Similarity 46.2%; Pred. No. 2.2;

Matches 12; Conservative 1; Mismatches 10; Indels 3; Gaps 1;

QY 2 RVPTAWYQHDLRAYRRFV---HRRP 24
 | : | | | | | | | | | |
 Db 44 rlprrfwpdhrdrdrdramvaahrp 69

RESULT 4

ABB69433
 ID ABB69433 standard; Protein; 512 AA.

XX ABB69433;

XX 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 35091.

KW Drosophila; developmental biology; cell signalling; insecticide;

KM pharmaceutical.

OS Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US09231.

XX 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

XX (PEKE) PE CORP NY.

PI Venter JC, Adams M, Li PMD, Myers EW;

DR WPI; 2001-656860/75.

DR N-PDB; ABL13536.

XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -

PS Disclosure: SEQ ID NO 35091; 21pp + Sequence Listing: English.

XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABB57737-ABB72072).
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.

XX Sequence 512 AA;

Query Match 35.9%; Score 51; DB 22; Length 512;
 Best Local Similarity 50.0%; Pred. No. 29;
 Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 7 AMYQHDLRAYRRFVHRP 24
 : : | | | | | : : | |
 Db 340 syfhdlnrlyertlsqr 357

RESULT 5

AAW42636
 ID AAW42636 standard; Protein; 833 AA.

XX AAW42636;

XX 22-OCT-1998 (first entry)

DE Protein sequence that is specific for Neisseria meningitidis.

KW N. gonorrhoeae; N. lactamica; chromosome 22491; region 1; region 2;

KM region 3; pathogenicity; blood-brain barrier; diagnosis; infection;

XX meningitis.

XX Neisseria meningitidis.

XX WO9802547-A2.

XX 22-JAN-1998.

XX 11-JUL-1997; 97WO-FR01295.

XX 12-JUL-1996; 96FR-0008768.

XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

XX (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

XX (SMIK) SMITHKLINE BEECHAM.

XX Nassif X, Tinsley C, Achtman M, Werker P, Ruelle J;

XX Vinals C;

XX WPI; 1998-110594/10.

XX N-PDB; AAV03553.

XX Genes present in Neisseria meningitidis but not other Neisseria

XX species - and related host cells, RNA, anti-sense sequences,

XX polypeptide(s) and antibodies, useful for diagnosing Neisseria

XX meningitidis infection and in protective vaccines

XX Claim 8; Pages 91-95; 150pp; French.

XX AAW42633-37 and AAW42639-41 are encoded by a DNA sequence found in region

XX 2 of Neisseria meningitidis. The specification describes DNA sequences

XX that are found in N. meningitidis, but not in N. gonorrhoeae or

XX N. lactamica, except for the genes involved in biosynthesis of the

XX capsule polysaccharide, frpA or C, opc, porA, rotamase, sequence IC1106,

XX IGA protease, pillin, pilC, proteins which bind transferrin and opacity

XX proteins. The DNA sequences are found on chromosome 22491, mainly (or

XX within 20 kb) between tufa and pilT (region 1), pilQ and lambda-740

XX (region 2) or argF and opaB (region 3). The DNA sequences are

XX responsible for the differences in pathogenicity between N. meningitidis

XX and N. gonorrhoeae, specifically they include the genes that allow

XX N. meningitidis to cross the blood-brain barrier. DNA sequences common

XX to N. meningitidis and N. gonorrhoeae, but absent from N. lactamica, are

XX responsible for colonisation and penetration of the mucosa. The DNA

XX sequences can be used to produce probes and primers, and antibodies

XX produced against the encoded proteins are used in standard

XX hybridisation/immunoassay processes for diagnosis of N. meningitidis

XX infection, particularly meningitis.

SQ Sequence 833 AA;

Query Match 35.9%; Score 51; DB 19; Length 833;
 Best Local Similarity 33.3%; Pred. No. 48;
 Matches 7; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 2 RVPTAWYQHDLRAYRRFVHR 22

KW colorectal carcinoma.
 XX
 OS Homo sapiens.
 XX
 PN WO200122920-A2.
 XX
 PD 05-APR-2001.
 XX
 PF 28-SEP-2000; 2000MO-US26524.
 XX
 PR 29-SEP-1999; 99US-0157137.
 PR 03-NOV-1999; 99US-0163280.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Barash SC, Birse CE, Rosen CA.
 XX
 DR WPI; 2001-235357/24.
 DR N-PSDB; AAH37150.
 XX
 PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
 useful for preventing, diagnosing and/or treating colorectal cancers -
 XX
 PS Claim 11: Page 9762-9763; 9803pp: English.
 XX
 CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where
 CC the proteins are collectively known as colon cancer antigens. The colon
 CC cancer antigens have cytostatic activity and can be used in gene
 CC therapy and vaccine production. N and P may be used in the prevention,
 CC diagnosis and treatment of diseases associated with inappropriate P
 CC expression. For example, N and P may be used to treat disorders
 CC associated with decreased expression by rectifying mutations or deletions
 CC in a patient's genome that affect the activity of P by expressing P.
 CC Inactive proteins or to supplement the patient's own production of P.
 CC Additionally, N may be used to produce the colon cancer-associated P,
 CC by inserting the nucleic acids into a host cell and culturing the cell
 CC to express the proteins. N and P can be used in the prevention, diagnosis
 CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
 CC and AAB77789 represent sequences used in the exemplification of the
 CC present invention.
 CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
 CC missing at time of publication, meaning no sequences are present for
 CC SEQ ID NO:1027 to 1052, 7921 and 7922.
 XX
 SO Sequence 84 AA;
 XX
 Query Match 34.5%; Score 49; DB 22; Length 84;
 Best Local Similarity 63.6%; Pred. No. 8.4;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 4 PWTAWYOHDLR 14
 | | | | | | : : |
 Db 63 pwtawxxhnr 73
 XX
 RESULT 9
 ABG22898
 ID ABG22898 standard; Protein; 63 AA.
 XX
 AC ABG22898;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #22889.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.

XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001MO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR N-PSDB; AAS87085.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 PS Claim 20: SEQ ID NO 53257; 103pp: English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
 XX
 SO Sequence 63 AA;
 XX
 Query Match 34.2%; Score 48.5; DB 22; Length 63;
 Best Local Similarity 45.8%; Pred. No. 7.4;
 Matches 11; Conservative 1; Mismatches 9; Indels 3; Gaps 1;
 QY 1 SRVPWTAWYOHDLRAVRRFVHRRP 24
 | | | | | | | | | | | |
 Db 25 srpwwksvtrprdrgrar---trp 45
 XX
 RESULT 10
 AAM39708
 ID AAM39708 standard; Protein; 233 AA.
 XX
 AC AAM39708;
 XX
 DT 22-OCT-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 2853.
 XX
 KW Human; neotropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.
 XX

OS	Homo sapiens.
XX	
PN	W020015312-A1.
XX	
PD	26-JUL-2001.
XX	
PE	26-DEC-2000; 2000WO-US34263.
XX	
PR	21-JAN-2000; 2000US-0486725.
PR	25-APR-2000; 2000US-0552317.
PR	09-JUL-2000; 2000US-0598042.
PR	19-JUL-2000; 2000US-0620312.
PR	03-AUG-2000; 2000US-0653450.
PR	14-SEP-2000; 2000US-0662191.
PR	19-OCT-2000; 2000US-0693036.
PR	29-NOV-2000; 2000US-0727344.
XX	
PA	(HYSEQ-) HYSEQ INC.
XX	
PI	Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI	Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI	Zhao QH, Zhou P, Goodrich R, Dirmacac RT;
XX	
DR	WPI: 2001-442253/47.
DR	N-PSDB: AAI38864.
XX	
PT	Novel nucleic acids and polypeptides, useful for treating disorders
PT	such as central nervous system injuries -
XX	
PS	Example 4; SEQ ID NO 2853; 10078bp; English.
XX	
CC	The invention relates to human nucleic acids (AA157798-AA161369) and
CC	the encoded polypeptides (AA38642-AA42213) with nootropic,
CC	immunosuppressant and cytostatic activity. The polynucleotides are useful
CC	in gene therapy. A composition containing a polypeptide or polynucleotide
CC	of the invention may be used to treat diseases of the peripheral nervous
CC	system, such as peripheral nervous injuries, peripheral neuropathy and
CC	localised neuropathies and central nervous system diseases, such as
CC	Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC	lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC	utilisation of the activities such as: Immune system suppression,
CC	Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC	and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC	assays for receptor activity, arthritis and inflammation, leukaemias and
CC	C.N.S disorders.
CC	Note: The sequence data for this patent did not form part of the printed
CC	specification.
XX	
SO	Sequence 233 AA;
XX	
Query Match	34.2%; Score 48.5; DB 22; Length 233;
Best Local Similarity	50.0%; Pred. No. 29;
Matches 9; Conservative	1; Mismatches 7; Indels 1; Gaps 1
QY	4 PWTANYQHDRAYYRRFVH 21
	:
Db	120 pwlwvysr-yrwregvnh 136
XX	
RESULT 11	
AAM41494	
ID	AAM41494 standard; Protein; 235 AA.
XX	
AC	AAM41494;
XX	
DT	22-OCT-2001 (first entry)
XX	
DE	Human polypeptide SEQ ID NO 6425.
XX	
KW	Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW	peripheral nervous system; neuropathy; central nervous system; CNS;
KW	Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;

KM	amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW	chemokine; chemokine; chemokine; drug screening; arthritis; inflammation;
KX	leukemia.
XX	
OS	Homo sapiens.
XX	
PN	W020015312-AL.
XX	
PD	26-JUL-2001.
XX	
PF	26-DEC-2000; 2000MO-US34263.
XX	
PR	21-JAN-2000; 2000US-0488725.
PR	25-APR-2000; 2000US-0552317.
PR	09-JUL-2000; 2000US-0598042.
PR	19-JUL-2000; 2000US-0620312.
PR	03-AUG-2000; 2000US-0653450.
PR	14-SEP-2000; 2000US-0662191.
PR	19-OCT-2000; 2000US-0693036.
PR	29-NOV-2000; 2000US-0727344.
XX	
PA	(HYSE-) HYSEQ. INC.
XX	
PI	Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI	Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI	Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX	
DR	WPI: 2001-442253/47.
DR	N-PSDB: AA60650.
XX	
PT	Novel nucleic acids and polypeptides, useful for treating disorders
PT	such as central nervous system injuries -
XX	
XX	Example 2: SEQ ID NO 6425; 10078pp; English.
XX	
CC	The invention relates to human nucleic acids (AA157798-AA161369) and
CC	the encoded polypeptides (AA136642-AA142213) with nootropic,
CC	immunosuppressant and cytostatic activity. The polynucleotides are useful
CC	in gene therapy. A composition containing a polypeptide or polynucleotide
CC	system, such as peripheral nervous injuries, peripheral neuropathy and
CC	localised neuropathies and central nervous system diseases, such as
CC	Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC	lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC	utilisation of the activities such as: immune system suppression,
CC	Activin/inhibin activity, chemotactic/chemokine activity, haemostatic
CC	and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC	assays for receptor activity, arthritis and inflammation, leukaemia and
CC	C.N.S disorders.
CC	Note: The sequence data for this patent did not form part of the printed
CC	specification.
XX	
XX	Sequence 235 AA:
QY	4 PWTAWYQHDRLAYRRFVH 21
DB	122 pWLVWysr-yrwregvh 138
XX	
XX	Query Match 34.2%; Score 48.5; DB 22; Length 235;
XX	Best Local Similarity 50.0%; Pred. No. 29;
XX	Matches 9; Conservative 1; Mismatches 7; Indels 1; Gaps 1
XX	
XX	RESULT 12
XX	AAU49192
XX	AAU49192 standard; Protein; 63 AA.
XX	AAU49192;
XX	
XX	27-FEB-2002 (first entry)
XX	Propionibacterium acnes immunogenic protein #10088.

```

XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KM uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KM inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KM dermatological; osteopathic; neuroprotectant.
XX
OS Propionibacterium acnes.
XX
PN W0200181581-A2.
XX
PD 01-NOV-2001.
XX
PF 20-APR-2001; 2001MO-US12865.
XX
PR 21-APR-2000; 2000US-199047P.
PR 02-JUN-2000; 2000US-208841P.
PR 07-JUL-2000; 2000US-216747P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX
DR WPI; 2001-616774/71.
DR N-PSDB; AAS59545.
XX
PT Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris -
XX
PS Example 1; SEQ ID No 10387; 10699p; English.
XX
CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA).
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_sequences.
XX
SQ Sequence 63 AA;

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Query Match 33.8%; Score 48; DB 22; Length 63;

Best Local Similarity 50.0%; Pred. No. 8.7; Mismatches 8; Indels 0; Gaps 0;

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Qy 2 RVPTAWYQHDLRAYRRFVH 21
   1 1 1 1 1 1 1 1 1 1 1
Db 24 rwpgtahwchrrcrrfrffh 43

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RESULT 13

AAU42419 standard; Protein: 150 AA.

AAU42419;

27-FEB-2002 (first entry)

DT XX

```

DE Propionibacterium acnes immunogenic protein #3315.
XX
KM SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KM uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KM inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KM dermatological; osteopathic; neuroprotectant.
XX
OS Propionibacterium acnes.
XX
PN W0200181581-A2.
XX
PD 01-NOV-2001.
XX
PF 20-APR-2001; 2001MO-US12865.
XX
PR 21-APR-2000; 2000US-199047P.
PR 02-JUN-2000; 2000US-208841P.
PR 07-JUL-2000; 2000US-216747P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX
DR WPI; 2001-616774/71.
DR N-PSDB; AAS59517.
XX
PT Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris -
XX
PS Example 1; SEQ ID No 3614; 10699p; English.
XX
CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA).
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_sequences.
XX
SQ Sequence 150 AA;

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Query Match 33.8%; Score 48; DB 22; Length 150;

Best Local Similarity 50.0%; Pred. No. 22; Mismatches 10; Indels 0; Gaps 0;

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Qy 3 VPWTAWYQHDLRAYRRFVHRP 24
   1 1 1 1 1 1 1 1 1 1 1
Db 30 vpggstaahdirlyfldvthnp 51

```

RESULT 14

AAU41400 standard; Protein: 151 AA.

AAU41400;

13-FEB-2002 (first entry)

DT XX

```

XX DE Propionibacterium acnes immunogenic protein #2296.
XX KW SAPHO syndrome; synovitis; acne; pustulosis; hyperostosis; osteomyelitis;
XX KW uveitis; endophthalmitis; bone joint; central nervous system; ELISA;
XX KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
XX KW dermatological; osteopathic; neuroprotectant.
XX OS Propionibacterium acnes.
XX PN WO200181581-A2.
XX PD 01-NOV-2001.
XX PF 20-APR-2001; 2001WO-US12865.
XX PR 21-APR-2000; 2000US-199047P.
XX PR 02-JUN-2000; 2000US-208841P.
XX PR 07-JUL-2000; 2000US-216747P.
XX PA (CORI-) CORIXA CORP.
XX PI Skeiky YAM, Persing DH, Mitcham JL, Wang SS, Bhatia A;
XX PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX DR WPI: 2001-616774/71.
XX DR N-PSDB: AAS59515.
XX PT Propionibacterium acnes polypeptides and nucleic acids useful for
XX PT vaccinating against and diagnosing infections, especially useful for
XX PT treating acne vulgaris -
XX PS Example 1; SEQ ID NO 2595; 1069pp; English.
XX SS
XX CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
XX CC polypeptides. The proteins and their associated DNA sequences are used in
XX CC the treatment, prevention and diagnosis of medical conditions caused by
XX CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
XX CC pustulosis, hyperostosis and osteomyelitis), uveitis and endophthalmitis.
XX CC P. acnes is also involved in infections of bone, joints and the central
XX CC nervous system, however it is particularly involved in the inflammatory
XX CC lesions associated with acne vulgaris. A method for detecting the
XX CC presence or absence of P. acnes in a patient comprises contacting a
XX CC sample with a binding agent that binds to the proteins of the invention
XX CC and determining the amount of bound protein in the sample. The
XX CC polypeptides may be used as antigens in the production of antibodies
XX CC specific for P. acnes proteins. These antibodies can be used to
XX CC downregulate expression and activity of P. acnes polypeptides and
XX CC therefore treat P. acnes infections. The antibodies may also be used as
XX CC diagnostic agents for determining P. acnes presence, for example, by
XX CC enzyme linked immunosorbent assay (ELISA).
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 151 AA:

Query Match 33.8%; Score 48; DB 22; Length 151;
Best Local Similarity 37.0%; Pred. No. 22;
Matches 10; Conservative 5; Mismatches 8; Indels 4; Gaps 1;

QY 2 RVPWTAWTQ---HDLRAYRFVHRP 24
| | | | | | | | | | | | | | |
| | | | | | | | | | | | | | |
Db 59 rpfqgwhvgsprdrprsrhrhrcp 85

RESULT 15
AAW70262
ID AAW70262 standard; Protein; 269 AA.
XX AC AAW70262;
XX

```

```

DT 20-NOV-1998 (first entry)
XX DE Amino acid sequence of Streptococcus pneumoniae l1cd2 protein.
XX KW l1cd2 gene; antagonist; inhibition; antibody; T cell; immune response;
XX KW vaccination; otitis media; conjunctivitis; pneumonia; bacteraemia;
XX KW pleural empyaema; meningitis; sinusitis; endocarditis.
XX OS Streptococcus pneumoniae.
XX PN EP861889-A1.
XX PD 02-SEP-1998.
XX PF 27-FEB-1998; 98EP-0301446.
XX PR 28-FEB-1997; 97US-0039225.
XX PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX PI Lonetto MA;
XX DR WPI: 1998-449106/39.
XX DR N-PSDB: AAV33008.
XX PT New DNA encoding Streptococcus pneumoniae l1cd2 polypeptides - used
XX PT to treat, prevent, diagnose and vaccinate against e.g. otitis media,
XX PT conjunctivitis, pneumonia, bacteraemia, meningitis, sinusitis,
XX PT pleural empyaema and endocarditis
XX PS Claim 1; Page 5; 29pp; English.
XX SS
XX CC This is the amino acid sequence of the Streptococcus pneumoniae l1cd2
XX CC protein, a choline kinase used in the method of an individual in need of
XX CC l1cd2 polypeptide is used for the treatment of an individual in need of
XX CC l1cd2 protein and the antagonist is used for the treatment of an
XX CC individual with the need to inhibit l1cd2 polypeptide. Inducing an
XX CC immunological response in a mammal comprises inoculating the mammal with
XX CC the l1cd2 polypeptide to produce antibody and/or T cell immune responses.
XX CC l1cd2 is used to prevent, treat, diagnose and vaccinate against e.g.
XX CC otitis media, conjunctivitis, pneumonia, bacteraemia, pleural empyaema,
XX CC meningitis, sinusitis and endocarditis.
XX SQ Sequence 269 AA:

Query Match 33.8%; Score 48; DB 19; Length 269;
Best Local Similarity 54.5%; Pred. No. 40;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 8 WYQHDLAYRR 18
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| | | | | | | | | | | | | | |
Db 258 wyshtskayrk 268

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Search completed: August 15, 2002, 11:59:16
Job time: 531 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 11:59:42 ; Search time 20.64 Seconds
(Without alignments)
28.402 Million cell updates/sec

Title: DEVI-613-COMBFRAG
Perfect score: 142
Sequence: 1 SRVPTAMVQHDLRAYRFRVHRRP 24

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
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4: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46.5	32.7	155	2	US-08-670-186-2
2	45	31.7	451	1	US-08-191-337-3
3	45	31.7	568	4	US-09-238-373-2
4	44	31.0	669	2	US-07-861-800-2
5	44	31.0	2465	2	US-08-596-291-3
6	44	31.0	2465	3	US-09-100-804-3
7	44	31.0	2466	3	US-09-080-855-12
8	44	31.0	2466	5	PCT-US94-09943-2
9	44	31.0	2485	2	US-09-290-640-46
10	43	30.3	310	2	US-08-640-765A-1
11	43	30.3	310	4	US-09-073-613-1
12	43	30.3	1257	1	US-08-340-428B-49
13	43	30.3	1312	4	US-08-989-299-8
14	42	29.6	17	1	US-08-465-391A-387
15	42	29.6	17	2	US-08-464-538B-384
16	42	29.6	17	2	US-08-463-076E-378
17	42	29.6	770	1	US-08-369-796-12
18	42	29.6	770	1	US-08-416-581B-1
19	42	29.6	770	1	US-08-416-581B-5
20	42	29.6	770	1	US-08-416-581B-9
21	42	29.6	770	2	US-08-852-091-12
22	42	29.6	770	2	US-08-820-754-12
23	42	29.6	770	3	US-08-956-652-12
24	42	29.6	770	3	US-08-956-869-12
25	42	29.6	770	3	US-09-012-710-8
26	42	29.6	770	3	US-08-948-547-12
27	42	29.6	770	4	US-09-087-465-6

28	42	29.6	770	4	US-09-364-970-3	Sequence 3, Appl1
29	42	29.6	770	4	US-09-364-970-5	Sequence 5, Appl1
30	42	29.6	770	4	US-09-556-273-8	Sequence 8, Appl1
31	42	29.6	770	4	US-08-956-653A-12	Sequence 12, Appl1
32	42	29.6	770	5	PCT-US95-17025-12	Sequence 12, Appl1
33	42	29.6	771	1	US-08-276-099A-14	Sequence 14, Appl1
34	42	29.6	771	1	US-08-781-890-14	Sequence 14, Appl1
35	42	29.6	1310	4	US-08-989-299-10	Sequence 10, Appl1
36	41	28.9	67	2	US-08-248-839C-100	Sequence 100, App
37	41	28.9	781	1	US-08-280-690-2	Sequence 2, Appl1
38	41	28.9	2409	6	5180808-2	Sequence 2, Appl1
39	40.5	28.5	471	4	US-09-160-494-6	Sequence 6, Appl1
40	40	28.2	148	2	US-09-193-877-1	Sequence 1, Appl1
41	40	28.2	260	2	US-09-193-877-3	Sequence 3, Appl1
42	40	28.2	294	1	US-08-325-562-2	Sequence 2, Appl1
43	40	28.2	294	1	US-08-437-795-2	Sequence 2, Appl1
44	40	28.2	318	4	US-09-199-637A-23	Sequence 23, Appl1
45	40	28.2	471	4	US-09-071-709-4	Sequence 4, Appl1

ALIGNMENTS

```
RESULT 1
US-08-670-186-2
: Sequence 2, Application US/08670186
: Patent No. 5859343
GENERAL INFORMATION:
APPLICANT: SUN, SAMUEL S. M.
APPLICANT: XIONG, LIMIN
APPLICANT: HU, ZHONG
APPLICANT: CHEN, HANG
TITLE OF INVENTION: RECOMBINANT SWEET PROTEIN MABINLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESS: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVE NW, STE. 5500
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/670,186
FILING DATE: 21-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MORASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 23461-20007.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 822-0168
TELEX: 90-4030 MRSNROERSM
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 155 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-670-186-2

Query Match 32.7%; Score 46.5; DB 2; Length 155;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 10; Conservative 2; Mismatches 2; Indels 1; Gaps 1;
QY 10 QHD-LRAYRFRVHRR 23
|| ||| :||:||||
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Db 46 QH0RLAC0PFIHRR 60

RESULT 2

US-08-191-337-3

; Sequence 3, Application US/08191337
; Patent No. 5643745

; GENERAL INFORMATION:

; APPLICANT: STUART, W. DORSEY

; TITLE OF INVENTION: HETEROLOGOUS DIMERIC PROTEINS PRODUCED

; TITLE OF INVENTION: IN HETEROKARYONS

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORRISON & FOERSTER

; STREET: 2000 Pennsylvania Ave. N.W.

; CITY: Washington, D.C.

; COUNTRY: USA

; ZIP: 20006-1812

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/191,337

; FILING DATE: 03-FEB-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: MURASHIGE, KATE H.

; REGISTRATION NUMBER: 29,959

; REFERENCE/DOCKET NUMBER: 3918-0002.00

; TELEPHONE: (202) 887-1500

; TELEFAX: (202) 887-0763

; TELEX: 90-4030

; INFORMATION FOR SEQ. ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 451 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-191-337-3

Query Match

Best Local Similarity 31.7%; Score 45; DB 1; Length 451;

Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 3 VPTWTAYQHDLRAYRRFV 20

Db 227 VPMSCWPKEDLSIAEGFI 244

RESULT 3

US-09-238-373-2

; Sequence 2, Application US/09238373A
; Patent No. 6187562

; GENERAL INFORMATION:

; APPLICANT: DUCKWORTH, DAVID MALCOLM

; APPLICANT: GODDEN, ROBERT JAMES

; APPLICANT: TESTA, TANIA TAMSON

; TITLE OF INVENTION: NOVEL COMPOUNDS

; FILE REFERENCE: GP-30034

; CURRENT APPLICATION NUMBER: US/09/238,373A

; CURRENT FILING DATE: 1999-01-27

; EARLIER FILING DATE: 1998-11-03 9824026.0

; EARLIER APPLICATION NUMBER: EP 98300625.5

; EARLIER FILING DATE: 1998-01-29

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 568

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-238-373-2

Query Match

Best Local Similarity 31.7%; Score 45; DB 4; Length 568;

Matches 10; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2 RVPWTAYQHDLRAYRRFVR 22

Db 258 RVPITKMEVDYRAMRAISR 278

RESULT 4

US-07-861-800-2

; Sequence 2, Application US/07861800
; Patent No. 5925515

; GENERAL INFORMATION:

; APPLICANT: VAN HARTINGSVELDT, WILLEM

; APPLICANT: VAN GORCOM, ROBERT

; APPLICANT: GOUKA, R. J.

; TITLE OF INVENTION: Transformant Selection Marker System

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORRISON & FOERSTER

; STREET: 755 Page Mill Road

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94304-1018

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy Disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/861,800

; FILING DATE: 19920611

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: MURASHIGE, KATE H.

; REGISTRATION NUMBER: 29,959

; REFERENCE/DOCKET NUMBER: 44615-20018.20

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 813-5600

; TELEFAX: (415) 494-0792

; TELEX: 706141

; INFORMATION FOR SEQ. ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 669 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-07-861-800-2

Query Match

Best Local Similarity 31.0%; Score 44; DB 2; Length 669;

Matches 7; Conservative 6; Mismatches 7; Indels 4; Gaps 1;

QY 1 SRVPWTA---WYQHDLRAYRRFV 20

Db 243 AEVPMTAGRDIMWHEVEYKPNYL 266

RESULT 5

US-08-596-291-3

; Sequence 3, Application US/08596291
; Patent No. 5821075

; GENERAL INFORMATION:

; APPLICANT: GONZALEZ, LEONEL JORGE

; APPLICANT: SARAS, JAN

```

: APPLICANT: CLAESSON-WELSH, LENA
: APPLICANT: HEIDIN, CARL-HENRIK
: TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
: TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
: TITLE OF INVENTION: TYROSINE PHOSPHATASES
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
: STREET: 600 ATLANTIC AVENUE
: CITY: BOSTON
: STATE: MASSACHUSETTS
: COUNTRY: USA
: ZIP: 02210
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/596,291
: FILING DATE: 09-AUG-1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/115,573
: FILING DATE: 01-SEP-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: GATES, EDWARD R.
: REGISTRATION NUMBER: 31,616
: REFERENCE/DOCKET NUMBER: L0461/7000
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617/720-3500
: TELEFAX: 617/720-2441
: TELEX: 92-11742 EZEKIEL
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2465 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-596-291-3

Query Match          31.0%; Score 44; DB 2; Length 2465;
Best Local Similarity 31.2%; Pred. No. 5.6e+02;
Matches 10; Conservative 4; Mismatches 8; Indels 10; Gaps 1;

QY 1 SRVPTAWYQHD-----LRAYRRFVHR 22
Db 2349 SHLNFTAMPDHDPSPDDLLTFISYMRHHR 2380

RESULT 6
US-09-100-804-3
: Sequence 3, Application US/09100804
: Patent No. 6066472
: GENERAL INFORMATION:
: APPLICANT: GONZ, LEONEL JORGE
: APPLICANT: SARAS, JAN
: APPLICANT: CLAESSON-WELSH, LENA
: APPLICANT: HEIDIN, CARL-HENRIK
: TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
: TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
: TITLE OF INVENTION: TYROSINE PHOSPHATASES
: NUMBER OF SEQUENCES: 34
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
: STREET: 600 ATLANTIC AVENUE
: CITY: BOSTON
: STATE: MASSACHUSETTS
: COUNTRY: USA
: ZIP: 02210
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
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: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/100,804
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/596,291
: FILING DATE: 09-AUG-1996
: APPLICATION NUMBER: US 08/115,573
: FILING DATE: 01-SEP-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/09943
: FILING DATE: 01-SEP-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: GATES, EDWARD R.
: REGISTRATION NUMBER: 31,616
: REFERENCE/DOCKET NUMBER: L0461/7003
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-720-3500
: TELEFAX: 617-720-2441
: TELEX:
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2465 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-09-100-804-3
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```

Query Match          31.0%; Score 44; DB 3; Length 2465;
Best Local Similarity 31.2%; Pred. No. 5.6e+02;
Matches 10; Conservative 4; Mismatches 8; Indels 10; Gaps 1;

QY 1 SRVPTAWYQHD-----LRAYRRFVHR 22
Db 2349 SHLNFTAMPDHDPSPDDLLTFISYMRHHR 2380
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RESULT 7
US-09-080-855-12
: Sequence 12, Application US/09080855A
: Patent No. 6083721
: GENERAL INFORMATION:
: APPLICANT: Saras, Jan
: APPLICANT: Franz, Petra
: APPLICANT: Aspenstrm, Pontus
: APPLICANT: Hellman, Ulf
: APPLICANT: Gopez, Leonel Jorge
: APPLICANT: Heidlin, Carl-Henrik
: TITLE OF INVENTION: PARC, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PPP1
: FILE REFERENCE: L0461/7030
: CURRENT APPLICATION NUMBER: US/09/080,855A
: CURRENT FILING DATE: 1998-05-18
: EARLIER APPLICATION NUMBER: 08/805,583
: EARLIER FILING DATE: 1997-02-25
: NUMBER OF SEQ ID NOS: 39
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 12
: LENGTH: 2466
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-080-855-12
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```

Query Match          31.0%; Score 44; DB 3; Length 2466;
Best Local Similarity 31.2%; Pred. No. 5.6e+02;
Matches 10; Conservative 4; Mismatches 8; Indels 10; Gaps 1;

QY 1 SRVPTAWYQHD-----LRAYRRFVHR 22
Db 2349 SHLNFTAMPDHDPSPDDLLTFISYMRHHR 2380
```



```

; GENERAL INFORMATION:
; APPLICANT: Tanuma, Sei-ichi
; TITLE OF INVENTION: ANTIBODY TO NOVEL DEOXYRIBONUCLEASE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voigt & Mayer
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073,613
; FILING DATE: 06-MAY-1998
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/640,765
; FILING DATE:
; APPLICATION NUMBER: JP 6239518
; FILING DATE: 06-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LARCHER, Carol
; REGISTRATION NUMBER: 35243
; REFERENCE/DOCKET NUMBER: 85519
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-073-613-1

Query Match      30.3%; Score 43; DB 4; Length 310;
Best Local Similarity 35.7%; Pred. No. 98;
Matches 10; Conservative 3; Mismatches 11; Indels 4; Gaps 1;

QY      1 SRVPTAWIOHDIRAYRREV----HRRP 24
DB      136 SREPFVWFQAPFTAKDFIVPLHTTP 163

RESULT 12
US-08-340-428B-49
; Sequence 49, Application US/08340428B
; Patent No. 5648465
; GENERAL INFORMATION:
; APPLICANT: MARGOLIS, Richard U.
; APPLICANT: RACH, Uwe
; APPLICANT: MARGOLIS, Renee K.
; TITLE OF INVENTION: CLONING, EXPRESSION AND USES FOR A
; TITLE OF INVENTION: CLEONOCAN AS A CHONDROITIN SULFATE PROTEOGLYCAN
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,428B
; FILING DATE: 14 NO. 5648465ember 1994
; CLASSIFICATION: 514
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 07/922,911
; FILING DATE: 03 August 1992
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: Margolis-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1257 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-340-428B-49

Query Match      30.3%; Score 43; DB 1; Length 1257;
Best Local Similarity 43.8%; Pred. No. 4e+02;
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY      8 WYOHDLRAYRFFVHRR 23
DB      1033 WHKFGCHCYRFPARR 1048

RESULT 13
US-08-989-299-8
; Sequence 8, Application US/08989299
; Patent No. 6194556
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Robinson, Keith E.
; TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
; TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,299
; FILING DATE: 11-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold E., Beth
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MIA-025.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1312 amino acids
; TYPE: amino acid
; STRANDEDNESS:

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Job time: 248 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 12:00:14 ; Search time 25.35 seconds
(without alignments)
90.972 Million cell updates/sec

Title: DEVI-613-COMBIFRAG
Perfect score: 142
Sequence: 1 SRVPTAWYQHDLRATRYRFRVRRP 24

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	39.4	133	2 C31211	T-cell receptor be
2	56	39.4	134	2 A49035	T-cell receptor be
3	56	39.4	135	2 B28823	T-cell receptor be
4	56	39.4	136	1 RWMSEI	T-cell receptor be
5	56	39.4	137	2 I71937	MHC class II I-A-B
6	54	38.0	345	2 T35357	hypothetical prote
7	52.5	37.0	267	2 S52347	hypothetical prote
8	52	36.6	85	2 JH0346	T-cell receptor be
9	51	35.9	389	2 H70841	probable amna prot
10	51	35.9	454	2 T26654	hypothetical prote
11	51	35.9	833	2 F81989	hypothetical prote
12	49.5	34.9	170	2 A12961	conserved hypotet
13	49.5	34.9	175	2 E98321	hypothetical prote
14	49	34.5	417	2 T33376	hypothetical prote
15	48.5	34.2	434	2 B69271	hypothetical prote
16	48.5	34.2	506	2 A81191	hypothetical prote
17	48	33.8	269	2 A95148	l1cd2 protein (imp
18	48	33.8	269	2 G98015	l1cd2 protein (imp
19	48	33.8	295	2 F70936	hypothetical prote
20	47	33.1	200	2 T34654	probable transmem
21	46.5	32.7	33	2 S28842	madulin II chain
22	46.5	32.7	135	2 JC5379	madulin II chain
23	46.5	32.7	1186	2 T03180	tyrosine protein k
24	46	32.4	461	2 A10279	hypothetical prote
25	45.5	32.0	382	2 E83322	probable PAD-depen
26	45.5	32.0	2290	1 GNNYE	genome polyprotein
27	45.5	32.0	2292	2 S35961	capsid polyprotein
28	45	31.7	253	2 A75252	conserved hypotet
29	45	31.7	302	2 AH2196	hypothetical prote

30	45	31.7	416	2 D83386	hypothetical prote
31	45	31.7	470	2 S47892	neutral amino acid
32	45	31.7	663	2 H82731	glutaryl-7-ACA acy
33	45	31.7	790	2 T34293	hypothetical prote
34	45	31.7	1776	2 G86280	protein T5E21.13 (
35	44.5	31.3	405	2 S61551	breast-regressing
36	44	31.0	62	2 S72792	hypothetical prote
37	44	31.0	125	2 F71276	holo-[acyl-carrier
38	44	31.0	209	2 A39759	photosystem I 18k
39	44	31.0	216	2 S31551	photosystem I chal
40	44	31.0	244	2 S50685	hypothetical prote
41	44	31.0	309	2 F83605	probable permease
42	44	31.0	314	2 B98232	probable 2-hydroxy
43	44	31.0	327	2 AC3054	2-hydroxyacid deny
44	44	31.0	354	2 S15660	(2'-5')oligo(A) sy
45	44	31.0	476	2 T43464	hypothetical prote

ALIGNMENTS

RESULT 1
C31211
T-cell receptor beta chain precursor V region (V2-D1.1-J1.2) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 23-Jul-1999
C:Accession: C31211
R:Malissen, M.; Trucy, J.; Letourneur, F.; Rebbi, N.; Dunn, D.E.; Fitch, F.W.; Hood,
Cell 55, 49-59, 1988
A>Title: A T cell clone expresses two T cell receptor alpha genes but uses one alpha-
A:Reference number: A94656; MUID:89003051
A:Accession: C31211
A:Molecule type: DNA
A:Residues: 1-133 <MAL>
A:Cross-references: GB:M22605; NID:q340718; PIDN:AAA63778.1; PID:q710557
C:Genetics:
A:Insertions: 19/1
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 39.4%; Score 56; DB 2; Length 133;
Best Local Similarity 57.1%; Pred. No. 0.9;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 SRVPTAWYQHDLR 14
DB 49 SQYPTAWYQDDIQ 62

RESULT 2
A49035
T-cell receptor beta chain variable region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 19-Dec-1993 #sequence_revision 25-Apr-1997 #text_change 23-Jul-1999
C:Accession: A49035
R:Iglesiass, A.; Hansen-Hagge, T.; Von Bonin, A.; Wetzien, H.U.
Eur J Immunol. 22, 335-341, 1992
A>Title: Increased frequency of 2,4,6-trinitrophenyl (TNP)-specific, H-2b-restricted
tri-allelic, TNP-specific cytolytic T cell clone.
A:Reference number: A49035; MUID:92164708
A:Accession: A49035
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-134 <TGL>
A:Cross-references: GB:S85477; NID:g246280; PIDN:AAB21544.1; PID:g246281
A>Note: sequence extracted from NCBI backbone (NCBIN:85477, NCBI:P:85529)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 39.4%; Score 56; DB 2; Length 134;
Best Local Similarity 57.1%; Pred. No. 0.91;

Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 SRPWTANYQHDLR 14
|:|:|:|:|:|:|:
Db 49 SQYPMSWYQODLQ 62

RESULT 3
B28823
T-cell receptor beta chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 23-Jul-1999
C:Accession: B28823
R:Tan, K.N.; Dattlof, B.M.; Gilmore, J.A.; Kronman, A.C.; Lee, J.H.; Maxam, A.M.; Rao, A.
Cell 54, 247-261, 1988
A:Title: The T cell receptor V-alpha-3 gene segment is associated with reactivity to p-
A:Reference number: A90900; MUID:88270504
A:Accession: B28823
A:Molecule type: DNA
A:Residues: 1-135 <TAN>
A:Cross-references: GB:M21203; NID:g201383; PIDN:AAA40254.1; PID:g554307
C:Genetics:
A:Introns: 18/3
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 39.4%; Score 56; DB 2; Length 135;
Best Local Similarity 57.1%; Pred. No. 0.91;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 SRPWTANYQHDLR 14
|:|:|:|:|:|:|:
Db 49 SQYPMSWYQODLQ 62

RESULT 4
RMMSE1
T-cell receptor beta chain precursor V region (E1) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 22-Jun-1999
C:Accession: A02009
R:Patten, P.; Yokota, T.; Rothbard, J.; Chien, Y.; Arai, K.; Davis, M.M.
Nature 312, 40-46, 1984
A:Title: Structure, expression and divergence of T-cell receptor beta-chain variable reg
A:Reference number: A93346; MUID:85036636
A:Accession: A02009
A:Molecule type: mRNA
A:Residues: 1-136 <PAT>
A:Cross-references: GB:X01642; NID:g54308; PIDN:CAA25799.1; PID:g762989
C:Comment: This sequence was derived from a T-helper clone.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; receptor; T-cell
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-136/Product: T-cell receptor beta chain precursor V region (E1) #status predicted <
F:21-116/Region: V segment
F:117-120/Region: D segment
F:121-136/Region: J segment
F:44-112/Disulfide bonds: #status predicted

Query Match 39.4%; Score 56; DB 1; Length 136;
Best Local Similarity 57.1%; Pred. No. 0.92;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 SRPWTANYQHDLR 14
|:|:|:|:|:|:|:
Db 49 SQYPMSWYQODLQ 62

RESULT 5
I71937
MHC class II I-A-beta protein precursor - mouse (fragment)

C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 23-Jul-1999
C:Accession: I71937
R:Spinelia, D.G.; Hansen, T.H.; Walsh, W.D.; Behlke, M.A.; Tillinghast, J.P.; Chou, H
J. Immunol. 138, 3991-3995, 1987
A:Title: Receptor diversity of insulin-specific T cell lines from C57BL (H-2b) mice.
A:Reference number: I55978; MUID:87224052
A:Accession: I71937
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-137 <RES>
A:Cross-references: GB:M6680; NID:g199471; PIDN:AAA39625.1; PID:g199472
C:Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 39.4%; Score 56; DB 2; Length 137;
Best Local Similarity 57.1%; Pred. No. 0.92;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 SRPWTANYQHDLR 14
|:|:|:|:|:|:|:
Db 49 SQYPMSWYQODLQ 62

RESULT 6
T35357
hypothetical protein SC5H1.41 - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C:Accession: T35357
R:Olliver, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, May 1999
A:Reference number: Z21575
A:Accession: T35357
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-345 <OLI>
A:Cross-references: EMBL:AL049863; PIDN:CAB42966.1; GSPDB:GN00070; SCOEDB:SC5H1.41
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SC5H1.41

Query Match 38.0%; Score 54; DB 2; Length 345;
Best Local Similarity 45.0%; Pred. No. 4.3;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 5 WTAWYQHDLRARFVRRP 24
|:|:|:|:|:|:|:
Db 82 WAERSRHEIGAYRSPVRRP 101

RESULT 7
S52347
hypothetical protein 1 - Lactobacillus leichmannii
C:Species: Lactobacillus leichmannii
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 05-Nov-1999
C:Accession: S52347
R:Schenk-Groeninger, R.
submitted to the EMBL Data Library, January 1995
A:Reference number: S52347
A:Accession: S52347
A:Molecule type: DNA
A:Residues: 1-267 <SCH>
A:Cross-references: EMBL:X81869; NID:g666067; PIDN:CAA57458.1; PID:g666068
A:Experimental source: DSM 20076

Query Match 37.0%; Score 52.5; DB 2; Length 267;
Best Local Similarity 52.4%; Pred. No. 5.4;
Matches 11; Conservative 2; Mismatches 5; Indels 3; Gaps 1;

OY 2 RVPWTANYQHDLRAY--RRF 19

Db 161 QVPLAVYNNHDLRTYNCORRF 181

RESULT 8

JH0346
T-cell receptor beta chain V region (MT1-6) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 23-Jul-1999
C:Accession: JH0346
R:Taylor, A.H.; Haberman, A.M.; Gerhard, W.; Caton, A.J.
J. Exp. Med. 172, 1643-1651, 1990
A:Title: Structure-function relationships among highly diverse T cells that recognize a
A:Reference number: JH0333; M0ID:91079767
A:Accession: JH0346
A:Molecule type: mRNA
A:Residues: 1-85 <TAY>
A:Cross-references: GB:M34203; NID:q201A18; PIDN:AAA58763.1; PID:q201A19
C:Comment: This T-cell receptor recognizes a determinant from Influenza virus hemagglutinin
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: receptor; T-cell

Query Match 36.6%; Score 52; DB 2; Length 85;
Best Local Similarity 63.6%; Pred. No. 2.1;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 4 PWTAWYQHDLRATYRRFVRRP 14
| | : | | | | |
Db 3 PMSWYQDDLD 13

RESULT 9

H70841
probable amIA protein - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: H70841
R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Ruter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; M0ID:98295987
A:Accession: H70841
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1389 <COL>
A:Cross-references: GB:AL021841; GB:AL123456; NID:g3261517; PIDN:CAA17077.1; PID:g289421
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: amIA
C:Superfamily: hippurate hydrolase

Query Match 35.9%; Score 51; DB 2; Length 389;
Best Local Similarity 45.0%; Pred. No. 13;
Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Oy 5 WTAMYQHDLRATYRRFVRRP 24
| | : | | | | |
Db 10 WLAHNDLWGWRRHRRP 29

RESULT 10

T26654
hypothetical protein Y38E10A.d - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T26654
R:Wallis, J.
submitted to the EMBL Data Library, September 1999

A:Reference number: Z20252
A:Accession: T26654
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-454 <MTL>
A:Cross-references: EMBL:AL110484; NID:e1542205; PIDN:CAB54395.1; CESP:Y38E10A.d
A:Experimental source: clone Y38E10A
C:Genetics:
A:Gene: CESP:Y38E10A.d
A:Introns: 67/3; 115/1; 159/1; 391/3; 434/2

Query Match 35.9%; Score 51; DB 2; Length 454;
Best Local Similarity 41.7%; Pred. No. 15;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Oy 1 SRVPTAWYQHDLRATYRRFVRRP 24
| | : | | | | |
Db 258 SWPTGSWYPCVCKASNSFLCKRP 281

RESULT 11

F81989
hypothetical protein NMA0692 [imported] - Neisseria meningitidis (strain Z2491 serogr
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: F81989
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo
; Holroyd, S.; Jagsels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, M.A.; Rogers, J.; Ruter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491
A:Reference number: AB1775; M0ID:20222556
A:Accession: F81989
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1833 <PAR>
A:Cross-references: GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB83978.1; PID:g737
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA0692

Query Match 35.9%; Score 51; DB 2; Length 833;
Best Local Similarity 33.3%; Pred. No. 26;
Matches 7; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Oy 2 RVPTAWYQHDLRATYRRFVRRP 22
| | : | | | | |
Db 666 RTGEPTWTRHDVOTYRQYNO 686

RESULT 12

AI2961
conserved hypothetical protein Atu3295 [imported] - Agrobacterium tumefaciens (strain
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C:Accession: AI2961
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo
erage, G.; Gillet, W.; Grant, C.; Guentlner, D.; Kutayavin, T.; Levy, R.; Li, M.; McCl
; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
ster, E.W.
A:Title: The genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; PMID:11743193
A:Accession: AI2961
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-170 <KUR>
A:Cross-references: GB:AE008689; PIDN:ALV4411.1; PID:g17741680; GSPDB:GN00187
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu3295

A:Map position: linear chromosome

Query Match 34.9%; Score 49.5; DB 2; Length 170;
Best Local Similarity 50.0%; Pred. No. 9.3;
Matches 10; Conservative 2; Mismatches 7; Indels 1; Gaps 1;

QY 4 PWT-AMYQHDLRAYRRFVHR 22
DB 134 PWTNAMYDYCSQRYRSEFSR 153

RESULT 13

hypothetical protein AGR_L_3047 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C:Species: Agrobacterium tumefaciens
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
C:Accession: E98321
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughly, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; PMID:11743194
A:Accession: E98321
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-175 <KUR>
A:Cross-references: GB:AE007870; PIDN:AAK90095.1; PID:q1516082; GSPDB:GN00170
C:Genetics:
A:Gene: AGR_L_3047
A:Map position: linear chromosome

Query Match 34.9%; Score 49.5; DB 2; Length 175;
Best Local Similarity 50.0%; Pred. No. 9.5;
Matches 10; Conservative 2; Mismatches 7; Indels 1; Gaps 1;

QY 4 PWT-AMYQHDLRAYRRFVHR 22
DB 139 PWTNAMYDYCSQRYRSEFSR 158

RESULT 14

hypothetical protein T07H3.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T33376
R:Beck, C.; O'Brien, D.; Kramer, J.
Submitted to the EMBL Data Library, July 1998
A:Description: The sequence of C. elegans cosmid T07H3.
A:Reference number: 221332
A:Accession: T33376
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-417 <BEC>
A:Cross-references: EMBL:AF077540; PIDN:AA26308.1; GSPDB:GN00020; CESP:T07H3.5
A:Experimental source: strain Bristol N2; clone T07H3
C:Genetics:
A:Gene: CESP:T07H3.5
A:Map position: 2
A:introns: 65/3; 152/1

Query Match 34.5%; Score 49; DB 2; Length 417;
Best Local Similarity 39.1%; Pred. No. 26;
Matches 9; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 2 RVPWTAWYQHDLRAYRRFVHR 24
DB 256 RQPWGLWYTGNCYDRKKFFCKRP 278

RESULT 15

hypothetical protein AF0170 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C:Accession: B69271
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
r.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E
Glodek, A.; Zhou, L.; Overbeek, R.; Cocayne, J.D.; Meldman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: utterback, T.; Cotton, M.D.; Spriggs, T.; Attiach, P.; Kaine, B.P.; Sykes,
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
A:Reference number: B69271
A:Accession: B69271
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-434 <KLE>
A:Cross-references: GB:AE001094; GB:AE000782; NID:g2689417; PIDN:AAB91065.1; PID:g265

Query Match 34.2%; Score 48.5; DB 2; Length 434;
Best Local Similarity 42.9%; Pred. No. 31;
Matches 9; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 3 VPTWAWYQHD-LRAYRRFVHR 22
DB 162 IPNVLMFKHDEIRALRLVLR 182

Search completed: August 15, 2002, 12:00:15
Job time: 205 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 12:05:55 ; Search time 16.31 Seconds
(without alignments)
56.975 Million cell updates/sec

Title: DEVI-613-COMBIFRAG
Perfect score: 142
Sequence: 1 SRVPTAWYQHDRLRAYRRFVHRP 24

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	56	39.4	136 1	TVB6_MOUSE
2	46.5	32.7	135 1	2SS2_CAPMA
3	45.5	32.0	2290 1	POIG_EMCV
4	45	31.7	470 1	MTR_NEUCR
5	44	31.0	125 1	ACPS_TREPA
6	44	31.0	209 1	PSAL_HORVU
7	44	31.0	216 1	PSAL_SPTOL
8	44	31.0	244 1	YE12_YEAST
9	44	31.0	586 1	ULB4_HCMVA
10	44	31.0	587 1	ULB4_HCMVT
11	44	31.0	669 1	ACSA_PENCH
12	44	31.0	775 1	MCD1_MOUSE
13	44	31.0	775 1	MCD1_MOUSE
14	44	31.0	778 1	MCD1_MOUSE
15	44	31.0	2485 1	MGDI_HUMAN
16	44	31.0	90 1	PTND_HUMAN
17	43	30.3	217 1	YPTJ_ECOLI
18	43	30.3	310 1	PSAL_CUCSA
19	43	30.3	367 1	DRNG_RAT
20	43	30.3	367 1	OASA_MOUSE
21	43	30.3	436 1	CP22_HORVU
22	43	30.3	515 1	AMYP_RAT
23	43	30.3	515 1	YJEF_ECOLI
24	43	30.3	1108 1	EMBA_MYCAV
25	43	30.3	1139 1	VRNA_BSMV
26	43	30.3	1257 1	PCGN_RAT
27	43	30.3	1268 1	PCGN_MOUSE
28	42.5	29.9	378 1	ACE_MOUSE
29	42.5	29.9	624 1	071A_DROME
30	42.5	29.9	624 1	HTPG_ECOLI
31	42.5	29.9	624 1	HTPG_SALTI
32	42	29.6	305 1	HTPG_SALTY
33	42	29.6	398 1	DRNG_HUMAN
				KR2_PPVN3

34	42	29.6	677 1	BGAL_HUMAN	P16278 homo sapien
35	42	29.6	770 1	STAG_HUMAN	P40763 homo sapien
36	42	29.6	770 1	STAG_MOUSE	P42237 mus musculu
37	42	29.6	770 1	STAG_RAT	P52631 rattus norv
38	42	29.6	1310 1	ACE_RABIT	P12822 oryctolagus
39	41.5	29.2	721 1	GLGX_MYCTU	Q10767 mycobacteri
40	41.5	29.2	1219 1	YMAZ_YEAST	Q04439 saccharomyc
41	41	28.9	107 1	HXAD_AMBME	P50210 ambystoma m
42	41	28.9	127 1	LYC_COLLI	P00708 columba liv
43	41	28.9	129 1	LYC2_ONCMY	P75406 mycoplasma
44	41	28.9	144 1	LYC2_ONCMY	P11941 oncorhynch
45	41	28.9	158 1	RACR_ECOLI	P70662 escherichia

ALIGNMENTS

RESULT	ID	TVB6_MOUSE	STANDARD	PRT	136 AA.
AC	P04214	TVB6_MOUSE	STANDARD	PRT	136 AA.
DT	20-MAR-1987	(Rel. 04, Created)			
DT	20-MAR-1987	(Rel. 04, Last sequence update)			
DT	15-JUL-1999	(Rel. 38, Last annotation update)			
DE	T-cell receptor beta chain V region E1 precursor.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=8503636; PubMed=6092964;				
RA	Patten P., Yokota T., Rothbard J., Chien Y., Aral K., Davis M.M.;				
RT	"Structure, expression and divergence of T-cell receptor beta chain				
RL	Nature 312:40-46(1984).				
CC	-I- MISCELLANEOUS: THIS SEQUENCE WAS DERIVED FROM A T-HELPER CLONE.				
CC	CC This SWISS-PROT entry is copyright. It is produced through a collaboration				
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CC	or send an email to license@sib-sib.ch).				
CC	-----				
DR	EMBL; X01642; CA25799.1; -.				
DR	PIR; A02009; RMWSE1.				
DR	InterPro; IPR003599; Ig.				
DR	InterPro; IPR003006; Ig_MHC.				
DR	Pfam; PF000047; Ig_1.				
DR	SMART; SM00409; Ig_1.				
DR	T-cell; Receptor; Signal.				
FT	SIGNAL	1	20		
FT	CHAIN	21	136		T-CELL RECEPTOR BETA CHAIN V REGION E1.
FT	DOMAIN	21	116		V SEGMENT.
FT	DOMAIN	117	120		D SEGMENT.
FT	DOMAIN	121	136		J SEGMENT.
FT	DISULFID	44	112		BY SIMILARITY.
FT	NON_TER	136	136		
SO	SEQUENCE	136 AA; 15538 MW; 2B93C4912E19B705 CRC64;			
Query Match		39.4%; Score 56; DB 1; Length 136;			
Best Local Similarity		57.1%; Pred. NO. 0.14;			
Matches	8; Conservative	3; Mismatches	3; Indels	0; Gaps	0;
Oy	1 SRVPTAWYQHDRL 14				
Db	49 SQYPMNMYQDDLO 62				
RESULT	2				

2SS2_CAPMA STANDARD: PRT: 155 AA.
ID CAPMA
AC p30233: C04774;
DT 01-APR-1993 (Rel. 25, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-Oct-2001 (Rel. 40, Last annotation update)
DE Mabinlin II precursor (MAB II) (sweet protein).
OS Capparis masaiikai (Mabianlang).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Capparidaceae;
OX NCBI_taxonomy=13395;

RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Seeds:
RX MEDLINE=97128796; PubMed=6973336;
RA Nitrasawa S., Masuda Y., Nakaya K., Kurihara Y.;
RT "Cloning and sequencing of a cDNA encoding a heat-stable sweet
RL protein, mabinlin II.";
Gene 181:225-227(1996).
[2]
RP SEQUENCE OF 36-68 AND 83-154.
RC TISSUE-Seeds:
RX MEDLINE=93145958; Pubmed=8425538;
RA Liu X., Maeda S., Hu Z., Aiuchi T., Nakaya K., Kurihara Y.;
RT "Purification, complete amino acid sequence and structural
characterization of the heat-stable sweet protein, mabinlin II.";
Eur. J. Biochem. 211:281-287(1993).
[3]
RP PARTIAL SEQUENCE, AND DISULFIDE BONDS.
RX MEDLINE=94002261; PubMed=8399391;
RA Niratsawa S., Lin X., Nishino T., Kurihara Y.;
RT "Disulfide bridge structure of the heat-stable sweet protein mabinlin
RI I.";
Biochim. Biophys. Acta 1202:277-280(1993).
CC -I- FUNCTION: HEAT STABLE 2S SEED STORAGE PROTEIN HAVING SWEETNESS-
INDUCING ACTIVITY
CC -I- SUBUNIT: HETERODIMER OF A SMALL A AND A LARGE B CHAIN LINKED BY
DISULFIDE BONDS.
CC -I- SIMILARITY: BELONGS TO THE 2S SEED STORAGE ALBUMINS FAMILY.

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DR EMBL: D83997; BAA12204.1; "-"
DR Mendel: 14634; Capma:1175;14634.
DR InterPro: IPRO03612; AAI.
DR InterPro: IPRO00617; Napin.
DR Pfam: PF01631; Seedstore_25; 1.
DR PRINTS: PR00496; NAPIN.
DR ProDom: PD002498; Napin: 1.
DR SMART: SM00499; AAI: 1.
CK Seed storage protein; Albumin; Signal; Sweet-taste.
CM SIGNAL 1 20 POTENTIAL.
FT PROPEP 21 35
FT CHAIN 36 68 MABINLIN II, A CHAIN.
FT PROPEP 69 82
FT CHAIN 83 154 MABINLIN II, B CHAIN.
FT PROPEP 155 155
FT DISUFPD 40 103
FT DISUFPD 53 92
FT DISUFPD 93 141
FT DISUFPD 105 149 PYROLIDONE CARBOXYLIC ACID.
FT MOD_RES 36 36
FT MOD_RES 83 83
FT CONFLICT 148 148 A->T (IN REF. 1).
FT CONFLICT 153 153 A->T (IN REF. 1).
SQ SEQUENCE 155 AA; 18089 MW; 72E8B5DECDC2D46A CRC64;

Query Match	32.7%	Score 46.5	DB 1	Length 155
Best Local Similarity	66.7%	Pred. NO. 4.2		
Matches 10	Conservative 2	Mismatches 2	Indels 1	Gaps 1
QY	10 QHD-LRAYRRFVHRR	23		
	: :			
Db	46 QHORLACORFIHRR	60		
RESULT	3			
POLG_EMCV	STANDARD;	PRT; 2290 AA.		
AC	P03304;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Genome polyprotein (Contains: Coat proteins VP1 TO VP4; Core proteins P2A TO P2C, P3A; Genome-linked protein VPg; Plicorain 3C (EC 3.4.22.28) (Protease 3c) (P3c); RNA-directed RNA polymerase P3D (EC 2.7.7.48)).			
DE	Encephalomyocarditis virus.			
OS	Viruses; ssRNA positive-strand viruses, no DNA stage; Plicornaviridae; Cardiovirus.			
CC	NCBI_TaxID=12104;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=84169586; PubMed=6324136;			
RA	Palmenberg A.C., Kirby E.M., Janda M.R., Drake N.L., Duke G.M., Potratz K.F., Collett M.S.,			
RT	"The nucleotide and deduced amino acid sequences of the encephalomyocarditis viral polyprotein coding region.";			
RL	Nucleic Acids Res. 12:2969-2985(1984).			
CC	-1- FUNCTION: P3C POLYPEPTIDE IS A PROTEASE THAT CLEAVES AT CERTAIN O/G SITES IN THE POLYPROTEIN. IT MAY BE A CYSTEINE PROTEASE.			
CC	-1- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHERAL UNITS.			
CC	EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2, VP3, AND VP4.			
CC	-1- PPM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.			
CC	-1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.			
CC	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/sib.ch).			
CC	or send an email to license@sib-sib.ch).			
DR	EMBL: X00463; CAA25152.1; -.			
DR	PIR: A03906; GNNYE.			
DR	HSSP; P12296; 2MEV.			
DR	MEROPS; C03.009; -.			
DR	MEROPS; U29.001; -.			
DR	InterPro: IPR000605; RNA_helicase.			
DR	InterPro: IPR001205; RNA_pol_P3D.			
DR	InterPro: IPR001676; Rnv.			
DR	PIfam; PF00073; Htv; 3.			
DR	PIfam; PF00680; RNA_dep_RNA_pol; 1.			
DR	PIfam; PF00910; RNA_helicase; 1.			
KW	Polyprotein; Coat protein; Core protein; Transferase; RNA-directed RNA polymerase; Hydrolyase; Thiol protease; Myristate.			
FT	PROPEP	1 67	LEADER PEPTIDE.	
FT	CHAIN	68 136	COAT PROTEIN VP4 (RH0).	
FT	CHAIN	137 391	COAT PROTEIN VP2 (BETA).	
FT	CHAIN	392 910	COAT PROTEIN VP3 (GAMMA).	
FT	CHAIN	623 922	COAT PROTEIN VP1 (ALPHA).	
FT	CHAIN	911 1056	CORE PROTEIN P2A (G).	
FT	CHAIN	1057 1192	CORE PROTEIN P2B (I).	
FT	CHAIN	1193 1517	CORE PROTEIN P2C (F).	
FT	CHAIN	1518 1605	CORE PROTEIN P3A.	
FT	CHAIN	1606 1625	GENOME-LINKED PROTEIN VPg (H).	

FT CHAIN 1626 1830 PICORNAIN 3C (P22).
 FT CHAIN 1831 2290 RNA-DIRECTED RNA POLYMERASE P3D (E).
 FT LIPID 68 68 MYRISTATE (BY SIMILARITY).
 FT ACT_SITE 1784 1784 PROTEASE (POTENTIAL).
 FT ACT_SITE 1802 1802 PROTEASE (POTENTIAL).
 SQ SEQUENCE 2290 AA; 255756 MW; 26BC81BB7CF68CB5 CRC64;

Query Match 32.0%; Score 45.5; DB 1; Length 2290;
 Best Local Similarity 55.6%; Pred. No. 99;
 Matches 10; Conservative 0; Mismatches 5; Indels 3; Gaps 1;

QY 1 SRVPMYAM---YOHDLRA 15
 || || | || ||
 Db 964 SRAPWNPKNYQAVLRA 981

RESULT 4

MTR_NEUCR STANDARD; PRT; 470 AA.
 AC P38680;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE N amino acid transport system protein (Methyltryptophan resistance protein).
 GN MTR.
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariales; Sordariaceae; Neurospora.
 OX NCBI_Taxid=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OAK RIDGE;
 RX MEDLINE=95095055; PubMed=1838345;
 RA Dillon D., Stadler D.;
 RT "Spontaneous mutation at the mtr locus in neurospora: the molecular spectrum in wild-type and a mutator strain.";
 RL Genetics 138:61-74(1994).
 RN [2]
 RP SEQUENCE OF 210-470 FROM N.A.
 RX MEDLINE=92146948; PubMed=1838345;
 RA Koo K., Stuart W.D.;
 RT "Sequence and structure of mtr, an amino acid transport gene of Neurospora crassa";
 RL Genome 34:644-651(1991).
 CC -1- FUNCTION: REQUIRED FOR THE TRANSPORT OF NEUTRAL ALIPHATIC AND ANOMATIC AMINO ACIDS VIA THE N SYSTEM.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -----
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 CC -----
 CC EMBL; L34605; AAA33600.1; -;
 DR EMBL; S81767; AAB21410.1; -;
 DR PIR; A54551; A54551.
 DR InterPro: IPR002422; AA_rel_permease_2.
 DR Pfam: PF01490; Aa_trans; 1.
 KW Transport; Amino-acid transport; Transmembrane.
 FT DOMAIN 1 56 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 57 77 POTENTIAL.
 FT TRANSMEM 78 98 POTENTIAL.
 FT DOMAIN 99 131 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 132 152 POTENTIAL.
 FT DOMAIN 153 168 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 169 189 POTENTIAL.
 FT TRANSMEM 191 211 POTENTIAL.
 FT DOMAIN 212 236 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 237 257 POTENTIAL.
 FT DOMAIN 258 275 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 276 296 POTENTIAL.
 FT DOMAIN 297 316 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 317 337 POTENTIAL.
 FT DOMAIN 338 357 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 358 378 POTENTIAL.
 FT DOMAIN 379 386 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 387 407 POTENTIAL.
 FT DOMAIN 408 427 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 428 448 POTENTIAL.
 FT DOMAIN 449 470 CYTOPLASMIC (POTENTIAL).
 SQ SEQUENCE 470 AA; 51162 MW; E8132D1A62373300 CRC64;

Query Match 31.7%; Score 45; DB 1; Length 470;
 Best Local Similarity 38.9%; Pred. No. 22;
 Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 3 VPMYAMYOHDRAVRRREV 20
 ||| | : || | :
 Db 227 VPMSCWPKEDLSAEGFT 244

RESULT 5

ACPS_TREPA STANDARD; PRT; 125 AA.
 ID ACPS_TREPA
 AC O83800;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Holo-[acyl-carrier protein] synthase (EC 2.7.8.7) (Holo-ACP synthase).
 GN ACPS OR TP0828.
 OS Treponema pallidum.
 OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
 OX NCBI_Taxid=160;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NICHOLS;
 RX MEDLINE=98332770; PubMed=9665876;
 RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwin M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utersback T., McDonald L., Artlisch P., Bowman C., Cotton M.D., Fujii C., Garland S., Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O., Venter J.C.;
 RT "Complete genome sequence of Treponema pallidum, the syphilis spirochete";
 RL Science 281:375-388(1998).
 CC -1- FUNCTION: TRANSFERS THE 4'-PHOSPHOPANTHETINE MOIETY FROM COENZYME A TO A SER OF ACYL-CARRIER PROTEIN (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine 3',5'-bisphosphate + holo-[acyl-carrier protein].
 CC -1- SIMILARITY: BELONGS TO THE ACPS FAMILY.
 CC -----
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 CC -----
 CC EMBL; AE001253; AAC65794.1; -;
 DR TIGR; TP0828; -;
 DR InterPro: IPR002582; ACPS.
 DR Pfam: PF01648; ACPS; 1.
 DR ProDom: PD004282; ACPS; 1.
 KW Lipid synthesis; Transferease; Complete proteome.
 SQ SEQUENCE 125 AA; 14118 MW; 88A05B5B0D20821F CRC64;

Query Match 31.0%; Score 44; DB 1; Length 125;
 Best Local Similarity 45.0%; Pred. No. 7.9;
 Matches 9; Conservative 3; Mismatches 4; Indels 4; Gaps 1;
 OY 3 PWTAWYQHDLRAYRRFVR 22
 1 11 1:1 111 1:
 DB 16 VSWT-----HNVRLLRRFFHQ 31

RESULT 6
 PSAL_HORVU STANDARD; PRT: 209 AA.
 AC P23933;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Photosystem I reaction center subunit XI, chloroplast precursor
 DE (PSI-L) (PSI subunit V).
 GN PSAL.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;
 OC Triticeae; Hordeum.
 OC NCB1_TaxID=4513;
 OX [1]
 RN
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 51-70 AND 72-74.
 RC STRAIN=CV. SVALOF'S BONUS;
 RA MEDLINE=91201317; PubMed=2016292;
 RA Okels J.S., Scheiller H.V., Svendsen I., Moeller B.L.;
 RT "Isolation and characterization of a cDNA clone encoding an 18-kDa
 RT hydrophobic photosystem I subunit (Pst-L) from barley (Hordeum
 RT vulgare L.).", 266:6767-6773(1991).
 RL J. Biol. Chem. 266:6767-6773(1991).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Chloroplast
 CC thylakoid membrane (Probable).
 CC -1- INDUCTION: BY LIGHT.
 CC -1- SIMILARITY: BELONGS TO THE PSAL FAMILY.
 CC -----
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 CC -----
 DR EMBL: M61146; AAA62700.1; -;
 DR PIR: A39759; A39759.
 DR InterPro: IPR003757; Psal.
 DR Pfam: PF02605; Psal. 1.
 DR Photosystem I; Photosynthesis; Chloroplast; Transit peptide;
 KM Thylakoid; Transmembrane; Acetylation.
 KW TRANSIT 1 40
 FT CHAIN 41 209 CHLOROPLAST.
 FT DOMAIN 41 124 PHOTOSYSTEM I REACTION CENTER SUBUNIT XI.
 FT TRANSMEM 125 146 POTENTIAL.
 FT TRANSMEM 147 179 POTENTIAL.
 FT DOMAIN 180 202 LUMENAL (POTENTIAL).
 FT TRANSMEM 203 209 STROMAL (POTENTIAL).
 FT DOMAIN 203 209 STROMAL (POTENTIAL).
 FT MOD_RES 41 41 ACETYLATION (PROBABLE).
 FT MOD_RES 209 209 ACETYLATION (PROBABLE).
 SO SEQUENCE 209 AA; 22211 MW; 95741FD3F290F9E1 CRC64;

Query Match 31.0%; Score 44; DB 1; Length 209;
 Best Local Similarity 52.9%; Pred. No. 13;
 Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

OY 4 PWTAWYQHDLRAYRRFVR 20
 1 111 1:1 111 1:
 DB 72 PLVAVYLSMLPAYRTAV 88

RESULT 7

PSAL_SPTOL STANDARD; PRT: 216 AA.
 ID PSAL_SPTOL
 AC Q41385;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Photosystem I reaction center subunit XI, chloroplast precursor
 DE (PSI-L) (PSI subunit V).
 GN PSAL.
 OS Spinacia oleracea (Spinach).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
 OX NCB1_TaxID=3562;
 OX [1]
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. MONATOL;
 RA MEDLINE=93344519; PubMed=8343606;
 RA Flieger K., Oelmüller R., Herrmann R.G.;
 RT "Isolation and characterization of cDNA clones encoding a 18.8 kDa
 RT polypeptide, the product of the gene psal, associated with
 RT photosystem I reaction center from spinach.",
 RL Plant Mol. Biol. 22:703-709(1993).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Chloroplast
 CC thylakoid membrane (Probable).
 CC -1- SIMILARITY: BELONGS TO THE PSAL FAMILY.
 CC -----
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 CC -----
 DR EMBL: X64445; CAA5775.1; -;
 DR InterPro: IPR003757; Psal.
 DR Pfam: PF02605; Psal. 1.
 DR Photosystem I; Photosynthesis; Chloroplast; Transit peptide;
 KM Thylakoid; Transmembrane.
 KW TRANSIT 1 47
 FT CHAIN 48 216 CHLOROPLAST (POTENTIAL).
 FT DOMAIN 48 134 PHOTOSYSTEM I REACTION CENTER SUBUNIT XI.
 FT TRANSMEM 135 155 POTENTIAL.
 FT TRANSMEM 156 188 LUMENAL (POTENTIAL).
 FT TRANSMEM 189 209 POTENTIAL.
 FT DOMAIN 210 216 STROMAL (POTENTIAL).
 SO SEQUENCE 216 AA; 22937 MW; 603DCA983C7C383B CRC64;

Query Match 31.0%; Score 44; DB 1; Length 216;
 Best Local Similarity 50.0%; Pred. No. 14;
 Matches 9; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
 OY 4 PWTAWYQHDLRAYRRFVR 21
 1 111 1:1 111 1:
 DB 79 PLVAVYLSMLPAYRTAVN 96

RESULT 8
 YE12_YEAST STANDARD; PRT: 244 AA.
 ID YE12_YEAST
 AC P40098;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Hypothetical 27.7 kDa protein in ISC10 3' region.
 GN YER182W.

OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCB1_TaxID=4932;
 OX [1]

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RP SEQUENCE FROM N.A.
RC STRAIN-5288C / AB972;
RA Dierich F.S., Mulligan J.T., Hennessey R.M., Allen E., Araujo R.,
RA Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M.,
RA Chung E., Duncan M., Guzman E., Hartzell G., Hudicke-Smith S.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C.,
RA Patel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V.,
RA Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBD databases.
CC -1- SIMILARITY: SOME, TO S.POMBE SPAC3A12.08.
CC
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CC
DR EMBL: U018922; AAB64709.1; -
DR SCD: S0000984; YER182W.
KW Hypothetical protein, Transmembrane.
FT TRANSMEM 29 49
FT TRANSMEM 139 159 POTENTIAL.
SQ SEQUENCE 244 AA; 27698 MW; A78338C86EA52766 CRC64;

Query Match
Best Local Similarity 31.0%; Score 44; DB 1; Length 244;
Matches 12; Conservative 2; Mismatches 3; Indels 14; Gaps 3;

OY 3 VPWT-----AWY--OH---DLRAYRRF 19
Db 30 IPWTIRGSGFLGSGWYLTQHMTFTDLAYRRY 60

RESULT 9
UL84_HCMVA STANDARD; PRT; 586 AA.
AC P16727;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE 65 kDa early nonstructural protein (UL84 protein).
GN UL84.
OS Human cytomegalovirus (strain AD169).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Cytomegalovirus.
OX NCBI_TaxID=10360;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-90269039; PubMed-2161319;
RA Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R.,
RA Horsnell T., Hutchinson C.A. III, Kouzarides T., Martignetti J.A.,
RA Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.;
RT "Analysis of the protein-coding content of the sequence of human
RT cytomegalovirus strain AD169."
RL Curr. Top. Microbiol. Immunol. 154:125-169(1990).
CC
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CC
DR EMBL: X17403; CAA35358.1; -
DR PIR: S09848; WMBEDE.
KW Nonstructural protein.
FT DOMAIN 9 19
FT DOMAIN 162 170
FT DOMAIN 162 170 LYS-RICH (BASIC).
FT DOMAIN 162 170 LYS-RICH (BASIC).

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FT DOMAIN 171 182 ASP/GLU-RICH (ACIDIC).
SQ SEQUENCE 586 AA; 65428 MW; 54AB912D6077223F CRC64;

Query Match
Best Local Similarity 31.0%; Score 44; DB 1; Length 586;
Matches 11; Conservative 1; Mismatches 6; Indels 2; Gaps 1;

OY 2 RVPW--TAWQHLRAYRRF 19
Db 427 RVPVELTKNSHRLRYRRF 446

RESULT 10
UL84_HCMVT STANDARD; PRT; 587 AA.
AC P29839;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE 65 kDa early nonstructural protein (UL84 protein).
GN UL84.
OS Human cytomegalovirus (strain Towne).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Cytomegalovirus.
OX NCBI_TaxID=10363;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-92114132; PubMed-1309892;
RA He Y.S., Xu L., Huang E.S.;
RT "Characterization of human cytomegalovirus UL84 early gene and
RT identification of its putative protein product."
RL J. Virol. 66:1098-1108(1992).
CC
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CC
DR EMBL: M81432; AAA45947.1; -
DR PIR: A41808; WMBETE.
KW Nonstructural protein.
FT DOMAIN 9 19
FT DOMAIN 162 170 LYS-RICH (BASIC).
FT DOMAIN 171 183 ASP/GLU-RICH (ACIDIC).
SQ SEQUENCE 587 AA; 65388 MW; 13C170E41FB3220B CRC64;

Query Match
Best Local Similarity 31.0%; Score 44; DB 1; Length 587;
Matches 11; Conservative 1; Mismatches 6; Indels 2; Gaps 1;

OY 2 RVPW--TAWQHLRAYRRF 19
Db 428 RVPVELTKNSHRLRYRRF 447

RESULT 11
ACSA_PENCH STANDARD; PRT; 669 AA.
ID ACSA_PENCH
AC P36333;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Acetyl-coenzyme A synthetase (EC 6.2.1.1) (Acetate--CoA ligase) (Acyl-L-
DE activating enzyme).
GN PACA OR ACUA.
OS Penicillium chrysogenum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.

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OX  NCBI_TaxID=5076;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=93366184; PubMed=8103029;
RA  Matinez-Blanco H., Orejas M., Reglero A., Luengo J.M., Penalva M.A.;
RT  "Characterisation of the gene encoding acetyl-CoA synthetase in
RT  penicillium chrysogenum: conservation of intron position in
RT  plectomyces.";
RL  Gene 130:265-270(1993).
RN  [2]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=93159753; PubMed=7765289;
RA  Gouka R.J., van Hartingsveldt W., Bovenberg R.A., van Zeijl C.M.,
RA  van den Hondel C.A., van Gorcom R.F.;
RT  "Development of a new transformant selection system for Penicillium
RT  chrysogenum: isolation and characterization of the P. chrysogenum
RT  acetyl-coenzyme A synthetase gene (faca) and its use as a homologous
RT  selection marker.";
RL  Appl. Microbiol. Biotechnol. 38:514-519(1993).
CC  -I- PATHWAY: Microbiol. Biotechnol. 38:514-519(1993).
CC  -I- CATALYTIC ACTIVITY: ATP + acetate + CoA = AMP + diphosphate +
CC  acetyl-CoA.
CC  -I- SIMILARITY: BELONGS TO THE ATP-DEPENDENT AMP-BINDING ENZYME
CC  FAMILY.
CC  -----
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CC  -----
DR  EMBL; S54801; AAC60546.1; -
DR  EMBL; L09598; AAA02921.1; -
DR  PIR; JN0781; JN0781.
DR  HSP; P08659; JICI.
DR  InterPro; IPR000873; AMP-bind.
DR  Pfam; PF00501; AMP-binding; 1.
DR  PRINTS; PR00154; AMPBINDING.
DR  PROSITE; PS00455; AMP_BINDING; 1.
KW  Ligase.
SQ  SEQUENCE 669 AA; 74287 MW; 7C05220D321D736C CRC64;

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RT  "Dlx1-1, a novel protein that binds Dlx5 and regulates its
RT  transcriptional function.";
RL  J. Biol. Chem. 276:5331-5338(2001).
RN  [2]
RP  SEQUENCE FROM N.A.
RA  Augier P.H., Chomez P.M., De Backer O.R., Bertrand M.J.M.;
RT  "Ten new murine members of the MAGE gene family.";
RT  Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.
RN  [3]
RP  SEQUENCE FROM N.A.
RC  STRAIN=C57BL/6J; TISSUE=Head;
RX  MEDLINE=21085660; PubMed=11217851;
RA  Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA  Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA  Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA  Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA  Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA  Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
RA  Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA  Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA  Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA  Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA  Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA  Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA  Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA  Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA  Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA  Suzuki H., Toyooka K., Wang K.H., Weitz C., Willeker C., Wilming L.,
RA  Wyshwan-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA  Hayashizaki Y.;
RT  "Functional annotation of a full-length mouse cDNA collection.";
RL  Nature 409:685-690(2001).
CC  -I- FUNCTION: Involved in the apoptotic response after nerve growth
CC  factor (NGF) binding in neuronal cells. Binds p75NTR and
CC  antagonizes its association with TrkA, inhibits cell cycle
CC  progression, and facilitates p75NTR-mediated apoptosis. May act as
CC  a regulator of the function of Dlx family members (by similarity).
CC  -I- SUBUNIT: INTERACTS WITH DLX5, DLX7 AND MSX2 AND FORMS
CC  HOMODIMERS.
CC  -I- SUBCELLULAR LOCATION: Cytoplasmic. Expression shifts from the
CC  cytoplasm to the plasma membrane upon stimulation with NGF (by
CC  similarity).
CC  -I- TISSUE SPECIFICITY: Ubiquitously expressed in many adult tissues,
CC  except for the spleen. Expressed in osteoblastic and
CC  chondrogenic cell lines and also during embryonic development.
CC  -I- SIMILARITY: CONTAINS 1 MAGE DOMAIN.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC  or send an email to license@sib-sib.ch).
CC  -----
DR  EMBL; AB029448; BAA87959.1; -
DR  EMBL; AF319975; AAK01203.1; -
DR  EMBL; AK017275; BAB30666.1; -
DR  EMBL; AK013231; BAB28729.1; ALT_INIT.
DR  MGD; MGI:1930187; Maged1.
DR  InterPro; IPR002190; MAGE.
DR  Pfam; PF01454; MAGE; 1.
DR  PROSITE; PS00838; MAGE; 1.
KW  Antigen; Multigene family; Repeat.
FT  DOMAIN 292 441
FT  22 X 6 AA TANDEM REPEATS OF W-[PQ]-X-P-X-
FT  REPEAT 292 297 X.
FT  REPEAT 298 303 1.
FT  REPEAT 304 309 2.
FT  REPEAT 304 309 3.
FT  REPEAT 329 334 4.
FT  REPEAT 335 340 5.
FT  REPEAT 341 346 6.
FT  REPEAT 347 352 7.

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FT REPEAT 436 441 22.
FT DOMAIN 468 666
SQ SEQUENCE 775 AA; 85669 MW; 224B82470816835A CRC64;

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Query Match 31.0%; Score 44; DB 1; Length 775;
Best Local Similarity 42.1%; Pred. No. 53;
Matches 8; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

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Oy 1 SRVPTAWYOHDLRAYRRF 19
Db 725 SRPFTWARYHONARSRF 743

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RESULT 13
MGDI_RAT STANDARD; PRT; 775 AA.
AC 09ES73: 09QX92: 09JH26;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Melanoma-associated antigen DI (MAGE-DI antigen) (Neurotrophin
DE receptor-interacting MAGE homolog) (Sertoli cell needin
DE related gene-1) (SNERG-1).
GN MAGDI OR NRAGE.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Neural crest;
RX MEDLINE=20439481; PubMed=10985348;
RA Salehi A.H., Roux P.P., Kuba C.J., Zeindler C., Bhakar A.,
RA Tannis L.-L., Verdi J.M., Barker P.A.;
RT *NRAGE, a novel MAGE protein, interacts with the p75 neurotrophin
RT receptor and facilitates nerve growth factor dependent apoptosis.";
RL Neuron 27:279-288(2000).
RN [2]
RP SEQUENCE OF 206-775 FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=20466167; PubMed=11014239;
RA Henny B., Reiter E., Cornet A., Bruyninx M., Daukandt M., Houssa P.,
RA N'Guyen V.-H., Closset J., Hennen G.;
RT *A novel messenger ribonucleic acid homologous to human MAGE-D is
RT strongly expressed in rat Sertoli cells and weakly in Leydig cells
RT and is regulated by folliculin, luteal phase, and prolactin.";
RL Endocrinology 141:3821-3831(2000).
RN [3]
RP SEQUENCE OF 178-775 FROM N.A.
RA Zhang C., He F.;
RT *Rattus norvegicus mRNA for SNERG-1 protein, partial cds.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
-1- FUNCTION: Involved in the apoptotic response after nerve growth
CC factor (NGF) binding in neuronal cells. Binds p75NTR and
CC antagonizes its association with TrkA, inhibits cell cycle
CC progression, and facilitates p75NTR-mediated apoptosis. May act as
CC a regulator of the function of DLX family members.

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CC -1- SUBUNIT: INTERACTS WITH DLX5, DLX7 AND MSX2 AND FORMS
CC HOMOMULTIMERS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Expression shifts from the
CC cytoplasm to the plasma membrane upon stimulation with NGF.
CC -1- TISSUE SPECIFICITY: Ubiquitous and in the seminiferous tubules
CC expressed in Sertoli cells but not in germ cells. Expression
CC decreases in all tissues with increased age and is detectable only
CC in brain cortex and lung.
CC -1- DEVELOPMENTAL STAGE: Expressed at low levels throughout the embryo
CC and is enriched in the developing brain and spinal cord.
CC -1- INDUCTION: Folliculin decreased expression while luteal phase and
CC prolactin stimulated expression.
CC -1- SIMILARITY: CONTAINS 1 MAGE DOMAIN.
CC -1- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
CC FRAMESHIFT IN POSITION 726.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF217964; MAG09705.1; -
DR EMBL: AJ133038; CAB65381.1; ALT_FRAME.
DR EMBL: AF274043; AAF75283.1; -
DR InterPro: IPR002190; MAGE.
DR Pfam: PF01454; MAGE; 1.
DR PROSITE: PS50838; MAGE; 1.
KW Antigen; Multigene family; Repeat.
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FT REPEAT 4090 4095
FT REPEAT 4096 4101
FT REPEAT 4102 4107
FT REPEAT 4108 4113
FT REPEAT 4114 4119
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FT REPEAT 4132 4137
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FT REPEAT 4396 4401
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FT REPEAT 4468 4473
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FT REPEAT 4480 4485
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FT REPEAT 4498 4503
FT REPEAT 4504 4509
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FT REPEAT 4534 4539
FT REPEAT 4540 4545
FT REPEAT 4546 4551
FT REPEAT 4552 4557
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FT REPEAT 4564 4569
FT REPEAT 4570 4575
FT REPEAT 4576 4581
FT REPEAT 4582 4587
FT REPEAT 4588 4593
FT REPEAT 4594 4599
FT REPEAT 4600 4605
FT REPEAT 4606 4611
FT REPEAT 4612 4617
FT REPEAT 4618 4623
FT REPEAT 4624 4629
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FT REPEAT 4702 4707
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FT REPEAT 4750 4755
FT REPEAT 4756 4761
FT REPEAT 4762 4767
FT REPEAT 4768 4773
FT REPEAT 4774 4779
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FT REPEAT 4786 4791
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FT REPEAT 4828 4833
FT REPEAT 4834 4839
FT REPEAT 4840 4845
FT REPEAT 4846 4851
FT REPEAT 4852 4857
FT RE
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ID	MDL	HUMAN	STANDARD:	PRF:	778 AA.
AC	09Y5V3		Q9UF36; Q9HBT4; Q9H355;		
DT	16-OCT-2001	(Rel. 40, Created)			
DT	01-MAR-2002	(Rel. 41, Last sequence update)			
DT	01-MAR-2002	(Rel. 41, Last annotation update)			
DE	Melanoma-associated antigen DI (MAGE-DI antigen) (Neurotrophin receptor-interacting MAGE homolog) (PRO2292).				
DE	MAGE-DI OR NRAGE.				
GN	Homo sapiens (Human).				
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID:9606;				
RN	[1]				
RN	SEQUENCE FROM N.A.				
RC	TISSUE=Bone marrow.				
RX	MEDLINE=99339980; PubMed=10409427;				
RA	Pold M., Zhou J., Chen G.L., Hall J.M., Vescio R.A., Berenson J.R.;				
RT	"Identification of a new, unorthodox member of the MAGE gene family.";				
RL	Genomics 59:161-167(1999).				
RN	[2]				
RN	SEQUENCE FROM N.A.				
RP	MEDLINE=20439481; PubMed=10985348;				
RC	TISSUE=Testis.				
RA	Blum H., Baurtsch S., Mewes H.-W., Gassenhuber J., Wiemann S.;				
RL	Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.				
RN	[4]				
RP	SEQUENCE OF 396-778 FROM N.A.				
RC	TISSUE=Fetal liver;				
RX	MEDLINE=21177478; PubMed=11280991;				
RA	Zhang C.G., Xing G.C., Wei H.D., Yu Y.T., He F.C.;				
RT	"A new melanoma antigen-encoding gene subfamily in human chromosome X.";				
RL	I Chuan Hsueh Pao 28:197-203(2001).				
RN	[5]				
RP	IDENTIFICATION OF THE TRANSLATIONAL INITIATION CODON.				
RX	MEDLINE=20541720; PubMed=11087672;				
RA	Kibu C.J., Goldhawk D.G., Barker P.A., Verdi J.M.;				
RT	"Identification of the translational initiation codon in human MAGE-DI.";				
RL	Genomics 70:150-152(2000).				
CC	-I- FUNCTION: INVOLVED IN THE APOPTOTIC RESPONSE AFTER NERVE GROWTH				
CC	factor (NGF) binding in neuronal cells. Binds p75NTR and				
CC	antagonizes its association with TRK, inhibits cell cycle				
CC	progression, and facilitates p75NTR-mediated apoptosis. May act as				
CC	a regulator of the function of Dlx family members.				
CC	-I- SUBUNIT: INTERACTS WITH THE p75 NEUROTROPHIN RECEPTOR.				
CC	-I- CYTOPLASMIC LOCATION: CYTOPLASMIC. Expression shifts from the				
CC	cytoplasm to the plasma membrane upon stimulation with NGF (By				
CC	similarity).				
CC	-I- TISSUE SPECIFICITY: EXPRESSED IN BONE MARROW STROMAL CELLS FROM				
CC	BOTH MULTIPLE MYELOMA PATIENTS AND HEALTHY DONORS. SEEMS TO BE				
CC	UBIQUITOUSLY EXPRESSED.				
CC	-I- SIMILARITY: CONTAINS 1 MAGE DOMAIN.				
CC	-I- CAUTION: REF.1 differs from that shown due to several frameshifts				
CC	that resulted in a N-terminally truncated protein.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on				
CC	use by non-profit institutions as long as its content is in no way				

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DR EMBL: AF217963; AAG09704.1; -.
DR EMBL: AL133628; CAB63752.1; -.
DR EMBL: AF132205; AAG35551.1; ALT_INIT.
DR MIM: 300224; -.
DR InterPro: IPR002190; MAGE.
DR Pfam: PF01454; MAGE; 1.
DR PROSITE: PS50838; MAGE; 1.
KW Antigen; Multigene family; Repeat.
FT DOMAIN 296 444
FT REPEAT 296 301
FT REPEAT 302 307
FT REPEAT 308 313
FT REPEAT 332 337
FT REPEAT 338 343
FT REPEAT 344 349
FT REPEAT 350 355
FT REPEAT 356 361
FT REPEAT 362 367
FT REPEAT 368 373
FT REPEAT 374 379
FT REPEAT 380 385
FT REPEAT 386 391
FT REPEAT 392 397
FT REPEAT 398 403
FT REPEAT 404 409
FT REPEAT 410 415
FT REPEAT 416 421
FT REPEAT 422 427
FT REPEAT 428 432
FT REPEAT 433 438
FT REPEAT 439 444
FT DOMAIN 471 669
SQ SEQUENCE 778 AA; 86150 MW; 0F8BEC7155326FC CRC64;

Query Match 31.0%; Score 44; DB 1; Length 778;
Best Local Similarity 42.1%; Pred. No. 53;
Matches 8; Conservative 4; Mismatches 7; Indels 0; Gaps

QY 1 SRVPMTAWOHDLAVYRRF 19
   ||:|:|:|:|:|:|:|:|:|
Db 728 SRDFTFMARYHONARSRF 746

RESULT 15
PTND_HUMAN PTND_HUMAN STANDARD; PRT; 2485 AA.
AC Q12923; Q15263; Q16826; Q15264; Q15265; Q15159;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein tyrosine phosphatase, non-receptor type 13 (EC 3.1.3.48)
DE (protein-tyrosine phosphatase 1E) (PTP-1E) (PTP-BAS) (Protein-tyrosine
DE phosphatase PTP1B) (Pas-associated protein-tyrosine phosphatase 1)
DE (PAP-1).
DE PTPN13 OR PTP1E OR PTP1L OR PNL1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
OX [1]
RN R1 TISSUE=Breast carcinoma;
RN R2 MEDLINE=94350988; PubMed=8071359;
RN RA Banville D., Ahmad S., Stocco R., Shen S.-H.;
RT "A novel protein-tyrosine phosphatase with homology to both the
RT cytoskeletal proteins of the band 4.1 family and junction-associated
RT guanylate kinases.";
RN RL J. Biol. Chem. 269:22320-22327(1994).
RN [2]
RN RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RN RP TISSUE=Leukemia;
OC

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RX MEDLINE-94116679; PubMed-8287977;
RA Maekawa K., Imagawa N., Nagamatsu M., Harada S.;
RT "Molecular cloning of a novel protein-tyrosine phosphatase containing
RT a membrane-binding domain and GUG repeats.";
RL FEBS Lett. 337:200-206(1994).
RN
RN [3]
RC SEQUENCE FROM N.A.
RC TISSUE=Fibroblast;
RX MEDLINE-95014139; PubMed-7929060;
RA Saras J., Claesson-Welsh L., Heldin C.-H., Gonen L.J.;
RT "Cloning and characterization of PRPL, a protein tyrosine phosphatase
RT with similarities to cytoskeletal-associated proteins.";
RL J. Biol. Chem. 269:24082-24089(1994).
RN [4]
RP SEQUENCE OF 1216-2490 FROM N.A.
RC TISSUE=Pancreas;
RA Wang H.Y.;
RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
RN [5]
RP STRUCTURE BY NMR OF 1361-1456.
RX MEDLINE-20170882; PubMed-10704206;
RA Kozlov G., Gehring K., Ekiel I.;
RT "Solution structure of the PDZ2 domain from human phosphatase hPRPL
RT and its interactions with C-terminal peptides from the Fas
RT receptor.";
RL Biochemistry 39:2572-2580(2000).
CC -1- FUNCTION: BINDS TO A NEGATIVE REGULATORY DOMAIN IN FAS THAT
CC INHIBITS FAS-INDUCED APOPTOSIS.
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: 1 (SHOWN HERE), 2 AND 3; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: PRESENT IN MOST TISSUES WITH THE EXCEPTION OF
CC THE LIVER AND SKELETAL MUSCLE. MOST ABUNDANT IN LUNG, KIDNEY AND
CC FETAL BRAIN.
CC -1- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U12128; AAB60339.1; -
DR EMBL; D12109; BAA04750.1; -
DR EMBL; D12110; BAA04751.1; -
DR EMBL; D12111; BAA04752.1; -
DR EMBL; X80289; CAA56563.1; -
DR EMBL; X79676; CAA56124.1; -
DR PDB; 3PDZ; 17-MAR-00.
DR MIM; 600267; -
DR InterPro: IPR000299; Band_4.1.
DR InterPro: IPR001478; PDZ.
DR InterPro: IPR000387; TYR_phosphatase.
DR InterPro: IPR000242; TYR_prot_phphatase.
DR Pfam; PF00373; Band_4.1; 1.
DR Pfam; PF00595; PDZ; 5.
DR Pfam; PR00102; Y_phosphatase; 1.
DR PRINTS; PR00935; BAND4.1.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00295; B4.1; 1.
DR SMART; SM00228; PDZ; 5.
DR SMART; SM00194; PTPC; 1.
DR PROSITE: PS00660; BAND_4.1; FALSE_NEG.
DR PROSITE: PS00661; BAND_4.1-2; FALSE_NEG.
DR PROSITE: PS00657; BAND_4.1-3; 1.
DR PROSITE: PS00106; PDZ; 5.

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DR PROSITE: PS00383; TYR_PHOSPHATASE_1; FALSE_NEG.
DR PROSITE: PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE: PS00055; TYR_PHOSPHATASE_PTP; 1.
KW Structural protein; Cytoskeleton; Hydrolase; Repeat; 3D-structure;
KW Alternative splicing; Coiled coil.
FT DOMAIN 56 59 POLY-DEU.
FT DOMAIN 585 879 BAND 4.1-LIKE.
FT DOMAIN 2237 2485 PROTEIN-TYROSINE PHOSPHATASE.
FT DOMAIN 379 399 COILED COIL (POTENTIAL).
FT DOMAIN 469 504 COILED COIL (POTENTIAL).
FT DOMAIN 1775 1804 COILED COIL (POTENTIAL).
FT DOMAIN 2057 2085 COILED COIL (POTENTIAL).
FT DOMAIN 1093 1178 PDZ 1.
FT DOMAIN 1368 1452 PDZ 2.
FT DOMAIN 1501 1588 PDZ 3.
FT DOMAIN 1788 1868 PDZ 4.
FT DOMAIN 1882 1965 PDZ 5.
FT DOMAIN 1742 1749 POLY-SER.
FT ACT_SITE 2408 2408 BY SIMILARITY.
FT VARSPPLIC 884 1074 MISSING (IN ISOFORM 2).
FT VARSPPLIC 1056 1074 MISSING (IN ISOFORM 3).
FT CONFLICT 1134 1135 LD -> FH (IN REF. 3).
FT CONFLICT 1216 1229 KDHMSRGTLRHIS -> DLSRSHCVLAHL (IN
FT REF. 4).
FT CONFLICT 1238 1239 GL -> A (IN REF. 4).
FT CONFLICT 1357 1357 S -> P (IN REF. 4).
FT CONFLICT 1362 1363 KP -> RS (IN REF. 4).
FT CONFLICT 1383 1383 T -> TVLFDK (IN REF. 1).
FT CONFLICT 1538 1538 P -> A (IN REF. 3).
FT CONFLICT 1649 1649 R -> K (IN REF. 4).
FT CONFLICT 1698 1714 KSEDICICMEFYPPQKI -> RVKKIPFVPCFTILKKR
FT (IN REF. 4).
FT CONFLICT 1797 1797 G -> A (IN REF. 3).
FT CONFLICT 1856 1857 AA -> G (IN REF. 4).
FT CONFLICT 2069 2069 A -> S (IN REF. 4).
FT CONFLICT 2206 2210 GLDQ -> VARS (IN REF. 4).
SQ SEQUENCE 2485 AA; 276903 MW; 8D1B31597C66962B CRC64;

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Query Match 31.08; Score 44; DB 1; Length 2485;
Best Local Similarity 31.28; Pred.No.1.8e+02;
Matches 10; Conservative 4; Mismatches 8; Indels 10; Gaps 1;
OY 1 SRVPTAWYQHD-----LRAVRFVHR 22
DB 2369 SHLFTAMPDHPSPDDLLTFISTYKRIHR 2400

```

Search completed: August 15, 2002, 12:05:56
Job time: 371 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 15, 2002, 12:05:33 ; Search time 41.42 Seconds
(Without alignments)
100.238 Million cell updates/sec

Title: DEVI-613-COMBFRRAG
Perfect score: 142
Sequence: 1 SRPWTAWYQHDLRAYRRFVHRP 24

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	38.0	345	2	Q9X7U8
2	52.5	37.0	267	2	Q48706
3	51	35.9	389	16	053357
4	51	35.9	454	5	Q9NAK6
5	51	35.9	512	5	Q9V820
6	51	35.9	833	16	Q9JORS
7	49.5	34.9	141	16	092K25
8	49	34.5	417	5	076609
9	49	34.5	431	10	094C00
10	48.5	34.2	104	2	Q9AFK4
11	48.5	34.2	434	17	030067
12	48.5	34.2	506	16	09K0S2
13	48.5	34.2	833	2	Q9JPE1
14	48	33.8	269	16	Q9X4D5
15	48	33.8	295	16	053514
16	48	33.8	702	2	Q9AD11

17	47.5	33.5	247	11	Q9D1Z3	Q9d1z3 mus musculu
18	47.5	33.5	417	13	013013	013013 ambystoma m
19	47	33.1	200	2	Q9ZBU7	Q9zbu7 streptomyce
20	47	33.1	361	16	092LW6	092lw6 rhizobium m
21	47	33.1	5388	5	Q9UID0	Q9uid0 leishmania
22	46.5	32.7	1186	12	055767	055767 chilo iride
23	46	32.4	119	2	Q9F3D7	Q9f3d7 streptomyce
24	46	32.4	332	12	082493	082493 influenza a
25	46	32.4	463	10	09FW03	09fw03 oryza sativ
26	46	32.4	467	2	Q9RL10	Q9rl10 streptomyce
27	45.5	32.0	282	5	Q9W5H9	Q9w5h9 drosophila
28	45.5	32.0	286	2	051376	051376 pseudomonas
29	45.5	32.0	378	5	Q9W5H8	Q9w5h8 drosophila
30	45.5	32.0	382	16	091000	091000 pseudomonas
31	45.5	32.0	2292	12	066765	066765 encephalomy
32	45.5	32.0	2292	12	066850	066850 encephalomy
33	45	31.7	173	2	Q04309	Q04309 salmonella
34	45	31.7	253	16	Q9RR75	Q9rr75 delnoccocus
35	45	31.7	416	16	091235	091235 pseudomonas
36	45	31.7	568	4	Q9UN89	Q9un89 homo sapien
37	45	31.7	568	4	095470	095470 homo sapien
38	45	31.7	580	4	Q9UL08	Q9ul08 homo sapien
39	45	31.7	642	2	Q9LJ06	Q9lj06 streptomyce
40	45	31.7	663	16	Q9PEJ9	Q9pej9 xylella fas
41	45	31.7	754	12	09JH33	09jh33 tt virus. o
42	45	31.7	790	5	Q20599	Q20599 caenorhabdi
43	45	31.7	842	5	Q950F5	Q950f5 caenorhabdi
44	45	31.7	1776	10	Q9MA20	Q9ma20 arabidopsis
45	45	31.7	2484	6	Q28006	Q28006 bos taurus

ALIGNMENTS

RESULT	ID	Q9X7U8	PRELIMINARY;	PRT;	345 AA.
AC	Q9X7U8	01-NOV-1999 (TREMblrel. 12, Created)			
DT	01-NOV-1999	(TREMblrel. 12, Last sequence update)			
DT	01-DEC-2001	(TREMblrel. 19, Last annotation update)			
DE	HYPOTHETICAL 37.1 KDA PROTEIN.				
GN	SC5H1.41.				
OS	Streptomyces coelicolor.				
OC	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;				
OC	Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.				
OX	NCBI_Taxid=1902;				
RN	[1]	SEQUENCE FROM N.A.			
RP	STRAIN=A3(2);				
RA	Oliver K., Harris D.,				
RL	Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.				
RN	[2]	SEQUENCE FROM N.A.			
RP	STRAIN=A3(2);				
RA	James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;				
RL	Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.				
RN	[3]	SEQUENCE FROM N.A.			
RP	STRAIN=A3(2);				
RC	MEDLINE=7000351; PubMed=8843436;				
RX	Redenbach M., Kleser H.M., Denapite D., Eichner A., Cullum J.,				
RA	Kinashi H., Hopwood D.A.;				
RT	"A set of ordered cosmids and a detailed genetic and physical map for				
RL	the 8 Mb Streptomyces coelicolor A3(2) chromosome.";				
DR	EMBL; AL049863; CAB42966.1; -				
KW	Hypothetical protein.				
SQ	SEQUENCE 345 AA; 37125 MW; 4DB68D28BB84F1BE CRC64;				

Query Match 38.0%; Score 54; DB 2; Length 345;
Best Local Similarity 45.0%; Pred. No. 5.4;

Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 5 WTAWYQHDRLRAYRPFVHRRP 24
 1 : : : | | | | : | |
 DB 82 WAERSRHEIGAYRSFVRRP 101

RESULT 2

O48706 PRELIMINARY; PRT; 267 AA.

AC O48706;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE ORF1 PROTEIN.
 GN ORF1.
 OS Lactobacillus leichmannii.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
 CC Lactobacillus
 OX NCBI_TaxID=28039;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-DSM 20076;
 RA Schenk-Groeninger R.;
 RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X81869; CAA57458.1; -;
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR PROSITE: PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
 SQ SEQUENCE 267 AA; 29995 MW; 29D060B935C559AB CRC64;

Query Match 37.0%; Score 52.5; DB 2; Length 267;
 Best Local Similarity 52.4%; Pred. No. 6.9;
 Matches 11; Conservative 2; Mismatches 5; Indels 3; Gaps 1;

OY 2 RYPWTAWYQHDRLAY---RRF 19
 : | | : | | | | | | | | | |
 DB 161 QVPLAVYTHHDLRYNCCORF 181

RESULT 3

O53357 PRELIMINARY; PRT; 389 AA.

AC O53357;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE PUTATIVE N-ACYL-L-AMINO ACID AMIDOHYDROLASE.
 GN AMIA OR RV3305C OR MT016.04C.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 CC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RA MEDLINE=96295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekoa F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltham T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagers K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;
 RA "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence."
 RL Nature 393:537-544(1998).
 DR EMBL; AL021841; CAA17077.1; -;
 DR MEROPS; M40.0NM; -;
 DR Tuberculist; RV3305C; -;
 DR InterPro: IPR002933; Peptidase_M20.
 DR InterPro: IPR000169; ThiolProt_act_site.

DR Pfam; PF01546; Peptidase_M20; 1.
 DR PROSITE: PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
 KW Hydrolase; Complete proteome.
 SQ SEQUENCE 389 AA; 41227 MW; B7D595748A1522A0 CRC64;

Query Match 35.9%; Score 51; DB 16; Length 389;
 Best Local Similarity 45.0%; Pred. No. 17;
 Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

OY 5 WTAWYQHDRLRAYRPFVHRRP 24
 1 : : : | | | | : | |
 DB 10 WLAHHDDLVGWRRIHRRP 29

RESULT 4

O9NAK6 PRELIMINARY; PRT; 454 AA.

AC O9NAK6;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Y38E10A.4 PROTEIN.
 GN Y38E10A.4.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 CC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wallis J.M.;
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 RT investigating biology."
 RL Science 282:2012-2018(1998).
 CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
 DR EMBL; AL110484; CAB54395.1; -;
 DR InterPro: IPR000859; CUB; 1.
 DR InterPro: IPR001304; Lectin_c.
 DR Pfam; PF00431; CUB; 1.
 DR Pfam; PF00059; Lectin_c; 2.
 DR SMART; SM00034; CLECT; 2.
 DR SMART; SM00042; CUB; 1.
 DR PROSITE; PS01180; CUB; 1.
 DR PROSITE; PS00615; C_TYPE_LECTIN_1; UNKNOWN_1.
 DR PROSITE; PS50041; C_TYPE_LECTIN_2; 2.
 SQ SEQUENCE 454 AA; 50121 MW; 452944C0E1454A39 CRC64;

Query Match 35.9%; Score 51; DB 5; Length 454;
 Best Local Similarity 41.7%; Pred. No. 19;
 Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

OY 1 SRYPWTAWYQHDRLAYRPFVHRRP 24
 1 : | | : | | : | | : | |
 DB 258 SMVPTGSGWIPVCKKASNSFLCKRP 281

RESULT 5

O9V820 PRELIMINARY; PRT; 512 AA.

AC O9V820; O9V821;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE BEST: LD13441 PROTEIN.
 GN BEST: LD13441 OR CG14478.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

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OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7227;
RN [1]
RP SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abri J.F., Agapayni A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolhakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier E.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harits N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalili M., Kalush F., Karpen G.H., Ke Z., Kenison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merklow G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Maasman D.A., Weinstein G.M., Weisenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A
CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
DR EMBL; AE003803; AAF57859.1; -
DR EMBL; AE003803; AAF57860.1; -
DR FlyBase; FBgn0028953; BEST:ID13441.
DR InterPro; IPR001525; C5_DNA_meth.
DR PROSITE; PS00095; C5_MTase_2; UNKNOWN_1.
KW Alternative splicing; Hypothetical protein.
FT VARSLIC 1 366 MISSING (IN SHORT ISOFORM).
SQ SQUONCE 512 AA; 56005 MW; 943FB812DD3C1B91 CRC64;

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DE HYPOTHETICAL PROTEIN NMA0692.
GN NMA0692 OR RTM4.
OS Neisseria meningitidis (serogroup A), and
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_Taxid=65699, 487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=22491 / SEROGROUP A / SEROTYPE 4A;
RX MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltham T., Hamlin N., Holtroyd S.,
RA Jagers K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajendram M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrall B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RL meningitidis 22491."
RL Nature 404:502-506(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=22491 / SEROGROUP A / SEROTYPE 4A;
RX MEDLINE=20187481; PubMed=10722605;
RA Klee S.R., Nassif X., Kusecek B., Merker P., Beretli J.L., Achtman M.,
RA Tinsley C.R.;
RT "Molecular and biological analysis of eight genetic islands that
RT distinguish neisseria meningitidis from the closely related pathogen
RT neisseria gonorrhoeae."
RT Infect. Immun. 68:2082-2095(2000).
DR EMBL; AL162753; CAB83978.1; -
DR EMBL; AJ391255; CAB71949.1; -
KW Hypothetical protein; Complete proteome.
SQ SQUONCE 833 AA; 88713 MW; DBC991A437511AC9 CRC64;

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Query Match 35.9%; Score 51; DB 16; Length 833;
Best Local Similarity 33.3%; Pred. No. 36;
Matches 7; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 2 RVPTATYQNDLRVRFVHR 22
Db 666 RTGEPWTRHDVQRYQYNO 686

RESULT 7
ID Q92K25 PRELIMINARY; PRT; 141 AA.
AC Q92K25;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE HYPOTHETICAL TRANSMEMBRANE PROTEIN SMC01586.
GN SMC01586.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_Taxid=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21368234; PubMed=11474104;
RA Galibert F., Finan T.M., Long S.R., Puehler A., Abola P., Ampe F.,
RA Barloy-Hubler F., Barnett M.J., Becker A., Boistard P., Bothe G.,
RA Boutry M., Bowser L., Buhrmester J., Cadieu E., Capela D., Chain P.,
RA Cowie A., Davis R.W., Dreano S., Federspiel N.A., Fisher R.F.,
RA Gloux S., Godrie T., Goffeau A., Golding B., Guzy J., Gurjal M.,
RA Hernandez-Lucas I., Hong A., Huitzer L., Hyman R.W., Jones T., Kahn D.,
RA Kahn M.L., Kalman S., Keating D.H., Kiss E., Komp C., Lelaure V.,
RA Mesny D., Palm C., Beck M.C., Pohl T.M., Portetelle D., Punnelle B.,
RA Ramsperger U., Surzycki R., Thebaud P., Vandenbol M.,
RA Vorhoeffer F.J., Weidner S., Wells D.H., Wong K., Yen K.-C., Batut J.;
RT "The composite genome of the legume symbiont Sinorhizobium meliloti."
RL Science 293:668-672(2001).

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DR EMBL: AL591790; CAC46910.1; -
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 141 AA; 15657 MW; D3B4CB1BIC93F879 CRC64;

Query Match 34.9%; Score 49.5; DB 16; Length 141;
 Best Local Similarity 52.9%; Pred. No. 9.7;
 Matches 9; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY 4 PWT-AMYOHDLRAYRRF 19
 ||| |||::: |||
 Db 105 PWT-AMYRYRCGRYRSF 121

RESULT 8
 ID 076609 PRELIMINARY; PRT; 417 AA.
 AC 076609;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE HYPOTHEITICAL 47.0 KDA PROTEIN.
 GN T07H3.5.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 CC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Beck C., O'Brien D., Kramer J.;
 RT "The sequence of C. elegans cosmid T07H3.";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 RN (3)
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RT "Direct Submission.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
 DR EMBL: AF077540; AAC26308.1; -
 DR HSP: P13727; IHB0.
 DR InterPro: IPR000859; CUB.
 DR InterPro: IPR001304; lectin_c.
 DR Pfam: PF00431; CUB; 1.
 DR Pfam: PF00059; lectin_c; 2.
 DR SMART: SM00034; CLECT; 2.
 DR SMART: SM00042; CUB; 1.
 DR PROSITE: PS01180; CUB; 1.
 DR PROSITE: PS00615; C-TYPE_LECTIN_1; UNKNOWN_1.
 DR PROSITE: PS50041; C-TYPE_LECTIN_2; 2.
 KW Hypothetical protein.
 SQ SEQUENCE 417 AA; 46974 MW; 090ABHFA20ABE5H CRC64;

Query Match 34.5%; Score 49; DB 5; Length 417;
 Best Local Similarity 39.1%; Pred. No. 35;
 Matches 9; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 2 RVPWTAMYOHDLRAYRRFVHRRP 24
 ||| |||::: |||
 Db 256 RQPMGLWYTGNDYDRKFFCKRP 278

RESULT 9

Q94C00
 ID 094C00 PRELIMINARY; PRT; 431 AA.
 AC 094C00;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE P0660F12.30 PROTEIN.
 GN P0660F12.30.
 OS Oryza sativa (Rice).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 CC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=4530;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
 RT clone:P0660F12.";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AP003687; BAB3864.1; -
 SQ SEQUENCE 431 AA; 46474 MW; 828E4E2554C2B8DB CRC64;

Query Match 34.5%; Score 49; DB 10; Length 431;
 Best Local Similarity 60.0%; Pred. No. 36;
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 7 AMYOHDLRAYRRFVH 21
 ||| |||::: |||
 Db 100 AMQPPDLRRFARFGH 114

RESULT 10
 ID 09AFX4 PRELIMINARY; PRT; 104 AA.
 AC 09AFX4;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE ORF, HYPOTHEITICAL.
 GN S0038.
 OS Shigella flexneri.
 OG Plasmid virulence plasmid pWR501.
 CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Shigella.
 OX NCBI_TaxID=623;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21189246; PubMed=11292750;
 RA Venkatesan M.M., Goldberg M.B., Rose D.J., Grotbeck E.J., Burland V.,
 RA Blatner F.R.;
 RT "Complete DNA sequence and analysis of the large virulence plasmid of
 RT Shigella flexneri.";
 RL Infect. Immun. 69:3271-3285(2001).
 DR EMBL: AF348706; AAK18349.1; -
 KW Plasmid.
 SQ SEQUENCE 104 AA; 11767 MW; 7F0C625CA72ED4FF CRC64;

Query Match 34.2%; Score 48.5; DB 2; Length 104;
 Best Local Similarity 35.0%; Pred. No. 9.9;
 Matches 14; Conservative 2; Mismatches 7; Indels 17; Gaps 2;

QY 1 SRVPW-----TAWYOHDLRAYRRFVHRRP 24
 ||||| |||:| | | | |
 Db 22 SRVPWKTSTKSSAPSLKSTCSTDW-KHYPLLRQSRHRRP 60

RESULT 11
 ID 030067 PRELIMINARY; PRT; 434 AA.
 AC 030067;

DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE HYPOTHEMETICAL 50.6 KDA PROTEIN.
 GN AF0170.
 OS Archaeoglobus fulgidus.
 OC Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
 OC Archaeoglobus.
 NCBI_TaxID=2234;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
 RX MEDLINE=98049343; PubMed=9389475;
 RA Klenk H.-P., Clayton R.A., Tomb J.-F., Nelson K.E.,
 RA Ketchum K.A., Dodson R.J., Gwin M., Hickey E.K., Peterson J.D.,
 RA Fleischmann D.L., Kierlavage A.R., Graham D.E., Kyriplides N.C., Gill S.,
 RA Kirness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
 RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodok A., Zhou L.,
 RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Uitterback T.,
 RA Cotton M.D., Spriggs T., Arlrich P., Kaine B.P., Sykes S.M.,
 RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
 RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
 RA Venter J.C.;
 RT "The complete genome sequence of the hyperthermophilic, sulphate-
 RT reducing archaeon Archaeoglobus fulgidus.";
 RL Nature 390:364-370(1997).
 DR EMBL: AE001094; AAB91065.1; -.
 DR TIGR: AF0170; -.
 DR InterPro: IPR000014; PAS.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 434 AA; 50640 MW; 777F8D5059347D2E CRC64;

Query Match 34.2%; Score 48.5; DB 17; Length 434;
 Best Local Similarity 42.9%; Pred. No. 43;
 Matches 9; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

OY 3 VPWTAWYOHDLRAYRFRVHR 22
 DB 162 IPVLMFKHDEIRALRVLRH 182

RESULT 12
 ID 09K0S2 PRELIMINARY; PRT; 506 AA.
 AC 09K0S2;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE HYPOTHEMETICAL PROTEIN NMB0506.
 GN NMB0506.
 OS Neisseria meningitidis (serogroup B).
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OC NCBI_TaxID=491;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MC58 / SEROGROUP B;
 RX MEDLINE=2017575; PubMed=10710307;
 RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
 RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
 RA Nelson W.C., Gwin M.L., Deboy R., Peterson J.D., Hickey E.K.,
 RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
 RA Cotton M.D., Uitterback T.R., Khouri H., Qin H., Vamathevan J.,
 RA Gill J., Scarlato V., Masignani V., Pizsa M., Grandi G., Sun L.,
 RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
 RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
 RT MC58.";
 RL Science 287:1809-1815(2000).
 DR EMBL: AE002407; AAF40938.1; -.
 DR TIGR: NMB0506; -.
 KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 506 AA; 52695 MW; A45ECDEA04046E5C CRC64;

Query Match 34.2%; Score 48.5; DB 16; Length 506;
 Best Local Similarity 38.1%; Pred. No. 50;
 Matches 8; Conservative 7; Mismatches 3; Indels 3; Gaps 1;

OY 2 RVPWTAWYOHDLRAYRFRVHR 22
 DB 342 REPWT---RHDVOTRYOYNO 359

RESULT 13
 ID 09JPE1 PRELIMINARY; PRT; 833 AA.
 AC 09JPE1;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DE HYPOTHEMETICAL 88.4 KDA PROTEIN.
 GN RTW4.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OC NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FAM18;
 RX MEDLINE=20187481; PubMed=10722605;
 RA Klee S.R., Nassif X., Kusecek B., Merker P., Beretti J.L., Achtman M.,
 RA Tinsley C.R.;
 RT "Molecular and biological analysis of eight genetic islands that
 RT distinguish neisseria meningitidis from the closely related pathogen
 RT neisseria gonorrhoeae.";
 RL Infect. Immun. 68:2082-2095(2000).
 DR EMBL: AJ391284; CAB72083.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 833 AA; 88396 MW; B967C8422CD71A12 CRC64;

Query Match 34.2%; Score 48.5; DB 2; Length 833;
 Best Local Similarity 38.1%; Pred. No. 83;
 Matches 8; Conservative 7; Mismatches 3; Indels 3; Gaps 1;

OY 2 RVPWTAWYOHDLRAYRFRVHR 22
 DB 669 REPWT---RHDVOTRYOYNO 686

RESULT 14
 ID 09X4D5 PRELIMINARY; PRT; 269 AA.
 AC 09X4D5;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE L1CD2 (L1CD2 PROTEIN).
 GN L1CD2 OR SPI274.
 OS Streptococcus pneumoniae.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 OC Streptococcus.
 OC NCBI_TaxID=1313;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=86X;
 RX MEDLINE=99217023; PubMed=10200966;
 RA Zhang J.R., Idanpaan-Helkkila I., Fischer W., Tuomanen E.I.;
 RT "Pneumococcal l1cd2 gene is involved in phosphorylcholine
 RT metabolism.";
 RL Mol. Microbiol. 31:1477-1486(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TIGR4;
 RX MEDLINE=21357209; PubMed=11463916;

RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
 RA Peterson S., Heidelberg J., Deboy R.T., Haft D.H., Dodson R.J.,
 RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
 RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
 RA Holtzapple E., Kouri H., Wolf A.M., Uterback T.R., Hansen C.L.,
 RA McDonald L.A., Feldlyum T.V., Anginoli S., Dickinson T., Hickey E.K.,
 RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
 RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
 RT "Complete genome sequence of a virulent isolate of Streptococcus
 RT pneumoniae.";
 RL Science 293:498-506(2001).
 DR EMBL: AF106539; AAD37094.1; -;
 DR EMBL: AE007426; AAK75378.1; -;
 DR TIGR: SP1274; -;
 KW Complete proteome.
 SQ SEQUENCE 269 AA; 32100 MM; 31A152DFAA480A10 CRC64;

Query Match 33.8%; Score 48; DB 16; Length 269;
 Best Local Similarity 54.5%; Pred. No. 31;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 8 WYOHDLRAYRR 18
 |||::|||:
 DB 258 WYSHSIKAYRK 268

RESULT 15
 OS3514
 ID 053514 PRELIMINARY; PRT; 295 AA.
 AC 053514.
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE PUTATIVE MEMBRANE PROTEIN.
 GN RV2180C OR MTW021.13C.
 GN
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RX MEDLINE=96295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.";
 RL Nature 393:537-544(1998).
 DR EMBL: AL021957; CAAT7484.1; -;
 DR TuberculList; RV2180C; -;
 KW Complete proteome.
 SQ SEQUENCE 295 AA; 33213 MM; 124501E68D4739CF CRC64;

Query Match 33.8%; Score 48; DB 16; Length 295;
 Best Local Similarity 26.3%; Pred. No. 34;
 Matches 10; Conservative 4; Mismatches 2; Indels 22; Gaps 1;

OY 8 WYOHDL-----RAYRRFVHRR 23
 |||||::|||:
 DB 6 WLOHDIYDRGRLLPCLCYAVFLVFLVTRSFVFTIHR 43

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 15, 2002, 11:49:01 ; Search time 73.67 seconds
(without alignments)
12.062 Million cell updates/sec

Title: US-09-613-092a-6_COPY_3_10
Perfect score: 46
Sequence: 1 YOHDLRAY 8

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A.Geneseq_032802:*
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2: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT:*
4: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT:*
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21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	100.0	15	20	AAV30352
2	35	76.1	187	18	AAW20436
3	35	76.1	432	18	AAW20733
4	35	76.1	447	22	AAU36020
5	34	73.9	316	20	AAV42795
6	34	73.9	1136	22	ABG14341
7	34	73.9	1136	22	ABG15880
8	34	73.9	1249	22	ABG26042
9	33	71.7	314	18	AAW11801
10	33	71.7	316	19	AAW69546
11	33	71.7	398	18	AAW11798

12	33	71.7	400	19	AAW69545
13	33	71.7	451	21	AAW10565
14	33	71.7	466	21	AAW10564
15	33	71.7	468	21	AAW32000
16	33	71.7	480	21	AAW31999
17	33	71.7	488	21	AAW10563
18	33	71.7	490	21	AAW31998
19	33	71.7	1563	22	ABW58432
20	32	69.6	89	22	AAW42343
21	32	69.6	107	22	ABG08859
22	32	69.6	137	22	AAU33553
23	32	69.6	138	22	AAU36056
24	32	69.6	354	22	AAU38322
25	32	69.6	356	22	AAU34471
26	32	69.6	370	22	AAU44615
27	32	69.6	464	22	ABG14467
28	32	69.6	512	22	ABW69433
29	32	69.6	604	22	ABW71943
30	32	69.6	676	22	ABG08862
31	32	69.6	708	21	AAV97550
32	32	69.6	1788	21	AAW85575
33	32	69.6	2396	22	ABW64047
34	31	67.4	28	17	AAW91380
35	31	67.4	86	21	AAW00043
36	31	67.4	239	22	ABG29619
37	31	67.4	295	22	ABG29618
38	31	67.4	380	20	AAV32053
39	31	67.4	432	20	AAW88236
40	31	67.4	441	22	ABW92783
41	31	67.4	442	22	ABW71447
42	31	67.4	449	21	AAW12572
43	31	67.4	533	10	AAW3091
44	31	67.4	554	22	ABG19731
45	31	67.4	554	22	ABG19785

ALIGNMENTS

RESULT 1	AAV30352	standard; Peptide; 15 AA.
XX	AAV30352:	
XX	09-NOV-1999	(first entry)
DE	Epitope derived from pneumococcal surface adhesion A protein.	
XX	Pneumococcal surface adhesion A protein; Psaa: monoclonal antibody;	
KW	vaccine; Streptococcus pneumoniae infection.	
XX		
OS	Streptococcus pneumoniae.	
XX		
PN	WO945121-A1.	
XX		
PD	10-SEP-1999.	
XX		
PF	26-FEB-1999; 99WO-US04326.	
XX		
PR	02-MAR-1998; 98US-0076565.	
XX		
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.	
PI	Ades EW, Carlone GM, Sampson JS, Tharpe JA, Westerink MAJ,	
PI	Zeller JL;	
XX	WPI; 1999-540849/45.	
DR		
XX		
PT	New peptides corresponding to Streptococcus pneumoniae Psaa, used	
PT	for treating or preventing Streptococcus pneumoniae infection in a	
XX	subject	

Dirofilaria immiti
Aradipops thalia
Aradipops thalia
Aradipops thalia
Aradipops thalia
Aradipops thalia
Aradipops thalia
Drosophila melanog
Protonibacterium
Novel human diagno
Klebsiella pneumonia
Klebsiella pneumonia
Salmonella typhi c
E. coli cellular p
Protonibacterium
Novel human diagno
Drosophila melanog
Drosophila melanog
Novel human diagno
Mouse PAMP protein
D. melanogaster BA
Drosophila melanog
H2-kappa-B binding
Human secreted pro
Novel human diagno
Novel human diagno
Bovine pregnancy a
Mouse prothrombina
Human protein sequ
Drosophila melanog
NDO related comple
Vire2 gene product
Novel human diagno
Novel human diagno

PS Claim 6; Page 43; 58pp; English.
XX
CC AAY0351-54 represent immunogenic peptides which are derived from
CC a pneumococcal surface adhesion A protein (PsaA). The specification
CC describes monoclonal antibodies which bind epitopes of the PsaA protein
CC (e.g present sequence). The peptides can be used in vaccines to prevent
CC Streptococcus pneumoniae infections. The antibodies of the invention
CC can also be used to detect S. pneumoniae in a sample or individual.
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 46; DB 20; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0068;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YOHDLRAY 8
Db 3 yghdlray 10

RESULT 2
ID AAM20436 standard; Protein: 187 AA.
XX
AC AAM20436;
XX
DT 14-JUL-1997 (first entry)
XX
DE H. pylori protein.
XX
KW Cytoplasmic; vaccine; prevention; treatment; infection; identification;
KW binding compound; bacterium; life cycle; activator; bacteria; inhibitor;
KW duodenal ulcer disease; chronic gastritis; diagnosis; envelope;
KW outer membrane; cell envelope; transporter.
XX
OS Helicobacter pylori.
XX
PN MO9640893-A1.
XX
PD 19-DEC-1996.
XX
PF 06-JUN-1996; 96WO-US09122.
XX
PR 01-APR-1996; 96US-0630405.
PR 07-JUN-1995; 95US-0487032.
XX
PA (ASTR) ASTRA AB.
XX
PI Berglindh OT, Smith D, Mellgaerd BL;
XX
DR WPI; 1997-052306/05.
DR N-PSDB; AAT67609.
XX
PT Helicobacter pylori nucleic acid sequences and related
PT polypeptide(s) - useful for vaccines to treat or prevent H. pylori
PT infection, and to detect Helicobacter
XX
PS Disclosure; Pages 613; 1481pp; English.
XX
CC The present sequence is a Helicobacter pylori protein of unknown
CC function. The protein may be used in a vaccine to prevent or treat
CC H. pylori infection or to identify H. pylori polypeptide binding
CC compounds, useful as potential H. pylori life cycle activators or
CC inhibitors. The genomic sequence of H. pylori (ATCC 55679) was
CC determined from overlapping contigs generated by mechanically shearing
CC the bacterial DNA. The sequences were analysed for ORF of at least 180
CC nucleotides, and the predicted coding regions defined by computer
CC evaluation. To identify likely H. pylori antigens for vaccine
CC development, the amino acid sequences predicted from various ORF were
CC analysed for significant homology to other known or exported membrane
CC proteins. Having identified and determined the sequences of interest,
CC particular regions can be isolated from H. pylori by PCR amplification

CC for recombinant polypeptide production, e.g. in E. coli hosts.
XX
SQ Sequence 187 AA;

Query Match 76.1%; Score 35; DB 18; Length 187;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YOHDLR 6
Db 103 yghdlr 108

RESULT 3
ID AAM20733 standard; protein: 432 AA.
XX
AC AAM20733;
XX
DT 16-JUL-1997 (first entry)
XX
DE H. pylori cell envelope protein, 06cp11722orf15.
XX
KW Cytoplasmic; vaccine; prevention; treatment; infection; identification;
KW binding compound; bacterium; life cycle; activator; bacteria; inhibitor;
KW duodenal ulcer disease; chronic gastritis; diagnosis; envelope.
XX
OS Helicobacter pylori.
XX
PN MO9640893-A1.
XX
PD 19-DEC-1996.
XX
PF 06-JUN-1996; 96WO-US09122.
XX
PR 01-APR-1996; 96US-0630405.
PR 07-JUN-1995; 95US-0487032.
XX
PA (ASTR) ASTRA AB.
XX
PI Berglindh OT, Smith D, Mellgaerd BL;
XX
DR WPI; 1997-052306/05.
DR N-PSDB; AAT67986.
XX
PT Helicobacter pylori nucleic acid sequences and related
PT polypeptide(s) - useful for vaccines to treat or prevent H. pylori
PT infection, and to detect Helicobacter
XX
PS Claim 56; Page 1148-1149; 1481pp; English.
XX
CC The present sequence is a Helicobacter pylori cell envelope protein.
CC The protein may be used in a vaccine to prevent or treat H. pylori
CC infection or to identify H. pylori polypeptide binding compounds,
CC useful as potential H. pylori life cycle activators or inhibitors.
CC The genomic sequence of H. pylori (ATCC 55679) was determined from
CC overlapping contigs generated by mechanically shearing the bacterial
CC DNA. The sequences were analysed for ORF of at least 180 nucleotides,
CC and the predicted coding regions defined by computer evaluation. To
CC identify likely H. pylori antigens for vaccine development, the amino
CC acid sequences predicted from various ORF were analysed for significant
CC homology to other known or exported membrane proteins. Having identified
CC and determined the sequences of interest, particular regions can be
CC isolated from H. pylori by PCR amplification for recombinant polypeptide
CC production, e.g. in E. coli hosts.
XX
SQ Sequence 432 AA;

Query Match 76.1%; Score 35; DB 18; Length 432;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YOHDLR 6
| | | | |
DB 239 yghdlr 244

RESULT 4
AAU36020
ID AAU36020 standard; Protein; 447 AA.

AC AAU36020;

DE 14-FEB-2002 (first entry)

DE Helicobacter pylori cellular proliferation protein #333.

KW Antisense; prokaryotic cellular proliferation protein;
antibiotic; antibacterial; drug design.

OS Helicobacter pylori.

PN WO200170955-A2.

PD 27-SEP-2001.

PF 21-MAR-2001; 2001WO-US09180.

PR 21-MAR-2000; 2000US-191078P.

PR 23-MAY-2000; 2000US-206848P.

PR 26-MAY-2000; 2000US-207727P.

PR 23-OCT-2000; 2000US-242578P.

PR 27-NOV-2000; 2000US-253625P.

PR 22-DEC-2000; 2000US-257931P.

PR 16-FEB-2001; 2001US-269308P.

PA (ELIT-) ELITRA PHARM INC.

PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
Yamamoto RT, Xu HH;

PI WPI: 2001-611495/70.

DR N-PSDB: AAS53879.

XX New polynucleotides for the identification and development of
antibiotics, comprise sequences of antisense nucleic acids -

PT Example 3; Seq ID No 11613; 511pp; English.

PS

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XX

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YOHDLR 6
| | | | |
DB 238 yghdlr 243

RESULT 5
AA42795
ID AA42795 standard; Protein; 316 AA.

AC AA42795;

DE 05-JAN-2000 (first entry)

DE Streptococcus pyogenes SAG-A processing protease.

KW Streptococcus; SAG-A; tissue necrosis; antibacterial; streptolysin S;
activity; oxygen-stable; non-immunogenic; cytotoxin; beta-haemolysis;

KW disease; strep throat; cellulitis; scarlet fever; impetigo;
rheumatic fever; acute glomerular nephritis; endocarditis;

KW necrotising fasciitis; brain abscess; meningitis; osteomyelitis;
pharyngitis; pneumonia; rheumatic carditis; toxic shock; protease.

OS Streptococcus pyogenes.

PF

FT Key Location/Qualifiers

FT Misc-difference 1 /note="Encoded by TG"

XX WO9949049-A1.

XX 30-SEP-1999.

XX 18-MAR-1999; 99WO-CA00240.

XX 20-MAR-1998; 98US-0078713.

XX (MOUN) MOUNT SINAI HOSPITAL.

XX De Azavedo J, Bast D, Borgia S, Betschel S, Low D;

XX WPI: 1999-591100/50.

XX N-PSDB: AA230815.

XX New isolated Streptococcus polypeptides, used to develop products for
treating, e.g. streptococcal infections, microbial infections in plants
and animals and cancers and as preservatives -

PS Disclosure; Page 92; 99pp; English.

XX

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Streptococcus pyogenes.

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Streptococcus pyogenes.

Streptococcus pyogenes.

CC preservative, or as an antibacterial agent for medical or agricultural
CC use. They may function synergistically with conventional therapeutic
CC agents such as antibiotics and anticancer treatments, and they may be
CC used as adjuvants. They may also be used to selectively lyse cells using
CC a chimeric toxin comprising a cytolytic polypeptide operatively linked
CC to a targeting agent. SAG-A peptides can also be used for detection and
CC diagnosis and in vaccines for preventing infections.

SQ Sequence 316 AA;

Query Match 73.9%; Score 34; DB 20; Length 316;
Best Local Similarity 75.0%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YQHDLRAY 8
| | | | |
Db 204 yqhalrcy 211

RESULT 6
ABG14341
ID ABG14341 standard; Protein: 1136 AA.
XX
AC ABG14341;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #14332.
XX
KW Human: chromosome mapping; gene mapping; gene therapy; forensic;
KM food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSED INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
DR N-PSDB: AAS78528.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID No 44700; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity

CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 1136 AA;

Query Match 73.9%; Score 34; DB 22; Length 1136;
Best Local Similarity 62.5%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YQHDLRAY 8
| | | | |
Db 615 yrhdkily 622

RESULT 7
ABG15880
ID ABG15880 standard; Protein: 1136 AA.
XX
AC ABG15880;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #15871.
XX
KW Human: chromosome mapping; gene mapping; gene therapy; forensic;
KM food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSED INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
DR N-PSDB: AAS80067.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID No 46239; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and

CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.

SQ Sequence 1136 AA;

Query Match 73.9%; Score 34; DB 22; Length 1136;
Best Local Similarity 62.5%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 YOHDLRAY 8
1:||||:|
Db 615 yrhdlkly 622

RESULT 8

ABG26042
ID ABG26042 standard; Protein; 1249 AA.

AC ABG26042;

DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #26033.

KM Human; chromosome mapping; gene mapping; gene therapy; forensic;
KM food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI: 2001-639362/73.

DR N-PSDB; AAS90229.

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity

PS Claim 20; SEQ ID NO 56401; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridization probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human

CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.

SQ Sequence 1249 AA;

Query Match 73.9%; Score 34; DB 22; Length 1249;
Best Local Similarity 62.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 YOHDLRAY 8
1:||||:|
Db 615 yrhdlkly 622

RESULT 9

AAW11801
ID AAW11801 standard; Protein; 314 AA.

AC AAW11801;

DT 06-MAY-1997 (first entry)

DE Dirofilaria immitis L3 cysteine protease PDICP314.

KM Cysteine protease; filarial nematode; helminth; vaccine; heartworm;
KM Onchocerca; ndicP942; PDICP314.

OS Dirofilaria immitis.

PN WO9640884-A1.

PD 19-DEC-1996.

PF 07-JUN-1996; 96WO-US09848.

PR 07-JUN-1995; 95US-0486036.

PA (HESK-) HESKA CORP.

PA (COLS) UNIV COLORADO STATE RES FOUND.

PI Frank GR, Grieve RB, Tripp CA, Wisniewski N;

DR WPI: 1997-099931/09.

DR N-PSDB; AAT59480.

PT Filarid nematode larval nucleic acid - capable of hybridizing with
PT dirofilaria immitis or Onchocerca volvulus L3 cysteine protease, to
PT protect against parasitic helminth diseases

PS Claim 16; Page 89-90; 115pp; English.

CC Cysteine protease (CP) polypeptide PDICP314 (AAW11801) comprises the
CC mature CP protein encoded by nucleic acid ndicP942 (AAT59478),
CC derived from a cDNA library of Dirofilaria immitis L3 larvae.
CC Novel filarid nematode CP polypeptides (AAW11798-802) are capable of
CC eliciting an immune response against native helminth CPs. They can
CC be used to identify CPs, capable of inhibiting the CP activity of
CC a parasitic helminth and to raise anti-CP antibodies. The
CC polypeptide (expressed e.g. by transformed host cells), inhibitor
CC or antibody can be used in therapeutic compns. to protect an
CC animal from a disease caused by a parasitic helminth, such as
CC Dirofilaria or Onchocerca.

SQ Sequence 314 AA;

Query Match 71.7%; Score 33; DB 18; Length 314;
Best Local Similarity 62.5%; Pred. No. 86;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YOHDLRAY 8
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 Db 239 yqhdffky 246

RESULT 10
 AAM69546
 ID AAM69546 standard; Protein: 316 AA.

XX AAM69546;

DT 09-OCN-1998 (first entry)

XX Dirofilaria immitis L3 larval cysteine protease #2.

XX Onchocerca volvulus; Dirofilaria immitis; L3 larval cysteine protease;
 KW filarid nematode; parasitic helminth; vaccine.

XX Dirofilaria immitis.

PN US5792624-A.

PD 11-AUG-1998.

PF 07-JUN-1995; 95US-0482282.

PR 07-JUN-1995; 95US-0482282.

PR 12-FEB-1991; 91US-0654226.

PR 12-NOV-1991; 91US-0792209.

PR 03-AUG-1993; 93US-0101283.

PR 16-NOV-1993; 93US-0153554.

XX (HESK-) HESKA CORP.

PA (COLS) UNIV COLORADO STATE RES FOUND.

XX Frank GR, Griveau RB, Richer JK, Tripp CA, Wisniewski N;

PI WPI: 1998-456128/39.

DR N-PSDB; AAV40249.

PT Nematode larval protease proteins - useful for vaccination, etc.

XX Example 1; Column 35-38; 22pp; English.

XX The present sequence represents an L3 larval protease protein from

CC Dirofilaria immitis. An embodiment of the present invention is an

CC isolated filarid nematode nucleic acid molecule that hybridises, under

CC stringent hybridisation conditions, with a Dirofilaria immitis L3 larval

CC cysteine protease gene and/or an Onchocerca volvulus L3 larval cysteine

CC protease gene. A filarid nematode cysteine protease protein of the

CC present invention preferably has cysteine protease activity and/or

CC comprises a protein that, when administered to an animal, is capable of

CC eliciting an immune response against a natural helminth cysteine protease

CC protein. This sequence can be used in a therapeutic composition

CC capable of protecting an animal from disease caused by a parasitic

CC helminth.

XX Sequence 316 AA;

XX

AC AAM11798;
 XX 06-MAY-1997 (first entry)

XX Dirofilaria immitis L3 cysteine protease PDICP398.

XX Cysteine protease; filarid nematode; helminth; vaccine; heartworm;

XX Onchocerca; ndICP1298; PDICP398.

XX Dirofilaria immitis.

XX Key Location/Qualifiers

FT Protein 85..398

FT /label= Mat_protein

FT /note= "polypeptide PDICP314"

PN WO9640884-A1.

PD 19-DEC-1996.

PF 07-JUN-1996; 96WO-US09848.

PR 07-JUN-1995; 95US-0486036.

XX (HESK-) HESKA CORP.

PA (COLS) UNIV COLORADO STATE RES FOUND.

XX Frank GR, Griveau RB, Tripp CA, Wisniewski N;

PI WPI: 1997-099931/09.

DR N-PSDB; AAT59477.

XX filarid nematode larval nucleic acid - capable of hybridising with

PT Dirofilaria immitis or Onchocerca volvulus L3 cysteine protease, to

PT protect against parasitic helminth diseases

XX Claim 16; Page 86-87; 115pp; English.

XX Cysteine protease (CP) polypeptide PDICP398 (AAM11798) is encoded by

CC nucleic acid ndICP1298 (AAT59477), ctd. from a cDNA library of

CC Dirofilaria immitis L3 larvae. Novel filarid nematode CP

CC polypeptides (AAM11798-802) are capable of eliciting an immune

CC response against native helminth CPs. They can be used to identify

CC cpds. capable of inhibiting the CP activity of a parasitic

CC helminth and to raise anti-CP antibodies. The polypeptide

CC (expressed e.g. by transformed host cells), inhibitor or antibody

CC can be used in therapeutic compns. to protect an animal from a

CC disease caused by a parasitic helminth, such as Dirofilaria or

CC Onchocerca.

XX Sequence 398 AA;

XX

XX

Query Match 71.7%; Score 33; DB 18; Length 398;
 Best Local Similarity 62.5%; Pred. NO. 1.1e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YOHDLRAY 8
 |||| : |
 Db 241 yqhdffky 248

RESULT 12
 AAM69545
 ID AAM69545 standard; Protein: 400 AA.

XX AAM69545;

DT 09-OCN-1998 (first entry)

XX Dirofilaria immitis L3 larval cysteine protease #1.

DE Onchocerca volvulus; Dirofilaria immitis; L3 larval cysteine protease;

XX

KW filarid nematode; parasitic helminth; vaccine.
XX
OS Dirofilaria immitis.
XX
PN US5792624-A.
XX
PD 11-AUG-1998.
XX
PF 07-JUN-1995; 95US-0482282.
XX
PR 07-JUN-1995; 95US-0482282.
PR 12-FEB-1991; 91US-0654226.
PR 12-NOV-1991; 91US-0792209.
PR 03-AUG-1993; 93US-0101283.
PR 16-NOV-1993; 93US-0153554.
XX
PA (HESK-) HESKA CORP.
PA (COLS) UNITV COLORADO STATE RES FOUND.
XX
PI Frank GR, Griewe RB, Richer JK, Tripp CA, Wisniewski N;
XX
DR WPI; 1998-456128/39.
DR N-PSDB; AAV40248.
XX
PT Nematode larval protease proteins - useful for vaccination, etc.
PS
XX Example 1; Column 31-34; 22pp; English.
XX
CC The present sequence represents an L3 larval protease protein from
CC Dirofilaria immitis. An embodiment of the present invention is an
CC isolated filarid nematode nucleic acid molecule that hybridises, under
CC stringent hybridisation conditions, with a Dirofilaria immitis L3 larval
CC cysteine protease gene and/or an Onchocerca volvulus L3 larval cysteine
CC protease gene. A filarid nematode cysteine protease protein of the
CC present invention preferably has cysteine protease activity and/or
CC comprises a protein that, when administered to an animal, is capable of
CC eliciting an immune response against a natural helminth cysteine protease
CC protein. This sequence can be used in a therapeutic composition
CC capable of protecting an animal from disease caused by a parasitic
CC helminth.
XX
XX
SO Sequence 400 AA;
Query Match 71.7%; Score 33; DB 19; Length 400;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 YOHDIRAY 8
Db 325 yghdtkfy 332
RESULT 13
AAG10565
ID AAG10565 standard; Protein; 451 AA.
XX
AC AAG10565;
XX
XX 17-OCT-2000 (first entry)
DE Arabidopsis thaliana protein fragment SEQ ID NO: 8937.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
XX Arabidopsis thaliana.
XX
XX EPI033405-A2.
XX
PD 06-SEP-2000.
XX

PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131444.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
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PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
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PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
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PR 21-MAY-1999; 99US-0135353.
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PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
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PR 07-JUN-1999; 99US-0137724.
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PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
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PR 29-JUN-1999; 99US-0140991.
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PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.

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PR 09-JUL-1999; 99US-0142920.
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PR 13-AUG-1999; 99US-0148684.
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PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149910.
PR 25-AUG-1999; 99US-0150586.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
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PR 24-SEP-1999; 99US-0155659.

PR 28-SEP-1999; 99US-0156458.
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PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
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PR 07-OCT-1999; 99US-0158029.
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PR 25-OCT-1999; 99US-0161406.
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PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 71.7%; Score 33; DB 21; Length 451;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YOHDRAY 8
Db 78 ydhlesy 85

RESULT 14
ID AAG10564 standard; Protein; 466 AA.
XX AAG10564;
AC AAG10564;
XX 17-OCT-2000 (first entry)
DT XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 8936.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
XX EPI033405-A2.
XX
XX PD 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123180.
XX 09-MAR-1999; 99US-0123548.
XX 23-MAR-1999; 99US-0125788.
XX 25-MAR-1999; 99US-0126264.
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PR 29-MAR-1999; 9905-0126785.
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PR 28-JUL-1999; 9905-0145951.
PR 02-AUG-1999; 9905-0146386.
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PR 02-AUG-1999; 9905-0146389.
PR 03-AUG-1999; 9905-0147038.
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PR 26-AUG-1999; 9905-0150884.
PR 27-AUG-1999; 9905-0151065.
PR 27-AUG-1999; 9905-0151066.
PR 27-AUG-1999; 9905-0151080.
PR 30-AUG-1999; 9905-0151303.
PR 31-AUG-1999; 9905-0151438.
PR 01-SEP-1999; 9905-0151930.
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PR 10-SEP-1999; 9905-0153070.
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Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Db 93 yhdhlesy 100

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XX 17-OCT-2000 (first entry)

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KW Protein identification: signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.

XX Arabidopsis thaliana.

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Query Match 71.7%; Score 33; DB 21; Length 468;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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DB 92 ydhdlresy 99

Search completed: August 15, 2002, 11:49:02
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GenCore version 4.5
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OM protein - protein search, using sw model

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Title: US-09-613-092a-6_COPY_3_10
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Sequence: 1 YOHDLRAY 8

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Searched: 231628 seqs, 24425594 residues

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Listing first 45 summaries

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ALIGNMENTS

RESULT 1
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; Sequence 100, Application US/08248839C
; Patent No. 5843702
; GENERAL INFORMATION:
; APPLICANT: McConnell, David
; APPLICANT: Devine, Kevin
; APPLICANT: O' Kane, Charles
; TITLE OF INVENTION: A Gene Expression System
; NUMBER OF SEQUENCES: 185
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 58437020 No. 5843702disk of No. 5843702ch America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/248,839C
; FILING DATE: 25-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gregg, Valera A.
; REGISTRATION NUMBER: 35,127
; REFERENCE/DOCKET NUMBER: 3614.214-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 67 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; US-08-248-839C-100

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Best Local Similarity 62.5%; Pred. No. 5.7;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Db 27 YNHDLRSF 34

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; GENERAL INFORMATION:
; APPLICANT: TRIPP, Cynthia A.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: NOVEL FILARIID NEMATODE CYSTEINE
; TITLE OF INVENTION: PROTEASE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09848
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/486,036
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2618-33-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 213 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YOHDLRAY 8
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Db 138 YOHDKFY 145

RESULT 3
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; Sequence 4, Application US/08486036A
; Patent No. 5795768
; GENERAL INFORMATION:
; APPLICANT: TRIPP, Cynthia A.
; APPLICANT: Wisniewski, Nancy
; APPLICANT: Grieve, Robert B.
; APPLICANT: Frank, Glenn R.
; TITLE OF INVENTION: NOVEL FILARIID NEMATODE
; TITLE OF INVENTION: CYSTEINE PROTEASE PROTEINS, NUCLEIC ACID
; MOLECULES AND USES THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
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COUNTRY: U.S.A.
ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,036A
; FILING DATE: June 7, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2618-33
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 4:
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Db 239 YOHDKFY 246

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; GENERAL INFORMATION:
; APPLICANT: TRIPP, Cynthia A.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: NOVEL FILARIID NEMATODE CYSTEINE
; TITLE OF INVENTION: PROTEASE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09848
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/486,036
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2618-33-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 4:
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LENGTH: 314 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-09848-4

Query Match 71.7%; Score 33; DB 5; Length 314;
Best Local Similarity 62.5%; Pred. No. 41;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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DB 239 YOHDFKFY 246

RESULT 5
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Patent No. 5792624
GENERAL INFORMATION:
APPLICANT: Tripp, Cynthia A.
APPLICANT: Wisniewski, Nancy
APPLICANT: Grieve, Robert B.
APPLICANT: Frank, Glenn R.
TITLE OF INVENTION: NOVEL FILARIID NEMATODE CYSTEINE
TITLE OF INVENTION: PROTEASE PROTEINS, NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,282B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: 2618-33-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (970) 493-7272
TELEFAX: (970) 484-9505
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-282B-4

Query Match 71.7%; Score 33; DB 1; Length 316;
Best Local Similarity 62.5%; Pred. No. 41;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YOHDLRAY 8
||||:|
DB 241 YOHDFKFY 248

RESULT 6
PCT-US96-09848-24

Sequence 24, Application PC/TUS9609848
GENERAL INFORMATION:
APPLICANT: Tripp, Cynthia A.
APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: NOVEL FILARIID NEMATODE CYSTEINE
TITLE OF INVENTION: PROTEASE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09848
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,036
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-33-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 356 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1172
PCT-US96-09848-24

Query Match 71.7%; Score 33; DB 5; Length 356;
Best Local Similarity 62.5%; Pred. No. 46;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YOHDLRAY 8
||||:|
DB 281 YOHDFKFY 288

RESULT 7
US-08-486-036A-2
Sequence 2, Application US/08486036A
Patent No. 5795768
GENERAL INFORMATION:
APPLICANT: Tripp, Cynthia A.
APPLICANT: Wisniewski, Nancy
APPLICANT: Grieve, Robert B.
APPLICANT: Frank, Glenn R.
TITLE OF INVENTION: NOVEL FILARIID NEMATODE
TITLE OF INVENTION: CYSTEINE PROTEASE PROTEINS, NUCLEIC ACID
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.

ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,036A
FILING DATE: June 7, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-33
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 398 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-486-036A-2

Query Match 71.7%; Score 33; DB 1; Length 398;
Best Local Similarity 62.5%; Pred. NO. 52;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 YOHDLRAY 8
||| : |
Db 323 YOHDFKFY 330

RESULT 8
PCT-US96-09848-2
Sequence 2, Application PC/TUS9609848
GENERAL INFORMATION:
APPLICANT: Tripp, Cynthia A.
APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: NOVEL FILARIID NEMATODE CYSTEINE
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESSES:
ADDRESS: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09848
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,036
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-33-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 398 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-09848-2

Query Match 71.7%; Score 33; DB 5; Length 398;
Best Local Similarity 62.5%; Pred. NO. 52;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 YOHDLRAY 8
||| : |
Db 323 YOHDFKFY 330

RESULT 9
US-08-482-282B-2
Sequence 2, Application US/08482282B
Patent No. 5792624
GENERAL INFORMATION:
APPLICANT: Tripp, Cynthia A.
APPLICANT: Wisniewski, Nancy
APPLICANT: Grieve, Robert B.
APPLICANT: Frank, Glenn R.
TITLE OF INVENTION: NOVEL FILARIID NEMATODE CYSTEINE
TITLE OF INVENTION: PROTEASE PROTEINS, NUCLEIC ACID MOLECULES AND USES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESS: Carol Talkington Verser, Ph.D.
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,282B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: 2618-33-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (970) 493-7272
TELEFAX: (970) 484-9505
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-282B-2

Query Match 71.7%; Score 33; DB 1; Length 400;
Best Local Similarity 62.5%; Pred. NO. 52;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 YOHDLRAY 8
||| : |
Db 325 YOHDFKFY 332

RESULT 10
US-08-066-167-3
Sequence 3, Application US/08066167

Patent No. 5618541
GENERAL INFORMATION:
APPLICANT: OQUENTIN-MILLET, Marie-Jose
TITLE OF INVENTION: VACCINE AGAINST NEISSERIA MENINGITIDIS
TITLE OF INVENTION: INFECTIONS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/066,167
FILING DATE: 02-JUN-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91 12177
FILING DATE: 03-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 016100-002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-6620
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 887 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORGANISM: Neisseria meningitidis 2169 subunit Tbp1.
US-08-066-167-3

Query Match 67.4%; Score 31; DB 1; Length 887;
Best Local Similarity 75.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YOHDLRAY 8
Db 493 YOHANRAY 500

RESULT 11
US-08-487-890A-95
Sequence 95, Application US/08487890A
Patent No. 5708149
GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Murdin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario

COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,890A
FILING DATE: 07-JUN-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-466 MIS:jfb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 911 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-487-890A-95

Query Match 67.4%; Score 31; DB 1; Length 911;
Best Local Similarity 75.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YOHDLRAY 8
Db 517 YOHANRAY 524

RESULT 12
US-08-478-435-95
Sequence 95, Application US/08478435
Patent No. 5923323
GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Murdin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,435
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-462 MIS:vg
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 911 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-478-435-95

Query Match 67.4%; Score 31; DB 2; Length 911;
Best Local Similarity 75.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 YOHDIRAY 8
Db 517 YOHANRAY 524

RESULT 13
US-08-337-483-95
Sequence 95, Application US/08337483
Patent No. 5922562
GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Mirdin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-410 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163

INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 911 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-337-483-95

Query Match 67.4%; Score 31; DB 2; Length 911;
Best Local Similarity 75.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 YOHDIRAY 8
Db 517 YOHANRAY 524

RESULT 14
US-08-478-373-95
Sequence 95, Application US/08478373
Patent No. 5922841
GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Mirdin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,373
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-463 MIS:vg
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 911 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-478-373-95

Query Match 67.4%: Score 31: DB 2: Length 911:
Best Local Similarity 75.0%: Pred. No. 2.8e+02:
Matches 6: Conservative 0: Mismatches 2: Indels 0: Gaps 0:

Db 517 YOHANRAY 524

Search completed: August 15, 2002, 11:49:35
Job time: 276 sec

Oy 1 YOHDLRAY 8
Db 517 YOHANRAY 524

RESULT 15

US-08-474-671-95
: Sequence 95, Application US/08474671
: Patent No. 6008326
: GENERAL INFORMATION:
: APPLICANT: Loosmore, Sheena
: APPLICANT: Harkness, Robin
: APPLICANT: Schryvers, Anthony
: APPLICANT: Chong, Pele
: APPLICANT: Gray-Owen, Scott
: APPLICANT: Yang, Yan-Ping
: APPLICANT: Mirdin, Andrew
: APPLICANT: Kieln, Michel
: TITLE OF INVENTION: Transferrin Receptor Genes
: NUMBER OF SEQUENCES: 147
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Sim & McBurney
: STREET: Suite 701, 330 University Avenue
: CITY: Toronto
: STATE: Ontario
: COUNTRY: Canada
: ZIP: M5G 1R7
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/474,671
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/337,483
: FILING DATE: 08-NOV-1994
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/175,116
: FILING DATE: 29-DEC-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/148,968
: FILING DATE: 08-NOV-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Stewart, Michael I
: REGISTRATION NUMBER: 24,973
: REFERENCE/DOCKET NUMBER: 1038-465 MIS:vg
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (416) 595-1155
: TELEFAX: (416) 595-1163
: INFORMATION FOR SEQ ID NO: 95:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 911 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-08-474-671-95

Query Match 67.4%: Score 31: DB 3: Length 911:
Best Local Similarity 75.0%: Pred. No. 2.8e+02:
Matches 6: Conservative 0: Mismatches 2: Indels 0: Gaps 0:

Oy 1 YOHDLRAY 8

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OM protein - protein search, using sw model

Run on: August 15, 2002, 11:50:17 ; Search time 35.29 Seconds
(without alignments)
21.783 Million cell updates/sec

Title: US-09-613-092a-6_COPY_3_10
Perfect score: 46
Sequence: 1 YOHDLRAY 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	80.4	284	2 B83236	conserved hypotet
2	36	78.3	267	2 S52347	hypothetical prote
3	36	78.3	451	2 T15718	hypothetical prote
4	36	78.3	563	2 T04598	hypothetical prote
5	35	76.1	447	2 D71812	udp-n-acetyluramy
6	35	76.1	502	2 B75287	sensor histidine k
7	34	73.9	167	2 JW0065	fast skeletal trop
8	34	73.9	481	2 F96802	hypothetical prote
9	34	73.9	1030	2 T51452	hypothetical prote
10	34	73.9	1224	2 T25770	hypothetical prote
11	33	71.7	317	2 B37388	hypothetical prote
12	33	71.7	330	2 B97368	probable DNA-bindi
13	33	71.7	330	2 AB2586	hypothetical sugar
14	33	71.7	436	2 S42160	MSS51 protein - ye
15	33	71.7	488	2 T47787	hypothetical prote
16	33	71.7	490	2 A84861	probable amine oxi
17	33	71.7	516	2 D96682	protein FIE22.18 l
18	33	71.7	762	2 H83415	cis/trans isomeras
19	33	71.7	949	2 B32105	clathrin-associate
20	32	69.6	199	2 H90024	hypothetical prote
21	32	69.6	213	2 S13398	chloroamphenicol O-
22	32	69.6	261	2 S72750	triose-phosphate 1
23	32	69.6	354	2 AD0552	S-adenosylmethioni
24	32	69.6	356	2 B38530	S-adenosylmethioni
25	32	69.6	356	2 D85536	S-adenosylmethioni
26	32	69.6	356	2 H90685	S-adenosylmethioni
27	32	69.6	385	2 T20701	hypothetical prote
28	32	69.6	479	2 D70676	probable PE protei
29	32	69.6	727	2 T10616	hypothetical prote

30	32	69.6	812	2 S64929	hypothetical prote
31	32	69.6	1101	2 T20881	hypothetical prote
32	32	69.6	1139	1 PAVB85	alpha-a protein -
33	32	69.6	2329	2 S44625	C50C3.6 protein -
34	31	67.4	98	2 G97041	hypothetical prote
35	31	67.4	104	2 B71180	hypothetical prote
36	31	67.4	133	2 D64609	conserved hypotet
37	31	67.4	158	2 G64885	ydar protein - Esc
38	31	67.4	158	2 B90817	probable phage rep
39	31	67.4	158	2 B85676	unknown protein en
40	31	67.4	260	2 E87577	glutamine cyclotra
41	31	67.4	263	1 A26147	egg-laying hormone
42	31	67.4	271	1 ONCAPA	egg-laying hormone
43	31	67.4	342	2 T14695	P2 protein homolog
44	31	67.4	348	2 G82645	alcohol dehydrogen
45	31	67.4	353	2 D83361	alcohol dehydrogen

ALIGNMENTS

RESULT 1
B83236
conserved hypothetical protein PA3283 [imported] - Pseudomonas aeruginosa (strain PAO
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: B83236
R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A:Reference number: A82950; PMID:20437337
A:Accession: B83236
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-284 <STO>
A:Cross-references: GB:AE004750; GB:AE004091; NID:9949400; PIDN:AMG06671.1; GSPDB:GN
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA3283

Query Match 80.4%; Score 37; DB 2; Length 284;
Best Local Similarity 85.7%; Pred. No. 7;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 QHDLRAY 8
|||||
Db 88 QHDLRAY 94

RESULT 2
S52347
hypothetical protein 1 - Lactobacillus leichmannii
C:Species: Lactobacillus leichmannii
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 05-Nov-1999
C:Accession: S52347
R:Schenk-Groeninger, R.
Submitted to the EMBL Data Library, January 1995
A:Reference number: S52347
A:Accession: S52347
A:Molecule type: DNA
A:Residues: 1-267 <SCH>
A:Cross-references: EMBL:X61869; NID:9666067; PIDN:CAA57458.1; PID:9666068
A:Experimental source: DSM 20076

Query Match 78.3%; Score 36; DB 2; Length 267;
Best Local Similarity 75.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 YOHDLRAY 8

Db 168 YNHDLRIT 175

RESULT 3

115718
|111111|
hypothetical protein C30G12.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T15718
R:Latreille, P.
Submitted to the EMBL Data Library, July 1995
A:Description: The sequence of C. elegans cosmid C30G12.
A:Reference number: Z18393
A:Accession: T15718
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-451 <LAT>
A:Cross-references: EMBL:U21319; NID:q687832; PID:q687833; PIDN:AAC46670.1; CESP:C30G12.
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:C30G12.1
A:Introns: 37/3; 71/2; 107/3; 153/2; 205/1; 289/1; 376/3

Query Match 78.3%; Score 36; DB 2; Length 451;
Best Local Similarity 75.0%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 YOHDLRAY 8
|111111|
Db 62 YOHDLRAF 69

RESULT 4

T04598
|111111|
hypothetical protein F23E13.180 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 15-Sep-2000
C:Accession: T04598
R:Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Jesse, T.
Submitted to the Protein Sequence Database, March 1998
A:Reference number: Z15378
A:Accession: T04598
A:Molecule type: DNA
A:Residues: 1-563 <BEV>
A:Cross-references: EMBL:AL022141
A:Experimental source: cultivar Columbia; BAC clone F23E13
C:Genetics:
A:Map position: 4
A:Introns: 80/1; 105/1; 116/3; 162/1; 192/1; 217/2; 243/3; 278/3; 327/3; 372/2; 467/3;
A:Note: F23E13.180
C:Superfamily: Arabidopsis thaliana hypothetical protein F23E13.180

Query Match 78.3%; Score 36; DB 2; Length 563;
Best Local Similarity 75.0%; Pred. No. 22;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 YOHDLRAY 8
|111111|
Db 273 YRHSURAY 280

RESULT 5

D71812
|111111|
udp-n-acetylmutamyl-tripeptide synthetase - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 20-Apr-2000
C:Accession: D71812
R:Alm, R.A.; Ling, L.S.L.; Molr, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Voyts, G.F.;

Nature 397, 176-180, 1999

A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric p
A:Reference number: A71800; MUID:99120557
A:Accession: D71812
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-447 <ARN>
A:Cross-references: GB:AE001561; GB:AE001439; NID:q415600; PIDN:AAD06968.1; PID:q415
A:Experimental source: strain J99
C:Genetics:
A:Gene: murF
C:Superfamily: UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase

Query Match 76.1%; Score 35; DB 2; Length 447;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YOHDLR 6
|111111|
Db 238 YOHDLR 243

RESULT 6

B75287
|111111|
sensor histidine kinase - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: B75287
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
M.; Shen, M.; Vamathevan, J.U.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896
A:Accession: B75287
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-502 <WH>
A:Cross-references: GB:AE002064; GB:AE000513; NID:q6460134; PIDN:APF11875.1; PID:q646
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR2328
A:Map position: 1
C:Superfamily: envz protein; sensor histidine kinase homology

Query Match 76.1%; Score 35; DB 2; Length 502;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YOHDLR 6
|111111|
Db 310 YOHDLR 315

RESULT 7

JW0065
|111111|
fast skeletal tropomyosin C - Entosphenus japonicus
N:Alternate names: ftnC
C:Species: Entosphenus japonicus
C:Date: 13-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 29-Sep-1999
C:Accession: JW0065
R:Yusasa, H.J.; Cox, J.A.; Takagi, T.
J. Biochem. 123, 1180-1190, 1998
A:Title: Diversity of the tropomyosin C genes during chordate evolution.
A:Reference number: JW0060; MUID:98265050
A:Accession: JW0065
A:Molecule type: mRNA
A:Residues: 1-167 <YUA>
A:Cross-references: DDBJ:AB008555; NID:q2589013; PIDN:BA23282.1; PID:q2589014
C:Comment: This protein belongs to the EF-hand Ca2+ binding protein family and functi
C:Genetics:

A:introns: 110/2
C:superfamily: calmodulin; calmodulin repeat homology
C:Keywords: EF hand
F:20-52/Domain: calmodulin repeat homology <EF1>
F:56-88/Domain: calmodulin repeat homology <EF2>
F:96-128/Domain: calmodulin repeat homology <EF3>
F:132-164/Domain: calmodulin repeat homology <EF4>

Query Match 73.9%; Score 34; DB 2; Length 167;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 YOHDLRAY 8
| | | | |
Db 10 QHDARAY 16

RESULT 8
F96802
hypothetical protein F2P24.7 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: F96802
R:Theologas, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Chn, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Jensen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luross, J.S.; Maitl, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; M0ID:21016719
A:Accession: F96802
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-481 <STO>
A:Cross-references: GB:AE005173; NID:g11079489; PIDN:AA629201.1; GSPDB:GN00141
C:Genetics:
A:Gene: F2P24.7
A:Map position: 1

Query Match 73.9%; Score 34; DB 2; Length 481;
Best Local Similarity 62.5%; Pred. No. 48;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 YOHDLRAY 8
| | | | |
Db 94 YEHSVRAY 101

RESULT 9
T51452
hypothetical protein F2G14.190 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000
C:Accession: T51452
R:Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Mew
submitted to the Protein Sequence Database, August 2000
A:Reference number: Z25394
A:Accession: T51452
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1030 <SAT>
A:Cross-references: EMBL:AL391146
A:Experimental source: cultivar Columbia; BAC clone F2G14
C:Genetics:
A:Map position: 5
A:introns: 29/3; 46/2; 74/2; 95/3; 147/1; 170/3; 205/3; 236/3; 261/3; 290/2; 359/2; 392/
/3

A>Note: F2G14.190
C:superfamily: Saccharomyces cerevisiae hypothetical protein YLR410W

Query Match 73.9%; Score 34; DB 2; Length 1030;
Best Local Similarity 62.5%; Pred. No. 1,1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 YOHDLRAY 8
| | | | |
Db 522 YRHDLKTY 529

RESULT 10
T25770
hypothetical protein F46F11.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T25770
R:Pauley, A.; Gattung, S.
submitted to the EMBL Data Library, February 1997
A:Description: The sequence of C. elegans cosmid F46F11.
A:Reference number: Z20083
A:Accession: T25770
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1224 <PAU>
A:Cross-references: EMBL:U88173; PIDN:ABA42264.1; GSPDB:GN00019; CESP:F46F11.1
A:Experimental source: strain Bristol N2; clone F46F11
C:Genetics:
A:Gene: CESP:F46F11.1
A:Map position: 1
A:introns: 16/3; 45/3; 84/3; 106/3; 189/3; 311/3; 429/3; 474/2; 523/1; 603/3; 742/3;

Query Match 73.9%; Score 34; DB 2; Length 1224;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 YOHDLRAY 8
| | | | |
Db 565 YRHDLKTY 572

RESULT 11
B37388
probable DNA-binding protein 1B - Thermus aquaticus insertion sequence IS1000B
N:Alternate names: hypothetical protein 1B
C:Species: Thermus aquaticus
C>Date: 17-Apr-1993 #sequence_revision 14-May-1993 #text_change 08-Oct-1999
C:Accession: B37388; S27740
R:Ashby, M.K.; Bergquist, P.L.
Plasmid 24, 1-11, 1990
A>Title: Cloning and sequence of IS1000, a putative insertion sequence from Thermus
A:Reference number: A37388; M0ID:91102148
A:Accession: B37388
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-317 <ASH>
A:Cross-references: EMBL:M33159; NID:g155103; PIDN:AAA27498.1; PID:g155109
A:Experimental source: strain HB8
A>Note: the source is designated as Thermus thermophilus
C:Genetics:
A:Mobile element: insertion sequence IS1000B
C:Keywords: DNA binding

Query Match 71.7%; Score 33; DB 2; Length 317;
Best Local Similarity 75.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 YOHDLRAY 8
| | | | |

Db 110 YHEDLRAY 117

RESULT 12
B97368
hypothetical sugar kinase slr0537 [imported] - Agrobacterium tumefaciens (strain C58, C6
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C:Accession: B97368
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughly, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; PMID:11743194
A:Accession: B97368
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-330 <KUR>
A:Cross-references: GB:AE007865; PIDN:AAK65899.1; PID:g15154944; GSPDB:GN00169
C:Genetics:
A:Gene: AGR_C_118
A:Map position: circular chromosome

Query Match 71.7%; Score 33; DB 2; Length 330;
Best Local Similarity 71.4%; Pred. No. 51;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 YOHDLRA 7
:|||||
Db 90 FOHDIRA 96

RESULT 13
AB2586
pfkF family carbohydrate kinase [imported] - Agrobacterium tumefaciens (strain C58, Dupc
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C:Accession: AB2586
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutlyavin, T.; Levy, R.; Li, M.; McCell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Bliddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; PMID:11743193
A:Accession: AB2586
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-330 <KUR>
A:Cross-references: GB:AE008688; PIDN:AAI41104.1; PID:g17738396; GSPDB:GN00186
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu0079
A:Map position: circular chromosome

Query Match 71.7%; Score 33; DB 2; Length 330;
Best Local Similarity 71.4%; Pred. No. 51;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 YOHDLRA 7
:|||||
Db 90 FOHDIRA 96

RESULT 14
S42160
MSS51 protein - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein L8167.17; protein YLR203c
C:Species: Saccharomyces cerevisiae
C:Date: 03-May-1994 #sequence_revision 07-Feb-1997 #text_change 21-Jul-2000

C:Accession: S48554; S42160; S25344
R:Pauley, A.
submitted to the EMBL Data Library, September 1994
A:Description: The sequence of S. cerevisiae cosmid 8167.
A:Reference number: S48545
A:Accession: S48554
A:Molecule type: DNA
A:Residues: 1-436 <PAU>
A:Cross-references: EMBL:U14913; NID:G544497; PID:G544513; MIPS:YLR203c
R:Faye, G.; Simon, M.
Cell 32, 77-87, 1983
A:Title: Analysis of a yeast nuclear gene involved in the maturation of mitochondrial
A:Reference number: S42160; MUID:83129417
A:Accession: S42160
A:Molecule type: DNA
A:Residues: 1-209, 'M', 211-436 <FAY>
A:Cross-references: EMBL:J01487; NID:G172009; PIDN:AAA66926.1; PID:g172010
R:Simon, M.; della Seta, F.; Sor, F.; Faye, G.
Yeast 8, 559-567, 1992
A:Title: Analysis of the MSS51 region on chromosome XII of Saccharomyces cerevisiae.
A:Reference number: S25342; MUID:92397593
A:Accession: S25344
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-209, 'M', 211-436 <SIM>
A:Cross-references: GB:S43721; NID:G255246; PIDN:AA823218.1; PID:g255249
C:Genetics:
A:Gene: SGD:MSS51
A:Cross-references: SGD:S0004193; MIPS:YLR203c
A:Map position: 12R
C:Superfamily: Saccharomyces cerevisiae MSS51 protein
C:Keywords: mitochondrion

Query Match 71.7%; Score 33; DB 2; Length 436;
Best Local Similarity 71.4%; Pred. No. 69;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 YOHDLRA 7
:|||||
Db 131 YEHDIRS 137

RESULT 15
T47787
hypothetical protein F17J16.100 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: T47787
R:D'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazz, M.; Valle, G.; Mewes, H.W.; Rudd, S.
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z24476
A:Accession: T47787
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-488 <DAN>
A:Cross-references: EMBL:AL163527
A:Experimental source: cultivar Columbia; BAC clone F17J16
C:Genetics:
A:Map position: 3
A:Introns: 14/1; 83/2; 121/2; 150/3; 179/2; 213/3; 246/2; 389/3
A>Note: F17J16.100

Query Match 71.7%; Score 33; DB 2; Length 488;
Best Local Similarity 62.5%; Pred. No. 77;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YOHDLRAY 8
:|||||
Db 115 YDHDESY 122

Fri Aug 16 10:35:59 2002

us-09-613-092a-6_copy_3_10.rpr

Page 5

Search completed: August 15, 2002, 11:50:18
Job time: 244 sec

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OM protein - protein search, using sw model

Run on: August 15, 2002, 11:58:16 ; Search time 18.61 Seconds

(without alignments)
16.645 Million cell updates/sec

Title: US-09-613-092a-6_COPY_3_10
Perfect score: 46
Sequence: 1 YOHDLRAY 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	78.3	451	1 YOB1_CAEEL	009355 caenorhabd
2	35	76.1	447	1 MURE_HELPJ	0923c6 helicobacte
3	34	73.9	301	1 RL5_NEUCR	059953 neuropept
4	33	71.7	436	1 MS51_YEAST	P32335 saccharomyc
5	33	71.7	949	1 A1B1_RAT	P52303 ratu
6	32	69.6	213	1 CAT2_ECOLI	P22615 escherichia
7	32	69.6	261	1 TPIS_MYCLE	P46711 mycobacteri
8	32	69.6	356	1 QUEA_ECOLI	P21516 escherichia
9	32	69.6	385	1 KUP1_CAEEL	P34705 caenorhabd
10	32	69.6	708	1 NICA_MOUSE	P57716 mus musculu
11	32	69.6	1139	1 VRNA_BSMV	P17595 barley stri
12	32	69.6	2329	1 YL16_CAEEL	P34369 caenorhabd
13	31	67.4	158	1 RACR_ECOLI	P76062 escherichia
14	31	67.4	263	1 ELH1_APLPA	P17685 aplysia par
15	31	67.4	271	1 ELH1_APLCA	P01362 aplysia cal
16	31	67.4	432	1 FGL2_MOUSE	P12804 mus musculu
17	31	67.4	533	1 VIE2_AGRTE	P07544 agrobacteri
18	31	67.4	587	1 YN14_YEAST	P53933 saccharomyc
19	31	67.4	830	1 MKT1_YEAST	P40850 saccharomyc
20	31	67.4	863	1 YP67_CAEEL	009216 caenorhabd
21	31	67.4	911	1 TB11_NEIMB	009056 neisseria m
22	31	67.4	937	1 MSH2_NEUCR	013336 neuropept
23	30.5	66.3	749	1 VP4_ROTGA	004916 rotavirus (
24	30	65.2	146	1 YD34_MYCTU	010645 mycobacteri
25	30	65.2	259	1 MORA_TREPA	007886 treponema p
26	30	65.2	342	1 Y1S5_BACSU	P40332 bacillus su
27	30	65.2	423	1 YB12_SFV1	P29170 simian foam
28	30	65.2	403	1 YCDB_ECOLI	P31545 escherichia
29	30	65.2	467	1 AFCA_ARATH	P51566 arabidopsi
30	30	65.2	528	1 YNH7_YEAST	P53940 saccharomyc
31	30	65.2	552	1 YHNE_YEAST	P38799 saccharomyc
32	30	65.2	593	1 FA12_BOVIN	P58140 bos taurus
33	30	65.2	615	1 FA12_HUMAN	P00748 homo sapien

34	30	65.2	686	1 HMCT_HELPJ	Q92153 helicobacte
35	30	65.2	686	1 HMCT_HELPJ	Q59465 helicobacte
36	30	65.2	770	1 STA3_HUMAN	P40763 homo sapien
37	30	65.2	770	1 STA3_MOUSE	P42227 mus musculu
38	30	65.2	770	1 STA3_RAT	P52631 ratu
39	30	65.2	869	1 AMPN_ECOLI	P04825 escherichia
40	30	65.2	942	1 HEX_ADEG1	P42671 avian adeno
41	30	65.2	1341	1 YL78_YEAST	Q05854 saccharomyc
42	30	65.2	1750	1 Y832_METUA	Q58242 methanococc
43	30	65.2	2388	1 SPCP_RAT	Q99488 ratu
44	30	65.2	2390	1 SPCP_HUMAN	O15020 homo sapien
45	29	63.0	91	1 XPR7_BACLI	Q99166 bacillus 11

ALIGNMENTS

```

RESULT 1
YOB1_CAEEL          STANDARD;          PRT;          451 AA.
AC 009255;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
DE Hypothetical 51.0 kDa protein C30G12.1 in chromosome II.
GN C30G12.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderae; Caenorhabditis.
OX NCBI_Taxid=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC SRRAIN-BRISTOL NZ;
RA Latreille P.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
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or send an email to license@sib-sib.ch).
DR EMBL: U21319; AAC46670.1; -.
DR WormRep: C30G12.1; CE01832.
KW Hypothetical protein.
SQ
SEQUENCE 451 AA; 51017 MW; 6AAAFD326751CCL CRC64;

```

Query Match 78.3%; Score 36; DB 1; Length 451;
Best Local Similarity 75.0%; Pred. No. 4.5;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YOHDLRAY 8
||| | | | | :
Db 62 YOHDLRAF 69

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RESULT 2
MURE_HELPJ          STANDARD;          PRT;          447 AA.
AC 0923c6;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE UDP-N-acetylmuramoylalanine-D-glutamate--2,6-diaminopimelate ligase
DE (EC 6.3.2.13) (UDP-N-acetylmuramyl-tripeptide synthetase) (Meso-
DE diaminopimelate-adding enzyme) (UDP-MurNAc-tripeptide synthetase).
GN MRE OR JHP1387.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.

```

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OX NCB1_TaxID=65963;
RN
RP SEQUENCE FROM N.A.
RA MRLME-99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., delonge B.L., Carmel G.,
RA Tummou P.J., Carruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jlang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori."
RL Nature 397:176-180(1999).
CC
CC -1- FUNCTION: CELL WALL FORMATION. DIAMINOPIMELIC ACID ADDING ENZYME
CC (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + UDP-N-acetylmuramoyl-L-alanyl-D-
CC glutamate + meso-2,6-diaminopentanedioate = ADP + phosphate +
CC UDP-N-acetylmuramoyl-L-alanyl-D-glutamyl-meso-2,6-
CC diaminopentanedioate.
CC -1- PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (probable).
CC -1- SIMILARITY: BELONGS TO THE MURCEP FAMILY.
CC
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CC
CC -----
DR EMBL: AEO01561; AAD06968.1; -
DR InterPro: IPR000713; Mur_1lgase.
DR InterPro: IPR004101; Mur_1lgase.C.
DR Pfam: PF01225; Mur_1lgase.1.
DR Pfam: PF02875; Mur_1lgase.C.1.
DR Pfam: PF02875; Mur_1lgase.C.1.
KW Peptidoglycan synthesis; Cell wall; Cell division; Llgase;
KW ATP-binding; Complete proteome.
FT NP_BIND 74 80
FT ATP (POTENTIAL).
SQ SEQUENCE 447 AA; 50660 MW; 639AB9D18F3740BD CRC64;

Query Match 76.1%; Score 35; DB 1; Length 447;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YOHDLR 6
Db 238 YOHDLR 243

RESULT 3
RL5_NEUCR STANDARD; PRT; 301 AA.
AC 059953;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 60S ribosomal protein L5 (CPR4).
GN CRP-4.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCB1_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=74-OR23-1A;
RC de la Serna I.L., Cujec T.P., Shi Y., Tyler B.M.;
RT "Non-coordinate regulation of 5S rRNA genes and the gene encoding the
RT 5S rRNA-binding ribosomal protein homolog in Neurospora crassa.";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THIS PROTEIN BINDS 5S RNA (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE L18P FAMILY OF RIBOSOMAL PROTEINS.
CC -----

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CC
CC -----
DR EMBL: AF054907; AAC09000.1; -
DR InterPro: IPR001149; Ribosomal_L18p.
DR Pfam: PF00861; Ribosomal_L18p.1.
DR PRINTS: PR00058; RIBOSOMAL15.
DR PRODOM: PD001394; Ribosomal_L18p.1.
DR Ribosomal protein; rRNA-binding.
SQ SEQUENCE 301 AA; 34411 MW; 289B0F0D1672A5F9 CRC64;

Query Match 73.9%; Score 34; DB 1; Length 301;
Best Local Similarity 62.5%; Pred. No. 7.5;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YOHDLR 8
Db 79 YSHEIKAY 86

RESULT 4
MS51_YEAST STANDARD; PRT; 436 AA.
AC P33335;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE MS51 protein.
GN MS51 OR YLR203C OR L8167.17.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCB1_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AB320;
RX MEDLINE=83129417; PubMed=6297789;
RA Faye G., Simon M.;
RT "Analysis of a yeast nuclear gene involved in the maturation of
RT mitochondrial pre-messenger RNA of the cytochrome oxidase subunit
RT I."
RT Cell 32:77-87(1983).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=D273-10B/A;
RX MEDLINE=92397593; PubMed=1523888;
RA Simon M., della Seta F., Sor F., Faye G.;
RT "Analysis of the MS51 region on chromosome XII of Saccharomyces
RT cerevisiae."
RL Yeast 8:559-567(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
RA Favell A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T.,
RA Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D.,
RA Johnston L., Langston Y., Latreille P., Mardis E., Meneses S.,
RA Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L.,
RA Taich S., Trevasakis E., Vaudin M., Vignati D., Wilcox L., Wilson R.,
RA Wohlman P., Waterston R.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=91117165; PubMed=2177521;
RA Decoster E., Simon M., Hatac D., Faye G.;
RT "The MS51 gene product is required for the translation of the COX1
RT mRNA in yeast mitochondria."

```

RL Mol. Genet. 224:111-118(1990).
 CC -1- FUNCTION: NECESSARY FOR THE CORRECT MATURATION OF THE
 CC MITOCHONDRIAL PRE-MRNA FOR CYTOCHROME OXIDASE SUBUNIT 1 (COX1). IT
 CC IS PROBABLY AN INITIATION FACTOR SPECIFIC FOR THE TRANSLATION OF
 CC THE COX1 MRNA.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial.
 CC -----
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 CC -----
 DR EMBL: J01487; AAA66926.1; -
 DR EMBL: S43721; AAB23218.1; -
 DR EMBL: U14913; AAB67438.1; -
 DR PIR: S25344; S25344.
 DR PIR: S42160; S42160.
 DR PIR: S48554; S48554.
 DR SGD: S0004193; MSS51.
 KM mRNA processing; mRNA splicing; Mitochondrion.
 FT VARIANT 210 210 M -> I (IN STRAINS D273-10B/A AND AB972).
 FT VARIANT 339 339 G -> S (IN STRAIN D273-10B/A).
 FT VARIANT 375 375 T -> M (IN STRAIN D273-10B/A).
 FT VARIANT 397 397 R -> K (IN STRAIN D273-10B/A).
 SQ SEQUENCE 436 AA; 50898 MW; B7616DDBAFC32FBI CRC64;

Query Match 71.7%; Score 33; DB 1; Length 436;
 Best Local Similarity 71.4%; Pred. No. 18;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 YOHDLRA 7
 DB 131 YEHDLRS 137

RESULT 5
 AIBL_RAT STANDARD; PRT; 949 AA.
 ID AIBL_RAT
 AC P52303;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Adapter-related protein complex 1 beta 1 subunit (beta-adaptin 1)
 DE (Plasma membrane adaptor HA2/Arp adaptin beta subunit) (Clathrin
 assembly protein complex 2 beta large chain) (AP105A).
 GN APLB1 OR ADTB1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=89202379; PubMed=2495531;
 RA Kirchhausen T., Nathanson K.L., Matsui W., Vaisberg A., Chow E.P.,
 RA Burne C., Keen J.H., Davis A.E.;
 RT "Structural and functional division into two domains of the large
 RT (100- to 115-kDa) chains of the clathrin-associated protein complex
 RT AP-2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:2612-2616(1989).
 CC -1- FUNCTION: ADAPTINS ARE COMPONENTS OF THE ADAPTOR COMPLEXES
 CC WHICH LINK CLATHRIN TO RECEPTORS IN COATED VESICLES. CLATHRIN-
 CC ASSOCIATED PROTEIN COMPLEXES ARE BELIEVED TO INTERACT WITH THE
 CC CYTOPLASMIC TAILS OF MEMBRANE PROTEINS, LEADING TO THEIR SELECTION
 CC AND CONCENTRATION. BETA ADAPTIN IS A SUBUNIT OF THE PLASMA
 CC MEMBRANE ADAPTOR.
 CC -1- SUBUNIT: ASSEMBLY PROTEIN COMPLEX 2 (AP-2) IS A HETEROTETRAMER
 CC COMPOSED OF TWO LARGE CHAINS (ALPHA AND BETA), A MEDIUM CHAIN
 CC (AP50) AND A SMALL CHAIN (AP17).

CC -1- SUBCELLULAR LOCATION: COMPONENT OF THE COAT SURROUNDING THE
 CC CYTOPLASMIC FACE OF COATED VESICLES IN THE PLASMA MEMBRANE.
 CC -1- PTM: THE N-TERMINUS IS BLOCKED.
 CC -1- SIMILARITY: BELONGS TO THE ADAPTOR COMPLEXES LARGE SUBUNITS
 CC FAMILY.
 CC -----
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 CC -----
 DR EMBL: M77245; AAA40807.1; -
 DR InterPro: IPR002553; Adaptin_N.
 DR InterPro: IPR001121; G_adapt_C.
 DR Pfam: PF01602; Adaptin_N_1.
 DR Pfam: PF02883; Alpha_adaptinC2_1.
 KM Coated pits.
 FT DOMAIN 576 728 PRO-RICH (STALK REGION).
 SQ SEQUENCE 949 AA; 104568 MW; CC5AE34EBACCD44 CRC64;

Query Match 71.7%; Score 33; DB 1; Length 949;
 Best Local Similarity 71.4%; Pred. No. 42;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 QHDLRAV 8
 DB 937 QHDLQAV 943

RESULT 6
 CAT2_ECOLI STANDARD; PRT; 213 AA.
 ID CAT2_ECOLI
 AC P22615;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Chloramphenicol acetyltransferase II (EC 2.3.1.28) (CAT-II).
 GN CMLA.
 OS Escherichia coli.
 OG Plasmid Incw psa.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=K12;
 RX MEDLINE=91097467; PubMed=2268278;
 RA Murray I.A., Martinez-Suarez J.V., Close T.J., Shaw W.V.;
 RT "Nucleotide sequences of genes encoding the type II chloramphenicol
 RT acetyltransferases of Escherichia coli and Haemophilus influenzae,
 RT which are sensitive to inhibition by thiol-reactive reagents.";
 RL Biochem. J. 272:505-510(1990).
 CC -1- FUNCTION: THIS ENZYME IS AN EFFECTOR OF CHLORAMPHENICOL RESISTANCE
 CC IN BACTERIA.
 CC -1- CATALYTIC ACTIVITY: Acetyl-CoA + chloramphenicol = CoA +
 CC chloramphenicol 3-acetate.
 CC -1- SUBUNIT: HOMOTRIMER.
 CC -1- MISCELLANEOUS: TYPE II CHLORAMPHENICOL ACETYLTRANSFERASES ARE
 CC SENSITIVE TO INHIBITION BY THIOL-REACTIVE REAGENTS. THE
 CC INACTIVATION OCCURS AS A RESULT OF CHEMICAL MODIFICATION OF
 CC CYS-26.
 CC -1- SIMILARITY: BELONGS TO THE CHLORAMPHENICOL ACETYLTRANSFERASE
 CC FAMILY.
 CC -----
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CC -----

DR EMBL: X53796; CAA37805.1; -

DR PIR: S13398; S13398.

DR HSSP: P00484; 10CA.

DR InterPro: IPR001707; CAT.

DR Pfam: PF00302; CAT: 1.

DR ProDom: PD002660; CAT: 1.

DR PROSITE: PS00100; CAT: 1.

KW Antibiotic resistance; Transferase; Acyltransferase; Plasmid.

FT ACT_SITE 189 189 BY SIMILARITY

SO SEQUENCE 213 AA; 24778 MW; 2E0DF150A730A7 CRC64;

Query Match 69.6%; Score 32; DB 1; Length 213;
Best Local Similarity 62.5%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YOHDLRAY 8
|||||
Db 122 YOHDLRLF 129

RESULT 7
TPIS_MYCLE STANDARD; PRT; 261 AA.

AC P46711;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Triosephosphate isomerase (EC 5.3.1.1) (TIM).

GN TPISA OR TPI OR ML0572 OR B1496_C1_127.

OS *Mycobacterium lepreae*.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; *Mycobacterium*.

OX NCBI_TaxID=1769;

RN [1]

RP SEQUENCE FROM N.A.

RA Smith D.R., Robison K.;

RL Submitted (MAR-1994) to the EMBL/Genbank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-TN;

RA MEDLINE-21128732; PubMed-11234002;

RA Cole S.T., Elglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holtroyd S., Hornsby T., Jagels K., Janczewska C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R., Barrell B.G.;

RT "Massive gene decay in the leprosy bacillus."

RL Nature 409:1007-1011(2001).

CC -1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glyceraldehyde 3-phosphate.

CC -1- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.

CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE TRIOSPHOSPHATE ISOMERASE FAMILY.

CC -----

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CC -----

DR EMBL: U00013; AAA17115.1; -

DR EMBL: AL583919; CAC30080.1; -

DR HSSP: P00943; 2B7M.

DR Leproma; ML0572; -

DR InterPro: IPR000652; Trioseph_isomerase.

DR Pfam: PF00121; TIM; 1.

DR ProDom: PD001005; Trioseph_isomerase; 1.

DR PROSITE: PS001071; TIM; 1

KW Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;

KW Pentose shunt; Complete proteome.

FT ACT_SITE 100 100 BY SIMILARITY

FT ACT_SITE 172 172 BY SIMILARITY

SO SEQUENCE 261 AA; 27557 MW; 598B5CDA6BBD822D CRC64;

Query Match 69.6%; Score 32; DB 1; Length 261;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 QHDLGAY 8
|||||
Db 73 QHDLGAY 79

RESULT 8
QOEA_ECOLI STANDARD; PRT; 356 AA.

AC P21516;

DT 01-MAY-1991 (Rel. 18, Created)

DT 01-MAY-1991 (Rel. 18, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE S-adenosylmethionine:tRNA ribosyltransferase-isomerase (EC 5.4.3.1) (QOEA).

GN QOEA OR B0405 OR Z0504 OR ECS0456.

OS *Escherichia coli*, and

OS *Escherichia coli* O157:H7.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.

OX NCBI_TaxID=562, 83334;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-K12;

RA MEDLINE-91177815; PubMed-1706703;

RA Reuter K., Slany R., Ullrich F., Kersten H.;

RT "Structure and organization of *Escherichia coli* genes involved in biosynthesis of the deazaguanine derivative queuine, a nutrient factor for eukaryotes."

RL J. Bacteriol. 173:2256-2264(1991).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-K12 / MG1655;

RA MEDLINE-97426617; PubMed-9278503;

RA Bletner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-VIDES J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;

RT "The complete genome sequence of *Escherichia coli* K-12."

RL Science 277:1453-1474(1997).

RN [3]

RP SEQUENCE FROM N.A.

RA Roberts D., Allen E., Araujo R., Aparicio A., Chung E., Davis K., Duncan M., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D., Namath A., Oefner P., Schramm S., Davis R.W.;

RL Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RC STRAIN-OL157:H7 / EDC933 / ATCC 700927;

RA MEDLINE-21074935; PubMed-11206551;

RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Godtcek E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Bletner F.R.;

RT "Genome sequence of enterohaemorrhagic *Escherichia coli* O157:H7."

RL Nature 409:529-533(2001).


```

RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN-0157:H7 / RIMD 050952;
RX MEDLINE-21156231; PubMed-11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
  Han C.-G., Ohtsuda E., Nakayama K., Murata T., Tanaka M., Tobe T.,
  Kida T., Takami H., Honda T., Sasaki C., Ogasawara N., Yasunaga T.,
  Kihara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
  O157:H7 and genomic comparison with a laboratory strain K-12."
RL DNA Res. 8:11-22(2001).
RN [6]
RP CHARACTERIZATION.
RX MEDLINE-93349860; PubMed-8347586;
RA Slany R.K., Boesl M., Crain P.F., Kersten H.;
RT "A new function of S-adenosylmethionine: the ribosyl moiety of AdoMet
  is the precursor of the cyclopentenol moiety of the tRNA wobble
  base queueine."
RL Biochemistry 32:7811-7817(1993).
CC -1- FUNCTION: SYNTHESIZES OO FROM PREQ1 IN A SINGLE S-
  ADENOSYLMETHIONINE- (ADOMET-) REQUIRING STEP. THE RIBOSYL MOIETY
  OF ADOMET IS TRANSFERRED AND ISOMERIZED TO THE EPOXYCYCLOPENTANE
  RESIDUE OF OO.
CC -1- PATHWAY: INVOLVED IN BIOSYNTHESIS OF THE DEAZAGUANINE DERIVATIVE
  QUEOSINE, WHICH IS USUALLY PRESENT IN TRNAS SPECIFIC FOR ASN,
  ASP, HIS, AND TYR.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (Potential).
CC -1- SIMILARITY: BELONGS TO THE QUEA FAMILY.
CC -----
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CC -----
DR EMBL: M37702; AAA16114.1; -
DR EMBL: AE000147; AAC73508.1; -
DR EMBL: U82664; AAB40161.1; -
DR EMBL: AE005220; AAG54752.1; -
DR EMBL: AF002551; BAB3879.1; -
DR PIR: B38530; B38530.
DR PIR: S35451; S35451.
DR EcoGene: EG10812; quea.
DR InterPro: IPR003699; Queosine_synth.
DR Pfam: PF02547; Queosine_synth.1.
KW Queosine biosynthesis; Transferase; Isomerase; Complete proteome.
SQ SEQUENCE 356 AA; 39430 MW; 47F7F0090812DCF3 CRC64;

Query Match 69.6%; Score 32; DB 1; Length 356;
Best Local Similarity 62.5%; Pred. No. 23;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YOHDLRAY 8
DB 317 YOHDMAY 324

RESULT 9
KUP1_CAEEL STANDARD; PRT; 385 AA.
AC P34705;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Protein kup-1.
GN KUP-1 OR F10C2.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
  Rhabditidae; Peloderae; Caenorhabditis.

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OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE-93258816; PubMed-8098272;
RA Spleth J., Brooke G., Kuersten S., Lea K., Blumenthal T.;
RT "Operations in C. elegans: polycistronic mRNA precursors are processed
  by trans-splicing of SL2 to downstream coding regions."
RL Cell 73:521-532(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA White S.;
RT Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -----
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  or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L12247; CAA28102.1; -
DR EMBL: Z81497; CAB04080.1; -
DR WormPeP: F10C2.2; CE09306.
SQ SEQUENCE 385 AA; 44188 MW; A023126D4E10A23B CRC64;

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Query Match 69.6%; Score 32; DB 1; Length 385;
Best Local Similarity 62.5%; Pred. No. 25;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YOHDLRAY 8
DB 281 YEHDTREY 288

RESULT 10
NICA_MOUSE STANDARD; PRT; 708 AA.
AC P57716;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Nicastrin precursor.
DR NCSTN.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20445163; PubMed-10993067;
RA Yu G., Nishimura M., Arawaka S., Levitan D., Zhang L., Tandon A.,
  Song Y.-O., Rogaeva E., Chen F., Kawarai T., Supala A., Levesque L.,
  Yu H., Yang D.S., Holmes E., Milman P., Zhang Y., Zhang D.M., Xu D.H.,
  Rado C., Rogaev E., Smith M., Janus C., Zhang Y., Aebersold R.,
  Farrer L.S., Sorbi S., Brunl A., Fraser P.E., St George-Hyslop P.H.;
RT "Nicastrin modulates presenilin-mediated notch/glp-1 signal
  transduction and betaAPP processing."
RL Nature 407:48-54(2000).
CC -1- FUNCTION: MAY FUNCTION IN THE CYTOPLASMIC PARTITIONING AND
  INTRAMEMBRANOUS PROTEOLYSIS OF PROTEINS. TOGETHER WITH PRESENILIN
  IS INVOLVED IN GAMMA-SECRETASE MEDIATED PROTEOLYTIC PROCESSING OF
  AMYLOID PRECURSOR PROTEIN (APP). MAY PLAY A ROLE IN NOTCH
  SIGNALING (BY SIMILARITY).
CC -1- SUBUNIT: ASSOCIATES WITH PSEN1 AND PSEN2 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: BELONGS TO THE NICASTRIN FAMILY.
CC -----
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 DR EMBL: AF240469; AAG11413.1; -
 DR MGD: MGI:1891700; Ncstn.
 KW Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 27
 FT CHAIN 28 708
 FT TRANSMEM 28 668
 FT DOMAIN 669 689
 FT DOVAIN 690 708
 FT CARBOHYD 44 44
 FT CARBOHYD 54 54
 FT CARBOHYD 128 128
 FT CARBOHYD 186 186
 FT CARBOHYD 203 203
 FT CARBOHYD 263 263
 FT CARBOHYD 386 386
 FT CARBOHYD 434 434
 FT CARBOHYD 463 463
 FT CARBOHYD 505 505
 FT CARBOHYD 529 529
 FT CARBOHYD 561 561
 FT CARBOHYD 572 572
 FT CARBOHYD 579 579
 FT CARBOHYD 593 593
 FT CARBOHYD 611 611
 SQ SEQUENCE 708 AA; 78489 MW; EB7B5FD9C9D3DECI CRC64;

Query Match 69.6%; Score 32; DB 1; Length 708;
 Best Local Similarity 71.4%; Pred. No. 49;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 QHDLRAY 8
 DB 538 KHLDSY 544

RESULT 11
 ID VRNA_BSMV STANDARD; PRT; 1139 AA.
 AC P17595;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Alpha-A protein.
 OS Barley stripe mosaic virus (BSMV).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hordeivirus.
 OX NCBI_TaxID=12327;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC PV43;
 RX MEDLINE=89268457; PubMed=2128343;
 RA Gustafson G., Armour S.L., Gamboa G.C., Burgett S.G., Shepherd J.W.;
 RT "Nucleotide sequence of barley stripe mosaic RNA alpha: RNA
 RT alpha encodes a single polypeptide with homology to corresponding
 RT proteins from other viruses."
 RL Virology 170:370-377(1989).
 CC -1- SIMILARITY: TO THE TMV 126 KDA PROTEIN, AND WITH RELATED PEPTIDES
 CC FROM OTHER VIRUSES. ITS C-TERMINUS HAS LIMITED HOMOLOGY WITH THE
 CC 58 KDA (BETA-B) PROTEIN FROM BSMV.
 CC -----
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CC -----
 DR EMBL: J04342; AAA46336.1; -
 DR PIR: J40109; PAVBBS.
 DR InterPro: IPR002588; V_methyltransf.
 DR InterPro: IPR000606; Viral_helicase1.
 DR Pfam: PF01443; Viral_helicase1.
 DR Pfam: PF01660; Vmethyltransf; 1.
 KW ATP-binding.
 FT NP_BIND 838 845
 FT SEQUENCE 1139 AA; 129627 MW; 24B1500F0D5362D9 CRC64;

Query Match 69.6%; Score 32; DB 1; Length 1139;
 Best Local Similarity 62.5%; Pred. No. 81;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YQHLRAY 8
 DB 294 YSHDLKY 301

RESULT 12
 ID YLJ6_CAEEL STANDARD; PRT; 2329 AA.
 AC P34369;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Hypothetical 272.0 kDa protein C50C3.6 in chromosome III.
 CN C50C3.6.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL NZ;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fraser A.,
 RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
 RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
 RA Lacroille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
 RA Sims M., Smaildon N., Smith A., Smith M., Sonhammer E., Staden R.,
 RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
 RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
 RA Wohldman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans."
 RL Nature 368:32-38(1994).
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- SIMILARITY: STRONG, TO YEAST PRP8.
 CC -----
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 DR EMBL: L14433; AAA2797.1; -
 DR PIR: S44625; S44625.
 DR WormPep: C50C3.6; CE00122.
 DR InterPro: IPR000555; MOV34.
 DR Pfam: PF01398; MOV34; 1.
 DR SMART: SM00232; JAB_MPN; 1.
 KW Hypothetical protein; Nuclear protein; RNA-binding.
 SQ SEQUENCE 2329 AA; 272025 MW; 626F9F97C800960C CRC64;

Query Match 69.6%; Score 32; DB 1; Length 2329;
 Best Local Similarity 62.5%; Pred. No. 1.8e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YQHDLRAY 8
 1:1111
 DB 71 YRHDKRVY 78

RESULT 13

RACR_ECOLI STANDARD; PRT; 158 AA.
 AC P76062;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Rac prophage repressor.
 GN RACR OR B1356.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Escherichia.
 OX NCBI_TaxId=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE-97426617; PubMed-9278503;
 RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden W.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [2]
 RP FUNCTION.
 RA Clark A.J.;
 RL Unpublished observations (JUN-1998).
 CC -1- FUNCTION: REPRESSOR PROTEIN FOR RAC PROPHAGE.
 CC -----
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 CC -----
 DR EMBL: AE000233; AAC74438.1; -.
 DR Ecogene; E613360; RACR.
 KW Transcription regulation; Repressor; DNA-binding; Complete proteome.
 SQ SEQUENCE 158 AA; 17663 MW; 110E900ED3847DDF CRC64;

Query Match 67.4%; Score 31; DB 1; Length 158;
 Best Local Similarity 83.3%; Pred. No. 16;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 HDLRAY 8
 1:1111
 DB 124 HDVRAY 129

RESULT 14

ELH1_APLPA STANDARD; PRT; 263 AA.
 AC P17685;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ELH type 1 precursor [Contains: Alpha-bag cell peptide (Alpha-BCP);
 DE Beta-bag cell peptide (Beta-BCP); Gamma-bag cell peptide (Gamma-BCP);
 DE Egg-laying hormone (ELH); Acidic peptide].
 GN ELH1.
 OS Aplysia parvula (little sea hare).

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidae;
 OC Aplysiidae; Aplysia.
 OX NCBI_TaxId=6503;

RP SEQUENCE FROM N.A.
 RX MEDLINE-86280675; PubMed-3734873;
 RA Nambu J.R., Scheller R.H.;
 RT "Egg-laying hormone genes of Aplysia: evolution of the ELH gene
 RT family";
 RT J. Neurosci. 6:2026-2036(1986)

-1- FUNCTION: ELH ACTS AS A NEUROTRANSMITTER LOCALLY, UPON NEURONS OF
 CC THE ABDOMINAL GANGLION AND AS A HORMONE BY DIFFUSING INTO THE
 CC CIRCULATING HEMOLYMPH AND MODULATING THE ACTIVITY OF OTHER ORGANS.
 CC IT SPECIFICALLY CAUSES CONTRACTION OF SMOOTH MUSCLE IN THE
 CC OVOTESTIS AND EXPULSION OF THE EGG STRING.
 CC -1- FUNCTION: ALPHA-BCP DECREASES THE ACTIVITY OF A CLUSTER OF NEURONS
 CC IN THE LEFT UPPER QUADRANT OF THE ABDOMINAL GANGLION.
 CC -1- FUNCTION: BETA-BCP SPECIFICALLY EXCITES 2 NEURONS, L1 AND R1, IN
 CC THE ABDOMINAL GANGLION.
 CC -1- TISSUE SPECIFICITY: BAG CELL NEURONS.
 CC -----

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 CC -----

DR EMBL: M30048; AAA27765.1; -.
 DR PIR: A26147; A26147.
 DR InterPro: IPR003424; ELH.
 DR Pfam: PF02323; ELH; 1.
 KW Hormone; Cleavage on pair of basic residues; Amidation; Neuropeptide;
 KW Signal; Multigene family.
 FT SIGNAL 1 29
 FT PEPPTIDE 88 92 BY SIMILARITY.
 FT PEPPTIDE 95 99 BETA-BAG CELL PEPPTIDE.
 FT PEPPTIDE 142 150 GAMMA-BAG CELL PEPPTIDE.
 FT PEPPTIDE 198 233 ALPHA-BAG CELL PEPPTIDE.
 FT PEPPTIDE 237 263 EGG-LAYING HORMONE.
 FT MOD.RES 233 253 ACIDIC PEPPTIDE.
 FT MOD.RES 233 253 AMIDATION (G-234 PROVIDE AMIDE GROUP).
 SQ SEQUENCE 263 AA; 29676 MW; E0C69F9E3E5FEF29 CRC64;

Query Match 67.4%; Score 31; DB 1; Length 263;
 Best Local Similarity 85.7%; Pred. No. 27;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YQHDLRA 7
 1:1111
 DB 136 YQDLRA 142

RESULT 15

ELH1_APLCA STANDARD; PRT; 271 AA.
 AC P01362;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ELH precursor [Contains: Alpha-bag cell peptide (Alpha-BCP); Beta-bag
 DE cell peptide (Beta-BCP); Gamma-bag cell peptide (Gamma-BCP); Egg-
 DE laying hormone (ELH); Acidic peptide].
 OS Aplysia californica (California sea hare).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidae;
 OC Aplysiidae; Aplysia.
 OX NCBI_TaxId=6500;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-83129416; PubMed-6687446;
 RA Scheller R.H., Jackson J.F., McAllister L.B., Rothman B.S.,
 RA Mayeri E., Axel R.;

RT "A single gene encodes multiple neuropeptides mediating a stereotyped
 RT behavior.";
 RL Cell 32:7-22(1983).
 RN [2]
 RP SEQUENCE OF 150-158.
 RA Rothman B.S., Mayeri E., Brown R.O., Yuan P.-M., Shively J.E.;
 RT "Primary structure and neuronal effects of alpha-bag cell peptide, a
 RT second candidate neuropeptide encoded by a single gene in bag cell
 RT neurons of Aplysia.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:5753-5757(1983).
 RN [3]
 RP SEQUENCE OF 206-241.
 RX MEDLINE-80101672; PubMed-293751;
 RA Chiu A.Y., Hunkapiller M.W., Heller E., Stuart D.K., Hood L.E.,
 RA Strumwasser F.;
 RT "Purification and primary structure of the neuropeptide egg-laying
 RT hormone of Aplysia californica.";
 RL Proc. Natl. Acad. Sci. U.S.A. 76:6656-6660(1979).
 RN [4]
 RP PROCESSING.
 RX MEDLINE-87168672; PubMed-3549995;
 RA Newcomb R., Scheller R.H.;
 RT "Proteolytic processing of the Aplysia egg-laying hormone and R3-14
 RT neuropeptide precursors.";
 RL J. Neurosci. 7:854-863(1987).
 CC -1- FUNCTION: ELH ACTS AS A NEUROTRANSMITTER LOCALLY, UPON NEURONS OF
 CC THE ABDOMINAL GANGLION AND AS A HORMONE BY DIFFUSING INTO THE
 CC CIRCULATING HEMOLYMPH AND MODULATING THE ACTIVITY OF OTHER ORGANS.
 CC IT SPECIFICALLY CAUSES CONTRACTION OF SMOOTH MUSCLE IN THE
 CC OVOTESTIS AND EXPUSION OF THE EGG STRING.
 CC -1- FUNCTION: ALPHA-BCP DECREASES THE ACTIVITY OF A CLUSTER OF NEURONS
 CC IN THE LEFT UPPER QUADRANT OF THE ABDOMINAL GANGLION.
 CC -1- FUNCTION: BETA-BCP SPECIFICALLY EXCITES 2 NEURONS, L1 AND R1, IN
 CC THE ABDOMINAL GANGLION.
 CC -1- TISSUE SPECIFICITY: BAG CELL NEURONS.
 CC -1- SIMILARITY: TO ATRIAL GLAND PEPTIDE A AND B PRECURSORS.
 DR PIR: A01632: ONGAPA.
 DR InterPro: IPR003424; ELH.
 DR Pfam: PF02323; ELH; 1.
 DR Pfam: PF02323; ELH; 1.
 KW Hormone; Cleavage on pair of basic residues; Amidation; Neuropeptide;
 KW Signal.
 FT SIGNAL. 1 34
 FT PROPEP 35 93 POTENTIAL.
 FT PEPTIDE 96 100 BETA-BAG CELL PEPTIDE.
 FT PEPTIDE 103 107 GAMMA-BAG CELL PEPTIDE.
 FT PROPEP 110 148
 FT PEPTIDE 150 158 ALPHA-BAG CELL PEPTIDE.
 FT PROPEP 162 203
 FT PEPTIDE 206 241 EGG-LAYING HORMONE.
 FT PEPTIDE 245 271 ACIDIC PEPTIDE.
 FT MOD_RES 241 241 AMIDATION (G-242 PROVIDE AMIDE GROUP).
 FT SIMILAR 206 241 TO LARGE SUBUNIT OF CALIFIN A, B AND
 FT C OF APLYSIA CALIFORNICA.
 FT C OF APLYSIA CALIFORNICA.
 FT SIMILAR 245 271
 FT SEQUENCE 271 AA; 30827 MM; FB2F1EBE3B9113A6 CRC64;

Query Match 67.4%; Score 31; DB 1; Length 271;
 Best Local Similarity 85.7%; Pred. No. 28;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 YQHDLRA 7
 11111
 Db 144 YQDRLRA 150

Search completed: August 15, 2002, 11:58:17
 Job time: 517 sec

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OM protein - protein search, using sw model

Run on: August 15, 2002, 11:57:51 ; Search time 58.57 Seconds
(without alignments)
23.629 Million cell updates/sec

Title: US-09-613-092a-6_COPY_3_10
Perfect score: 46
Sequence: 1 YOHDLRAY 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	37	80.4	284	16	Q9HYW0	Q9HYW0 pseudomonas
2	37	80.4	1763	6	Q9YU16	Q9YU16 monodelphis
3	36	78.3	267	2	Q48706	Q48706 lacobacilli
4	36	78.3	408	10	Q23245	Q23245 arabidopsis
5	36	78.3	563	10	Q65520	Q65520 arabidopsis
6	36	78.3	635	10	Q9C5D9	Q9C5D9 arabidopsis
7	36	78.3	756	10	Q93XR9	Q93XR9 bruguiera
8	35	76.1	345	16	Q987E1	Q987E1 rhizobium
9	35	76.1	392	12	Q919J4	Q919J4 culx nigri
10	35	76.1	502	16	Q9RS01	Q9RS01 deinococcus
11	34	73.9	167	13	Q42136	Q42136 lampetra ja
12	34	73.9	242	5	Q9U0R8	Q9U0R8 plasmodium
13	34	73.9	316	16	Q85470	Q85470 streptococc
14	34	73.9	481	10	Q9FVX2	Q9FVX2 arabidopsis
15	34	73.9	531	17	Q9HIE2	Q9HIE2 thermoplasm
16	34	73.9	1015	10	Q9SRH8	Q9SRH8 arabidopsis

17	34	73.9	1030	10	Q9LFP8	Q9LFP8 arabidopsis
18	34	73.9	1049	10	Q93YV1	Q93YV1 arabidopsis
19	34	73.9	1243	4	Q43314	Q43314 homo sapien
20	34	73.9	1339	5	P91309	P91309 caenorhabd
21	33	71.7	317	2	Q56421	Q56421 thermus the
22	33	71.7	400	5	Q18348	Q18348 dirofilaria
23	33	71.7	488	10	Q9LYT1	Q9LYT1 arabidopsis
24	33	71.7	490	10	Q9SKX5	Q9SKX5 arabidopsis
25	33	71.7	497	10	Q94JZ7	Q94JZ7 arabidopsis
26	33	71.7	516	10	Q9SHX4	Q9SHX4 arabidopsis
27	33	71.7	706	10	Q9FY97	Q9FY97 arabidopsis
28	33	71.7	762	16	Q912P9	Q912P9 pseudomonas
29	33	71.7	823	5	Q9FGW3	Q9FGW3 arabidopsis
30	33	71.7	1563	5	Q9VAF5	Q9VAF5 drosophila
31	32	69.6	199	16	Q99S03	Q99S03 staphylococ
32	32	69.6	230	3	Q38003	Q38003 bacterioph
33	32	69.6	479	16	P71862	P71862 mycobacteri
34	32	69.6	512	5	Q9V820	Q9V820 drosophila
35	32	69.6	604	5	Q9V1S4	Q9V1S4 drosophila
36	32	69.6	727	10	Q9SVH3	Q9SVH3 arabidopsis
37	32	69.6	812	3	Q12072	Q12072 saccharomyc
38	32	69.6	1101	5	Q45818	Q45818 caenorhabd
39	32	69.6	1130	12	Q82718	Q82718 indian pean
40	32	69.6	1138	12	Q65713	Q65713 barley stri
41	32	69.6	1138	12	Q65715	Q65715 barley stri
42	32	69.6	1138	12	Q65716	Q65716 barley stri
43	32	69.6	1139	12	Q65714	Q65714 barley stri
44	32	69.6	1145	12	Q84687	Q84687 peanut clum
45	32	69.6	2391	10	Q9XE40	Q9XE40 oryza sativ

ALIGNMENTS

RESULT	ID	Q9HYW0	PRELIMINARY:	PRT:	284 AA.
AC	Q9HYW0	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)				
DT	01-OCT-2001 (TREMBLrel. 18, Last annotation update)				
DE	HYPOTHETICAL PROTEIN PA3283.				
GN	PA3283.				
OS	Pseudomonas aeruginosa.				
OC	Bacteria: Proteobacteria; gamma subdivision; Pseudomonadaceae;				
OX	NCBI_TaxID=287;				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-ATCC 15692 / PA01;				
RX	MEDLINE=20437337; PubMed=10984043;				
RA	Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warren P.,				
RA	Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,				
RA	Garber R.L., Goltz L., Tolentino E., Westbrook-Wadman S., Yuan Y.,				
RA	Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,				
RA	Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,				
RA	Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;				
RT	Complete genome sequence of Pseudomonas aeruginosa PA01, an				
RT	opportunistic pathogen.				
RL	Nature 406:959-964 (2000).				
DR	EMBL: AE004750; AAG06671.1;				
KW	Hypothetical protein; Complete proteome.				
SO	SEQUENCE 284 AA; 31683 MW; 6FP966F3C7D0B7D6 CRC64;				

Query Match 80.4%; Score 37; DB 16; Length 284;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QHDLRAY 8
DB 88 QHDLRAY 94

RESULT 2
Q97U16 PRELIMINARY; PRT; 1763 AA.
AC Q97U16;
DT 01-MAY-2000 (TRMBLrel. 13, Created)
DT 01-MAY-2000 (TRMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TRMBLrel. 19, Last annotation update)
DE Apolipoprotein B (FRAGMENT).
OS Monodelphis domestica (Short-tailed grey opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Monodelphis.
OX NCBI_TaxID=13616;
RN [1]
RP SEQUENCE FROM N.A.
RA Fujino T., Navaratnam N., Jarmuz A., von Haeselaer A., Scott J.;
RT "C to U editing of apolipoprotein B mRNA in marsupials :
RT Identification and characterisation of APOBEC-1 from the American
RT opossum Monodelphaus domestica.";
RL Nucleic Acids Res. 0:0-0(1999).
DR EMBL; AB027413; BAA86052.1; -.
DR InterPro; IPR001747; Vitellogenin_N.
KW Pfam; PF01347; Vitellogenin_N; 1.
FT NON_TER
SO SEQUENCE 1763 AA; 192330 MW; DBE8F87ED2D6289 CRC64;

Query Match 80.4%; Score 37; DB 6; Length 1763;
Best Local Similarity 75.0%; Pred. No. 1,le+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YOHDLRAY 8
1:1:1111
Db 1576 YDHDLQAY 1583

RESULT 3
Q48706 PRELIMINARY; PRT; 267 AA.
AC Q48706;
DT 01-NOV-1996 (TRMBLrel. 01, Created)
DT 01-NOV-1996 (TRMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TRMBLrel. 19, Last annotation update)
DE ORF1 PROTEIN.
GN ORF1.
OS Lactobacillus leichmannii.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=28039;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-DSM 20076;
RA Schenk-Groeninger R.;
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; X81869; CAA57458.1; -.
DR InterPro; IPR001899; Gram_pos_anchor.
DR PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN.1.
SQ SEQUENCE 267 AA; 29995 MW; 29D606B935C559AB CRC64;

Query Match 78.3%; Score 36; DB 2; Length 267;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YOHDLRAY 8
1:111111
Db 168 YNHDLRIT 175

RESULT 4
023245 PRELIMINARY; PRT; 408 AA.
ID 023245

AC 023245;
DT 01-JAN-1998 (TRMBLrel. 05, Created)
DT 01-MAY-1999 (TRMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TRMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 45.3 KDA PROTEIN (FRAGMENT).
GN C7A10.1020.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eusoids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Terryn N., Vos P., Heijnen L., Mewes H.W., Mayer K.F.X.,
RA Schueller C.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z99708; CAB16854.1; -.
KW Hypothetical protein.
FT NON_TER
SO SEQUENCE 408 AA; 45344 MW; 64DDCC0D3889NAAC CRC64;

Query Match 78.3%; Score 36; DB 10; Length 408;
Best Local Similarity 75.0%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YOHDLRAY 8
1:1:1111
Db 365 YRHSRLAY 372

RESULT 5
O65520 PRELIMINARY; PRT; 563 AA.
AC O65520;
DT 01-AUG-1998 (TRMBLrel. 07, Created)
DT 01-AUG-1998 (TRMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TRMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 62.5 KDA PROTEIN.
GN F23E13.180 OR A74G36290.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eusoids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
RA Hohnel J., Jesse T., Heijnen L., Vos P., Mewes H.W., Mayer K.,
RA Schueller C.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
RA Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL022141; CAA18135.1; -.
DR EMBL; AL161589; CAB80300.1; -.
KW Hypothetical protein.
SO SEQUENCE 563 AA; 62526 MW; BE176FF1601C4C8D CRC64;

Query Match 78.3%; Score 36; DB 10; Length 563;
Best Local Similarity 75.0%; Pred. No. 52;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 YOHDLRAY 8
1:11111
DB 273 YRHSRLRAY 280

RESULT 6
O9C5D9 PRELIMINARY; PRT: 635 AA.

DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE HYPOTHEICAL 70.8 KDA PROTEIN.
GN ATAG36290
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;

RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA Carninci P., Chen H., Chauk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinzaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Full Length cDNA of gene AT4g36290 (GI:7270582)."
RL Submitt (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF360314; AAK26024.1; -
DR InterPro: IPR003594; HATPase_C.
DR SMART; SM00387; HATPase_C; 1.
KW Hypothetical protein.
FT VARIANT 77
SQ SEQUENCE 635 AA; 70819 MW; 30D2718E8CFBAF53 CRC64;

Query Match 78.3%; Score 36; DB 10; Length 635;
Best Local Similarity 75.0%; Pred. No. 60;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 YOHDLRAY 8
1:11111
DB 330 YRHSRLRAY 337

RESULT 7
O93XR9 PRELIMINARY; PRT: 756 AA.

DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE BG55 PROTEIN.
GN BG55.
OS Bruguiera gymnorhiza.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Malpighiales; Rhizophoraceae; Bruguiera.
OX NCBI_TaxID=39984;

RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LEAF;
RA Banzai T., Hershkovits G., Katcoff D.J., Hanagata N., Dubinsky Z.,
RA Karube I.;
RT "Identification of mRNA transcripts differentially expressed in
RT mangrove plant, Bruguiera gymnorhiza,"
RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB061795; BAB55653.1; -
SQ SEQUENCE 756 AA; 84482 MW; 1597F3D46C3E0809 CRC64;

Query Match 78.3%; Score 36; DB 10; Length 756;
Best Local Similarity 85.7%; Pred. No. 72;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YOHDLRA 7
1111:11
DB 480 YOHDLRA 486

RESULT 8
O987E1 PRELIMINARY; PRT: 345 AA.

DT 01-OCT-2001 (TREMBLrel. 18, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DE MLT7088 PROTEIN.
GN MLT7088

OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MAFF303099;
RX MEDLINE=21082930; PubMed=11214568;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa K., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti."
RL DNA Res. 7:331-338(2000).
DR EMBL; AP003011; BAB53262.1; -
DR InterPro: IPR001173; Glycos_transf_2.
DR Pfam; PF00535; Glycos_transf_2; 1.
KW Complete proteome.
SQ SEQUENCE 345 AA; 39450 MW; 131B52D5E56507E1 CRC64;

Query Match 76.1%; Score 35; DB 16; Length 345;
Best Local Similarity 75.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 YOHDLRAY 8
111111
DB 217 YOHDLRAY 224

RESULT 9
O919J4 PRELIMINARY; PRT: 392 AA.

DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE CUN082 HYPOTHEICAL PROTEIN.
GN CUN082.
OS Culex nigripalpus baculovirus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae.
OX NCBI_TaxID=130556;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FLORIDA1997;
RX MEDLINE=21488685; PubMed=11602755;
RA Afonso C.L., Tlilman E.R., Lu Z., Balinsky C.A., Moser B.A.,
RA Becnel J.J., Rock D.L., Kutish G.F.;
RT "Genome Sequence of a Baculovirus Pathogenic for Culex nigripalpus,"
RL J. Virol. 75:11157-11165(2001).
RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=FLORIDA1997;
 RA Alfonso C.L., Tulman E.R., Lu Z., Balinsky C.A., Moser B.A.,
 RA Begen J.J., Rock D.L., Kutish G.F.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF403738; AAK94160.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 392 AA; 45338 MW; 49BE7B36DF3767E2 CRC64;

Query Match 76.1%; Score 35; DB 12; Length 392;
 Best Local Similarity 75.0%; Pred. No. 56;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YOHDLR 8
 |||||
 Db 229 YOHDLRH 236

RESULT 10
 Q9RS01 PRELIMINARY; PRT; 502 AA.
 AC Q9RS01;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE SENSOR HISTIDINE KINASE.
 GN DR3328.
 OS Deinococcus radiodurans.
 OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
 OX NCBI_TaxID=1299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RI;
 RX MEDLINE=20036896; PubMed=10567266;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 RA Dodson R.J., Halt D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
 RA Fraser C.M.;
 RT "Genome sequence of the radioresistant bacterium Deinococcus
 radiodurans RI.";
 RL Science 286:1571-1577(1999).
 CC -I- SIMILARITY: TO PROKARYOTE SENSOR TRANSDUCTION PROTEINS.
 DR EMBL: AE002064; AAF11875.1; -.
 DT TIGR: DR3328; -.
 DR InterPro: IPR004358; BCTRSENSOR.
 DR InterPro: IPR003660; HAMP.
 DR InterPro: IPR003594; HATPase_C.
 DR InterPro: IPR003661; His_KinA.
 DR InterPro: IPR004359; HIS_KIN_sig.
 DR Pfam: PF00672; HAMP; 1.
 DR Pfam: PF02518; HATPase_C; 1.
 DR Pfam: PF00512; signal; 1.
 DR PRINTS: PR00344; BCTRSENSOR.
 DR SMART: SM00304; HAMP; 1.
 DR SMART: SM00387; HATPase_C; 1.
 DR SMART: SM00388; HisK_A; 1.
 KW Complete proteome; Kinase; Phosphorylation; Sensory transduction;
 KW Transference.
 SQ SEQUENCE 502 AA; 52988 MW; 295FD8FD050ECD0B CRC64;

Query Match 76.1%; Score 35; DB 16; Length 502;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YOHDLR 6
 |||||
 Db 310 YOHDLR 315

RESULT 11
 O42136 PRELIMINARY; PRT; 167 AA.
 ID O42136
 AC O42136
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE TROPONIN C.
 OS Lampetra japonica (Japanese lamprey) (Entosphenus japonicus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hypochoartia;
 OC Petromyzontiformes; Petromyzontidae; Leptocheilichthys.
 OX NCBI_TaxID=94989;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98265050; PubMed=9604009;
 RA Yusa H.J., Cox J.A., Takagi T.;
 RT "Diversity of the troponin C genes during chordate evolution.";
 RL J. Biochem. 123:1180-1190(1998).
 CC -I- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
 DR EMBL: AB008555; BAA33282.1; -.
 DR HSSP: P10246; TRF.
 DR InterPro: IPR002048; EF-hand.
 DR Pfam: PF00036; ehand; 4.
 DR SMART: SM00034; EFh; 4.
 DR PROSITE: PS00018; EF_HAND; UNKNOWN_4.
 KW Calcium-binding.
 SQ SEQUENCE 167 AA; 18596 MW; C907CF1716AAAF20B CRC64;

Query Match 73.9%; Score 34; DB 13; Length 167;
 Best Local Similarity 85.7%; Pred. No. 35;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QHDLR 8
 |||||
 Db 10 QHDLR 16

RESULT 12
 O9U0R8 PRELIMINARY; PRT; 242 AA.
 ID O9U0R8
 AC O9U0R8;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE DELTA-AMINOLEVULINIC ACID DEHYDRATASE (EC 4.2.1.24) (PORHOBILINOGEN
 DE SYNTHASE) (ALADH) (FRAGMENT).
 GN HEM2.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20198189; PubMed=10731566;
 RA Sato S., Tews I., Wilson R.J.M.;
 RT "Impact of a plastid-beating endocytobiont on apicomplexan genomes.";
 RL Int. J. Parasitol. 30:427-439(2000).
 CC -I- CATALYTIC ACTIVITY: 2 5-AMINOLEVULINATE = PORHOBILINOGEN + 2
 H(2)O.
 CC -I- PATHWAY: SECOND STEP IN PORPHYRIN AND HEME BIOSYNTHESIS.
 CC -I- SUBUNIT: HOMOOCTAMER (BY SIMILARITY).
 CC -I- SIMILARITY: BELONGS TO THE ALADH FAMILY.
 DR EMBL: AJ249365; CAB65342.1; -.
 DR HSSP: P15002; 1BAE.
 DR InterPro: IPR001731; D_ala_dehydratase.
 DR Pfam: PF00490; ALAD; 2.
 DR PRINTS: PR00144; DALDHDRATASE.
 DR PROSITE: PD002304; D_ala_dehydratase; 1.
 DR PROSITE: PS00169; D_ALA_DEHYDRATASE; 1.
 KW Lyase; Porphyrin biosynthesis.
 FT NON_TER 1
 FT NON_TER 242

SQ SEQUENCE ~ 242 AA; 28534 MW; 7257D98516F82BBB CRC64;

Query Match 73.9%; Score 34; DB 5; Length 242;

Best Local Similarity 62.5%; Pred. No. 53;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YOHDLRAY 8
| | | | |
Db 204 YOHDLRAY 211

RESULT 13

085470

ID 085470 PRELIMINARY; PRT; 316 AA.

AC 085470;

DT 01-NOV-1998 (TREMBLrel. 08, Created)

DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE SAGB (STREPTOLYSIN S ASSOCIATED ORF).

GN SAGB OR SPY0739.

OS Streptococcus pyogenes.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;

OC Streptococcus.

OX NCBI_TaxID=1314;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=N2131;

RA Beall B., Nicholson M.L.;

RT "A Locus Required for Oxygen-Stable Hemolysis in Streptococcus

pyogenes.";

RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=SF370 / ATCC 700294 / SEROTYPE M1;

RA MEDLINE=21192684; PubMed=11296296;

RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,

RA Primeaux C., Szate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,

RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,

RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;

RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";

RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).

DR EMBL: AF067649; AAC25178.1; -

DR EMBL: AE006526; AAC33685.1; -

DR InterPro: IPR000102; MAP1B_neuraxln.

DR PROSITE: PS00230; MAP1B_NEURAXIN; UNKNOWN_1.

KW Complete proteome.

SQ SEQUENCE 316 AA; 35989 MW; D8926FB38E68E765 CRC64;

Query Match 73.9%; Score 34; DB 16; Length 316;

Best Local Similarity 75.0%; Pred. No. 70;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 YOHDLRAY 8
| | | | |
Db 204 YOHDLRAY 211

RESULT 14

09FVX2

ID 09FVX2 PRELIMINARY; PRT; 481 AA.

AC 09FVX2;

DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE HYPOTHETICAL 55.7 KDA PROTEIN.

GN F2P24.7.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC Eurosid II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=CV. COLUMBIA;

RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,

RA Maiti R., Konning C.M., Koo H., Fujii C.Y., Utterback T.R.,

RA Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;

RT "Arabidopsis thaliana chromosome 1 BAC F2P24 genomic sequence.";

RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AC078898; AAC29201.1; -

DR InterPro: IPR002885; PPR.

DR Pfam: PF01535; PPR; 10.

KW Hypothetical protein.

SQ SEQUENCE 481 AA; 55688 MW; 8F3E13B4D2FF3EDB CRC64;

Query Match 73.9%; Score 34; DB 10; Length 481;

Best Local Similarity 62.5%; Pred. No. 11e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 YOHDLRAY 8
| | | | |
Db 94 YEHVRAV 101

RESULT 15

09HIE2

ID 09HIE2 PRELIMINARY; PRT; 531 AA.

AC 09HIE2;

DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

DE HYPOTHETICAL PROTEIN TAI1398.

GN TAI1398.

OS Thermoplasma acidophilum.

OC Archaea; Euryarchaeota; Thermoplasmales; Thermoplasmaeae;

OC Thermoplasma.

OX NCBI_TaxID=2303;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=DSM 1728;

RA MEDLINE=20479972; PubMed=11029001;

RA Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,

RA Newes H.-W., Fishman D., Stocker S., Lupas A.N., Baumeister W.;

RT "The genome sequence of the thermophilic scavenger Thermoplasma

acidophilum.";

RL Nature 407:508-513(2000).

DR EMBL: AF445067; CAC12518.1; -

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 531 AA; 60041 MW; 8F0C0BCD478307F6 CRC64;

Query Match 73.9%; Score 34; DB 17; Length 531;

Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 YOHDLRAY 8
| | | | |
Db 271 YDNDLRAY 278

Search completed: August 15, 2002, 11:57:52
Job time: 527 sec

GenCore version 4.5
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OW protein - protein search, using sw model

Run on: August 15, 2002, 11:39:44 ; Search time 73.67 Seconds
(without alignments)
12.062 Million cell updates/sec

Title: US-09-613-092a-5_COPY_3_10
Perfect score: 51
Sequence: 1 SRVPMPTAM 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT : *
2: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT : *
3: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT : *
4: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1983.DAT : *
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6: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1985.DAT : *
7: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1986.DAT : *
8: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1987.DAT : *
9: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1988.DAT : *
10: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1989.DAT : *
11: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1990.DAT : *
12: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1991.DAT : *
13: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1992.DAT : *
14: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1993.DAT : *
15: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1994.DAT : *
16: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1995.DAT : *
17: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1996.DAT : *
18: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1997.DAT : *
19: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT : *
20: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT : *
21: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT : *
22: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	15	20	AAV30351
2	42	82.4	34	22	ABB38515
3	42	82.4	34	22	ABB23664
4	42	82.4	34	22	AAW59133
5	42	82.4	34	22	AAW71668
6	42	82.4	34	22	AAW19262
7	42	82.4	34	22	AAW31962
8	42	82.4	81	22	AAW69150
9	39	76.5	1189	20	AAV15217
10	39	76.5	1189	20	AAV15218
11	38	74.5	10	16	AAW69771

12	38	74.5	15	21	AAW13080	Vascular endothel
13	38	74.5	27	22	AAW27332	Protein #9311 enco
14	38	74.5	53	20	AAW92467	Rat F-spondin PSP
15	38	74.5	58	22	AAW61606	Protonibacterium
16	38	74.5	72	22	AAW52332	Protonibacterium
17	38	74.5	76	22	AAW15813	Human nervous syst
18	38	74.5	84	22	AAW77743	Human colon cancer
19	38	74.5	102	22	AAW16216	Human nervous syst
20	38	74.5	106	22	AAW16994	Human nervous syst
21	38	74.5	128	22	AAW09709	Human gene 5 encod
22	38	74.5	157	22	AAW61821	Protonibacterium
23	38	74.5	168	22	AAW97743	H. annus SCIP-1 pr
24	38	74.5	182	21	AAW58354	Lung cancer associ
25	38	74.5	185	21	AAW14880	Arabidopsis thalia
26	38	74.5	343	22	AAW93099	Human protein sequ
27	38	74.5	436	21	AAW30975	Arabidopsis thalia
28	38	74.5	445	21	AAW5039	Arabidopsis thalia
29	38	74.5	454	21	AAW30974	Arabidopsis thalia
30	38	74.5	463	21	AAW52038	Arabidopsis thalia
31	38	74.5	525	22	AAW09697	Human gene 8 encod
32	38	74.5	568	14	AAW44243	Xenopus F-spondin
33	38	74.5	616	22	AAW39256	Human polypeptide
34	38	74.5	646	22	AAW41042	Human polypeptide
35	38	74.5	802	14	AAW44242	F-spondin (FP5-9) .
36	38	74.5	807	14	AAW44241	F-spondin (FP5-9) .
37	38	74.5	807	20	AAW04262	Human vascular smo
38	38	74.5	807	20	AAW04263	Bovine vascular sm
39	38	74.5	807	20	AAW04264	Rat vascular smoot
40	38	74.5	807	21	AAW13072	Vascular endothel
41	38	74.5	807	21	AAW13073	Vascular endothel
42	38	74.5	807	21	AAW13074	Vascular endothel
43	38	74.5	807	22	AAW93799	Human polypeptide
44	38	74.5	807	22	AAW74401	Human ovarian canc
45	38	74.5	817	22	AAW30223	Novel human diagno

ALIGNMENTS

RESULT 1	AAV30351	standard; Peptide: 15 AA.
AC	AAV30351;	
XX		
DE	09-NOV-1999 (first entry)	
XX		
DE	Epitope derived from pneumococcal surface adhesion A protein.	
XX		
KW	Pneumococcal surface adhesion A protein; PsaA; monoclonal antibody;	
KW	vaccine; Streptococcus pneumoniae infection.	
XX		
OS	Streptococcus pneumoniae.	
XX		
PN	WO9945121-A1.	
XX		
PD	10-SEP-1999.	
XX		
PF	26-FEB-1999; 99WO-US04326.	
XX		
PR	02-MAR-1998; 98US-0076565.	
XX		
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.	
PI	Ades EW, Carlone GW, Sampson JS, Tharpe JA, Westerink MAJ;	
PI	Zeller JL;	
XX		
DR	WPI; 1999-540849/45.	
XX		
PT	New peptides corresponding to Streptococcus pneumoniae PsaA, used	
PT	for treating or preventing Streptococcus pneumoniae infection in a	
PT	subject	
XX		

PS Claim 6; Page 43; 58pp; English.

XX AAY30351-54 represent immunogenic peptides which are derived from
CC a pneumococcal surface adhesion A protein (PsaA). The specification
CC describes monoclonal antibodies which bind epitopes of the PsaA protein
CC (e.g present sequence). The peptides can be used in vaccines to prevent
CC Streptococcus pneumoniae infections. The antibodies of the invention
CC can also be used to detect S. pneumoniae in a sample or individual.

XX Sequence 15 AA;

Query Match 100.0%; Score 51; DB 20; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.08;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RVPWTAW 8
| | | | |
Db 3 RVPWTAW 10

RESULT 2

ID ABB38515 standard; Peptide; 34 AA.

XX ABB38515;

XX 04-FEB-2002 (first entry)

XX Peptide #6021 encoded by human foetal liver single exon probe.

XX Human; foetal liver; gene expression; single exon nucleic acid probe.

XX Homo sapiens.

XX MO200157277-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001MO-US00669.

XX 04-FEB-2000; 2000US-0180312.

XX 26-MAY-2000; 2000US-0207456.

XX 30-JUN-2000; 2000US-0608408.

XX 03-AUG-2000; 2000US-0632366.

XX 21-SEP-2000; 2000US-0234687.

XX 27-SEP-2000; 2000US-0236359.

XX 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483447/52.

XX Human genome-derived single exon nucleic acid probes useful for

XX analyzing gene expression in human fetal liver -

XX Claim 27; SEQ ID NO 31150; 639pp + sequence listing; English.

XX The invention relates to a single exon nucleic acid probe for

XX measuring human gene expression in a sample derived from human foetal

XX liver. The single exon nucleic acid probes may be used for predicting,

XX measuring and displaying gene expression in samples derived from human

XX fetal liver. The present sequence is a peptide encoded by a single exon

XX nucleic acid probe of the invention.

XX Note: The sequence data for this patent did not form part of the

XX printed specification, but was obtained in electronic format directly

XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 34 AA;

Query Match 82.4%; Score 42; DB 22; Length 34;

Best Local Similarity 71.4%; Pred. No. 4.6;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 2 RVPWTAW 8
| | | | |
Db 25 RVPWTAW 31

RESULT 3

ID ABB23664 standard; Protein; 34 AA.

XX ABB23664;

XX 23-JAN-2002 (first entry)

XX Protein #5663 encoded by probe for measuring heart cell gene expression.

XX Human; gene expression; heart; microarray; vascular system;

XX cardiovascular disease; hypertension; cardiac arrhythmia;

XX congenital heart disease.

XX Homo sapiens.

XX MO200157274-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001MO-US00666.

XX 04-FEB-2000; 2000US-0180312.

XX 26-MAY-2000; 2000US-0207456.

XX 30-JUN-2000; 2000US-0608408.

XX 03-AUG-2000; 2000US-0632366.

XX 21-SEP-2000; 2000US-0234687.

XX 27-SEP-2000; 2000US-0236359.

XX 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-48899/53.

XX Single exon nucleic acid probes for analyzing gene expression in human

XX hearts -

XX Claim 15; SEQ ID NO 25434; 530pp; English.

XX The present invention relates to single exon nucleic acid probes for

XX measuring human gene expression in a sample derived from human heart (see

XX ABA21535-ABA41305). The present sequence is a protein encoded by one such

XX probe. The probes may be used for predicting, measuring and displaying

XX gene expression in samples derived from the human heart via microarrays.

XX By measuring gene expression, the probes are useful for predicting,

XX diagnosing, grading, staging, monitoring and prognosing diseases of the

XX human heart and vascular system e.g. cardiovascular disease,

XX hypertension, cardiac arrhythmias and congenital heart disease.

XX Note: The sequence data for this patent did not form part of the printed

XX specification, but was obtained in electronic format directly from WIPO

XX at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 34 AA;

Query Match 82.4%; Score 42; DB 22; Length 34;

Best Local Similarity 71.4%; Pred. No. 4.6;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 2 RVPWTAW 8
| | | | |
Db 25 RVPWTAW 31

RESULT 4

AAM59133
ID AAM59133 standard; Protein; 34 AA.

AC AAM59133;

DT 05-NOV-2001 (first entry)

DE Human brain expressed single exon probe encoded protein SEQ ID NO: 31238.

XX Human; brain expressed exon; gene expression analysis; probe;

KM microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;

KW epilepsy; cancer.

XX Homo sapiens.

OS Homo sapiens.

PN WO200157275-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00667.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483446/52.

XX Single exon nucleic acid probes for analyzing gene expression in human

XX brains -

XX Example 4; SEQ ID NO: 31238; 650pp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid

XX probes which are derived from genomic sequences expressed in the human

XX brain. They can be used to measure gene expression in brain cell samples,

XX which may enable the diagnosis and improved treatment of nervous system

XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,

XX epilepsy and cancers. The present sequence is a protein encoded by one of

XX the probes of the invention.

SQ Sequence 34 AA;

Query Match 82.4%; Score 42; DB 22; Length 34;

Best Local Similarity 71.4%; Pred. No. 4.6;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RVPWTAW 8

XX 1:11111

DB 25 ripwtlw 31

RESULT 5

AAM71668

ID AAM71668 standard; Protein; 34 AA.

AC AAM71668;

DT 06-NOV-2001 (first entry)

DE Human bone marrow expressed probe encoded protein SEQ ID NO: 31974.

KM Human; bone marrow expressed exon; gene expression analysis; probe;

KM microarray; cancer; leukaemia; lymphoma; myeloma.

OS Homo sapiens.

PN WO200157276-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00668.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488900/53.

XX Human genome-derived single exon nucleic acid probes useful for

XX analyzing gene expression in human bone marrow -

XX Example 4; SEQ ID NO: 31974; 658pp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid

XX probes which are derived from genomic sequences expressed in the human

XX bone marrow. They can be used to measure gene expression in bone marrow

XX samples, which may enable the improved diagnosis and treatment of cancers

XX such as lymphoma, leukaemia and myeloma. The present sequence is a

XX protein encoded by one of the probes of the invention.

SQ Sequence 34 AA;

Query Match 82.4%; Score 42; DB 22; Length 34;

Best Local Similarity 71.4%; Pred. No. 4.6;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RVPWTAW 8

XX 1:11111

DB 25 ripwtlw 31

RESULT 6

AAM19262

ID AAM19262 standard; Protein; 34 AA.

AC AAM19262;

DT 12-OCT-2001 (first entry)

DE Peptide #5696 encoded by probe for measuring cervical gene expression.

XX Probe; human; microarray; gene expression; cervical epithelial cell;

XX cervical cancer.

OS Homo sapiens.

PN WO200157278-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00670.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-488901/53.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human cervical epithelial cells -
 XX
 PS Claim 27: SEQ ID NO 24088; 487pp; English.
 XX
 CC The present invention relates to human single exon nucleic acid probes
 CC (SENP: see AAI10068-AA128459). The present sequence is a peptide encoded
 CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs
 CC can be used to produce a single exon microarray, which can be used for
 CC measuring human gene expression in a sample derived from human cervical
 CC epithelial cells. By measuring gene expression, the probes are therefore
 CC useful in grading and/or staging of diseases of the cervix, notably
 CC cervical cancer.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
 CC
 SQ Sequence 34 AA;
 XX
 Query Match 82.4%; Score 42; DB 22; Length 34;
 Best Local Similarity 71.4%; Pred. No. 4.6;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 RVPTTAW 8
 Db 25 ripwtw 31
 XX
 RESULT 7
 AAM31962
 ID AAM31962 standard; Protein; 34 AA.
 XX
 AC AAM31962;
 XX
 DT 17-OCT-2001 (first entry)
 XX
 DE Peptide #5999 encoded by probe for measuring placental gene expression.
 XX
 KW Probe: microarray; human; placenta; antenatal diagnosis;
 KW genetic disorder.
 XX
 OS Homo sapiens.
 OS
 PN WO200157272-A2.
 PD
 PD 09-AUG-2001.
 PD
 PF 30-JAN-2001; 2001WO-US00663.
 PF
 XX
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 PA
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 PI
 XX

DR WPI; 2001-488897/53.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human placenta -
 XX
 PS Claim 27: SEQ ID NO 32231; 654pp; English.
 XX
 CC The present invention relates to single exon nucleic acid probes (SENP:
 CC see AAI31315-AA157546). The present sequence is a peptide encoded by one
 CC such probe. The probes are useful for producing a microarray for
 CC predicting, measuring and displaying gene expression in samples derived
 CC from human placenta. The probes are useful for antenatal diagnosis of
 CC human genetic disorders.
 CC
 SQ Sequence 34 AA;
 XX
 Query Match 82.4%; Score 42; DB 22; Length 34;
 Best Local Similarity 71.4%; Pred. No. 4.6;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 RVPTTAW 8
 Db 25 ripwtw 31
 XX
 RESULT 8
 ABB69150
 ID ABB69150 standard; Protein; 81 AA.
 XX
 AC ABB69150;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 34242.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX
 OS Drosophila melanogaster.
 OS
 PN WO200171042-A2.
 PD
 PD 27-SEP-2001.
 PD
 PF 23-MAR-2001; 2001WO-US009231.
 PF
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 PA
 PI Venter JC, Adams M, Li PWD, Myers EW;
 PI
 DR WPI; 2001-656860/75.
 DR N-PSDB; ABL13253.
 DR
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 PT
 XX
 PS Disclosure; SEQ ID NO 34242; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 81 AA:

Query Match 82.4%; Score 42; DB 22; Length 81;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 3 VPWTAW 8
|||||
Db 58 VPWTAW 63

RESULT 9
AA15217
ID AA15217 standard; Protein: 1189 AA.
XX
AC AA15217;
XX
DT 09-NOV-1999 (first entry)
XX

DE Human Hairless wildtype protein amino acid sequence.
XX
KW alopecia; congenital alopecia; congenital atrichia;
KW androgenetic alopecia; alopecia areata; alopecia universalis;
KW wildtype; hair follicle.
XX

OS Homo sapiens.
XX
PN MO9938965-A1.
XX
PD 05-AUG-1999.
XX

PF 29-JAN-1999; 99WO-US02128.
XX
PR 29-JAN-1998; 98US-0073043.
XX
PA (UYCO) UNIV COLUMBIA NEW YORK.
XX

PI Christiano AM;
XX
DR WPI: 1999-479184/40.
DR N-PSDB; AA206349.
XX

PT Human hairless gene and protein, useful for identifying modulators
of hair growth
XX
PS Claim 21; Fig 6; 127pp; English.
XX

CC This is the amino acid sequence for the wildtype human hairless
protein.
CC The gene was discovered by genotyping a Pakistani kindred (comprising of
CC 4 affected males and 7 affected females) with an inherited form of
CC congenital alopecia universalis. The pedigree is strongly suggestive of
CC autosomal recessive inheritance.
CC The invention provides methods and sequences for the recombinant
CC production of wild-type human hairless, mutant human hairless and
CC wild-type human whn (winged-helix-nude) proteins, assays for screening
CC for blinding compounds, modulators and homologues, and animal models of
CC hairlessness. Human hairless conditions such as androgenetic alopecia
CC (male pattern baldness), alopecia areata, alopecia totalis,
CC congenital alopecia universalis, congenital alopecia and severe T-cell
CC immunodeficiency can be treated with compounds identified in the assays.
CC The methods are also useful for identifying compounds that can be used
CC to inhibit hair growth.
XX

SQ Sequence 1189 AA;

Query Match 76.5%; Score 39; DB 20; Length 1189;
Best Local Similarity 83.3%; Pred. No. 4.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 VPWTAW 8
|||||
Db 274 VPWTAW 279

RESULT 10
AA15218
ID AA15218 standard; Protein: 1189 AA.
XX
AC AA15218;
XX
DT 09-NOV-1999 (first entry)
XX

DE Human Hairless mutant amino acid sequence, Thr(1022)Ala.
XX

KW alopecia; congenital alopecia; congenital atrichia;
KW androgenetic alopecia; alopecia areata; alopecia universalis;
KW mutant; hair follicle.
XX

OS Homo sapiens.
XX

FH Key Location/Qualifiers
FT Misc-difference 1022 /label= T1022A
FT /note= "Wild-type Thr substituted by Ala"
XX

PN MO9938965-A1.
XX

PD 05-AUG-1999.
XX

PF 29-JAN-1999; 99WO-US02128.
XX

PR 29-JAN-1998; 98US-0073043.
XX

PA (UYCO) UNIV COLUMBIA NEW YORK.
XX

PI Christiano AM;
XX

DR WPI: 1999-479184/40.
XX

PT Human hairless gene and protein, useful for identifying modulators
of hair growth
XX
PS Claim 8; Page -: 127pp; English.
XX

CC This is the amino acid sequence for the mutant human hairless
protein, which has Alanine substituted for Threonine at position
CC 1022.
CC The gene was discovered by genotyping a Pakistani kindred (comprising of
CC 4 affected males and 7 affected females) with an inherited form of
CC congenital alopecia universalis. The pedigree is strongly suggestive of
CC autosomal recessive inheritance.
CC The invention provides methods and sequences for the recombinant
CC production of wild-type human hairless, mutant human hairless and
CC wild-type human whn (winged-helix-nude) proteins, assays for screening
CC for blinding compounds, modulators and homologues, and animal models of
CC hairlessness. Human hairless conditions such as androgenetic alopecia
CC (male pattern baldness), alopecia areata, alopecia totalis,
CC congenital alopecia universalis, congenital alopecia and severe T-cell
CC immunodeficiency can be treated with compounds identified in the assays.
CC The methods are also useful for identifying compounds that can be used
CC to inhibit hair growth.
XX

SQ Sequence 1189 AA;

Query Match 76.5%; Score 39; DB 20; Length 1189;
Best Local Similarity 83.3%; Pred. No. 4.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 3 VPWTAW 8
|||||

DB 274 vpwtsw 279

RESULT 11

ID AAR69771 standard; peptide; 10 AA.

AC AAR69771;

DT 13-OCT-1995 (first entry)

DE Thrombospondin peptide #6 for activating latent TGF-beta.

KM Thrombospondin type 1 repeat sequence; transforming growth factor-beta; wound healing; fibrosis; endothelial cell proliferation.

OS Synthetic.

PN WO9505191-A.

PD 23-FEB-1995.

PF 12-AUG-1994; 94WO-US09193.

PR 13-AUG-1993; 93US-0106120.

PR 04-MAY-1994; 94US-0238169.

PA (UABR-) UAB RES FOUND.

PI Kruttsch HC, Murphy-Ullrich JE, Roberts DD, Schultz-Cherry S;

DR WPI; 1995-098579/13.

XX Stimulating or inhibiting transforming growth factor-beta by

PT contacting with thrombo-spondin or an activating enzyme - used

PT to enhance wound healing or prevent fibrosis

XX Claim 4; Page 62; 67pp; English.

PS The peptides AAR6976-79 are active peptide fragments based on the

CC second type 1 repeat sequence (amino acids 412-473) of thrombospondin

CC (sequence not given in the specification) which can be used to convert

CC latent transforming growth factor-beta (TGF-b) to active TGF-b.

CC Thrombospondin, or the activating peptides, can be used to stimulate

CC TGF-b for use in wound healing. Peptides (see AAR69780-90) which inhibit

CC the stimulation of TGF-b can be used to prevent fibrosis or block TGF-b

CC mediated endothelial cell proliferation.

XX SQ Sequence 10 AA;

Query Match

Best Local Similarity 74.5%; Score 38; DB 16; Length 10;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 21-DEC-2000 (first entry)

DE Vascular endothelial cell migration inhibitory protein SEQ ID 9.

KM Vascular endothelial cells migration; inhibition; abnormal angiogenesis;

KM solid tumour; inflammatory disease; arthritis; ocular angiogenic disease;

KM diabetic retinopathy.

XX OS Synthetic.

XX Key Location/Qualifiers

XX FT Modified-site 15 /note="C-terminal amide"

XX FT WO200047606-A1.

XX PD 17-AUG-2000.

PF 09-FEB-2000; 2000WO-JP00703.

PR 12-FEB-1999; 99JP-0033772.

PA (KYOW) KYOWA HAKKO KOGYO KK.

PI Shibata K, Yamasaki M, Tsukuda E, Oda S, Miyamoto K;

DR WPI; 2000-549131/50.

XX New peptides inhibiting the migration of vascular endothelial cells for

PT treating diseases associated with abnormal angiogenesis including solid

PS tumors

PS Claim 4; Page 11; 58pp; Japanese.

CC This invention relates to peptides which inhibit the migration of

CC vascular endothelial cells. The peptides of the invention (sequences

CC AAB13075-B13085 including the present sequence) are fragments of the

CC human, bovine and rat sequences represented by sequences AAB13072-B13074.

CC The peptides are inhibitors of the migration of vascular endothelial

CC cells and are used for treating diseases associated with abnormal

CC angiogenesis including solid tumours, inflammatory diseases (e.g.

CC arthritis) and ocular angiogenic diseases (e.g. diabetic retinopathy).

XX SQ Sequence 15 AA;

Query Match

Best Local Similarity 74.5%; Score 38; DB 21; Length 15;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 23-JAN-2002 (first entry)

DE Protein #9331 encoded by probe for measuring heart cell gene expression.

KM Human: gene expression; heart; microarray; vascular system;

KM cardiovascular disease; hypertension; cardiac arrhythmia;

KM congenital heart disease.

OS Homo sapiens.

PN WO200157274-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00666.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488899/53.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT hearts -
XX
PS Claim 15; SEQ ID No 29102; 530pp; English.
XX
CC The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart (see
CC ABA21535-ABA1305). The present sequence is a protein encoded by one such
CC probe. The probes may be used for predicting, measuring and displaying
CC gene expression in samples derived from the human heart via microarrays.
CC By measuring gene expression, the probes are useful for predicting
CC diagnosing, grading, staging, monitoring and prognosing diseases of the
CC human heart and vascular system e.g. cardiovascular disease,
CC hypertension, cardiac arrhythmias and congenital heart disease.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 27 AA:

Query Match 74.5%; Score 38; DB 22; Length 27;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 VPWTAW 8
:||||:
DB 20 lpwtsw 25

RESULT 14
AAW92467
ID AAW92467 standard; Protein: 53 AA.
XX
AC AAW92467;
XX
DT 21-APR-1999 (first entry)
XX
DE Rat F-spondin FSP-TSR-6 protein domain.
XX
XX NAF-1; neuronal attachment factor-1; F-spondin analogue; treatment;
KW spinal cord injury; peripheral nerves damage; neural cell adhesion;
KW neurite extension; tumour cell metastasis; inhibitor; mobility; disease;
KW endothelial cell proliferation; tumour neovascularisation; haemostasis;
KW angiostatic agent; wound healing; diagnostic; neurotrophic; anticancer;
KW antimetastatic; anti-angiogenic; antimalarial; rat; FSP; TSP; TSR;
KW thrombospondin; thrombospondin type 1 repeat; FSP-TSR-6.
XX
OS Rattus sp.
XX
PN US5871969-A.
XX
PD 16-FEB-1999.
XX
PF 12-FEB-1997; 97US-0799173.
XX
PR 12-FEB-1996; 96US-0011519.
XX
PR 12-FEB-1997; 97US-0799173.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Dillon PJ, Hastings G;

XX WPI; 1999-166644/14.
DR
XX
PT Nucleic acid encoding human neuronal attachment factor-1 - used to
PT e.g. treat spinal cord injuries, and inhibit tumor cell metastasis
PT and neovascularization
XX
PS Disclosure; Fig 3; 29pp; English.
XX

CC This sequence represents a rat F-spondin (FSP) thrombospondin (TSP) type
CC 1 repeat domain, FSP-TSR-6 which is used in a method resulting in the
CC isolation of a novel human neuronal attachment factor-1, NAF-1. NAF-1 is
CC an analogue of rat F-spondin and is used to treat spinal cord injuries
CC and damage to peripheral nerves (by promoting neural cell adhesion and
CC neurite extension), to inhibit tumor cell metastasis (particularly in
CC small cell and breast carcinoma) and endothelial cell proliferation,
CC adhesion and mobility, to reduce tumor neovascularisation, as angiostatic
CC agents for tumor cells, to promote wound healing and to modulate
CC hemostasis. NAF-1 may also be used to identify treatments and diagnoses
CC for human disease. Fragments of the nucleic acid that do not encode NAF-1
CC peptides are useful as probes to isolate the NAF-1 gene, its allelic
CC variants, full-length cDNA or related sequences, in chromosomal location
CC by in situ hybridization or in Northern blotting, and as diagnostic
CC probes or primers. The protein has neurotrophic, anticancer,
CC antimetastatic, anti-angiogenic, antimalarial and modulates adhesion,
CC proliferation and mobility of cells.
XX
SQ Sequence 53 AA:

Query Match 74.5%; Score 38; DB 20; Length 53;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PWTAW 8
|||||
DB 5 pwtaw 9

RESULT 15
AAU61606
ID AAU61606 standard; Protein: 58 AA.
XX
AC AAU61606;
XX
DT 27-FEB-2002 (first entry)
XX
DE Propionibacterium acnes immunogenic protein #22502.
XX
XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.
XX
OS Propionibacterium acnes.
XX
PN WO200181581-A2.
XX
PD 01-NOV-2001.
XX
PF 20-APR-2001; 2001WO-US12865.
XX
PR 21-APR-2000; 2000US-199047P.
XX
PR 02-JUN-2000; 2000US-20841P.
XX
PR 07-JUL-2000; 2000US-216747P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Skelky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
XX
XX L'Maisonneuve J, Zhang Y, Jen S, Carter D;
XX
DR WPI; 2001-616774/71.
DR N-PSDB; AAS59618.

XX Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris -
XX

PS Example 1: SEQ ID No 22801; 1069pp; English.

XX
CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA).
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX

SQ Sequence 58 AA;

Query Match

Best Local Similarity 74.58; Score 38; DB 22; Length 58;

Matches 5; Conservatively 1; Mismatches 1; Indels 0; Caps 0;

QY 2 RVPWTAW 8

Db 20 repvltsw 26

Search completed: August 15, 2002, 11:49:01
Job time: 557 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 11:44:59 ; Search time 27.13 Seconds
(without alignments)
7.203 Million cell updates/sec

Title: US-09-613-092a-5_COPY_3_10
Perfect score: 51
Sequence: 1 SRVPMWTAW 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

- 1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
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- 6: /cgn2_6/ptodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	76.5	984	4	US-09-287-354-2
2	39	76.5	1189	4	US-09-287-354-3
3	39	76.5	1189	4	US-09-287-354-4
4	38	74.5	53	2	US-07-999-173A-13
5	38	74.5	55	1	US-07-862-021B-20
6	38	74.5	55	5	PCT-US93-03164-20
7	38	74.5	568	1	US-07-862-021B-14
8	38	74.5	568	1	PCT-US93-03164-14
9	38	74.5	802	1	US-07-862-021B-12
10	38	74.5	802	1	US-08-313-288B-12
11	38	74.5	802	5	PCT-US93-03164-12
12	38	74.5	807	1	US-07-862-021B-10
13	38	74.5	807	1	US-08-313-288B-10
14	38	74.5	807	5	PCT-US93-03164-10
15	36	70.6	150	4	US-08-334-179A-6
16	36	70.6	150	4	US-08-334-179A-10
17	36	70.6	323	1	US-07-913-107-2
18	36	70.6	323	1	US-08-459-201-2
19	36	70.6	323	1	US-08-281-248-2
20	36	70.6	323	5	PCT-US93-06421-1
21	36	70.6	582	4	US-08-334-179A-4
22	36	70.6	870	2	US-08-732-192A-2
23	36	70.6	870	4	US-09-172-339-8
24	36	70.6	1038	4	US-08-334-179A-2
25	36	70.6	1038	4	US-08-334-179A-8
26	35	66.6	387	1	US-08-539-798-2
27	35	66.6	387	1	US-08-329-560-2

28	34	66.7	32	2	US-08-078-311-25	Sequence 25, Appl
29	34	66.7	32	2	US-08-460-402-25	Sequence 25, Appl
30	34	66.7	45	2	US-08-078-311-10	Sequence 10, Appl
31	34	66.7	45	2	US-08-460-402-10	Sequence 10, Appl
32	34	66.7	184	2	US-08-078-311-4	Sequence 4, Appl
33	34	66.7	184	2	US-08-460-402-4	Sequence 4, Appl
34	34	66.7	284	2	US-08-078-311-14	Sequence 14, Appl
35	34	66.7	284	2	US-08-460-402-14	Sequence 14, Appl
36	34	66.7	284	2	US-08-460-402-14	Sequence 14, Appl
37	34	66.7	284	2	US-08-460-402-24	Sequence 24, Appl
38	34	66.7	285	2	US-08-712-072C-5	Sequence 5, Appl
39	34	66.7	382	2	US-08-078-311-3	Sequence 3, Appl
40	34	66.7	382	2	US-08-460-402-3	Sequence 3, Appl
41	34	66.7	422	2	US-08-712-072C-2	Sequence 2, Appl
42	34	66.7	451	1	US-08-191-337-3	Sequence 3, Appl
43	34	66.7	482	1	US-08-184-327A-8	Sequence 8, Appl
44	34	66.7	482	5	PCT-US95-00670-8	Sequence 8, Appl
45	34	66.7	572	6	5200183-5	Patent No. 5200183

ALIGNMENTS

RESULT 1
US-09-287-354-2
; Sequence 2, Application US/09287354
; Patent No. 6348348
; GENERAL INFORMATION:
; APPLICANT: THOMPSON, Catherine C.
; TITLE OF INVENTION: HUMAN HAIRLESS GENE AND PROTEIN
; FILE REFERENCE: Thompson-20263/0243435
; CURRENT APPLICATION NUMBER: US/09/287,354
; CURRENT FILING DATE: 1999-04-07
; EARLIER FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 984
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-287-354-2

Query Match Best Local Similarity 76.5%; Score 39; DB 4; Length 984;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 VPWTAW 8
DB 69 VPWTAW 74

RESULT 2
US-09-287-354-3
; Sequence 3, Application US/09287354
; Patent No. 6348348
; GENERAL INFORMATION:
; APPLICANT: THOMPSON, Catherine C.
; TITLE OF INVENTION: HUMAN HAIRLESS GENE AND PROTEIN
; FILE REFERENCE: Thompson-20263/0243435
; CURRENT APPLICATION NUMBER: US/09/287,354
; CURRENT FILING DATE: 1999-04-07
; EARLIER FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-287-354-3

Query Match 76.5%; Score 39; DB 4; Length 1189;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 VPWTAW 8
||||:|
Db 274 VPWTAW 279

RESULT 3
US-09-287-354-4
; Sequence 4, Application US/09287354
; Patent No. 6348348
; GENERAL INFORMATION:
; APPLICANT: THOMPSON, Catherine C.
; TITLE OF INVENTION: HUMAN HAIRLESS GENE AND PROTEIN
; FILE REFERENCE: Thompson-20263/0243435
; CURRENT APPLICATION NUMBER: US/09/287,354
; CURRENT FILING DATE: 1999-04-07
; EARLIER APPLICATION NUMBER: US 60/080,888
; EARLIER FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-287-354-4

Query Match 76.5%; Score 39; DB 4; Length 1189;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 VPWTAW 8
||||:|
Db 274 VPWTAW 279

RESULT 4
US-08-799-173A-13
; Sequence 13, Application US/08799173A
; Patent No. 5871969
; GENERAL INFORMATION:
; APPLICANT: HASTINGS, GREGG,
; APPLICANT: PATRICK J. DILLON
; TITLE OF INVENTION: HUMAN NEURONAL ATTACHMENT FACTOR-1
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/799,173A
; FILING DATE: 11-FEB-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF226
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:
; LENGTH: 53 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-799-173A-13

Query Match 74.5%; Score 38; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PWTAW 8
|||||
Db 5 PWTAW 9

RESULT 5
US-07-862-021B-20
; Sequence 20, Application US/07862021B
; Patent No. 5279966
; GENERAL INFORMATION:
; APPLICANT: Jessell, Thomas M
; APPLICANT: Klar, Avihu
; TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
; TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/862,021B
; FILING DATE: 19920405
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 40028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 55 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-862-021B-20

Query Match 74.5%; Score 38; DB 1; Length 55;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PWTAW 8
|||||
Db 7 PWTAW 11

RESULT 6
PCT-US93-03164-20

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; Sequence 20, Application PC/TUS9303164
; GENERAL INFORMATION:
; APPLICANT: Jessell, Thomas M
; APPLICANT: Klar, Avihu
; TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
; TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/03164
; FILING DATE: 19930402
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 40028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 55 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US93-03164-20

Query Match          74.5%; Score 38; DB 5; Length 55;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PWTAW 8
    |||||
Db 7 PWTAW 11

RESULT 7
US-07-862-021B-14
; Sequence 14, Application US/07862021B
; Patent No. 5279966
; GENERAL INFORMATION:
; APPLICANT: Jessell, Thomas M
; APPLICANT: Klar, Avihu
; TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
; TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/03164
; FILING DATE: 19930402
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 40028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 568 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-862-021B-14
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/07/862,021B
; APPLICATION NUMBER: 520 PWTAW 524
; FILING DATE: 19920405
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 40028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 568 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-862-021B-14

Query Match          74.5%; Score 38; DB 1; Length 568;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PWTAW 8
    |||||
Db 520 PWTAW 524

RESULT 8
PCT-US93-03164-14
; Sequence 14, Application PC/TUS9303164
; GENERAL INFORMATION:
; APPLICANT: Jessell, Thomas M
; APPLICANT: Klar, Avihu
; TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
; TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/03164
; FILING DATE: 19930402
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 40028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 568 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
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; MOLECULE TYPE: protein
PCT-US93-03164-14

Query Match          74.5%; Score 38; DB 5; Length 568;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PWTAM 8
    |||||
Db 520 PWTAM 524

RESULT 9
US-07-862-021B-12
; Sequence 12, Application US/07862021B
; Patent No. 5279966
; GENERAL INFORMATION:
; APPLICANT: Jessell, Thomas M
; TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
; TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/862,021B
; FILING DATE: 19920405
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 40028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 802 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-862-021B-12

Query Match          74.5%; Score 38; DB 1; Length 802;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PWTAM 8
    |||||
Db 754 PWTAM 758

RESULT 10
US-08-313-288B-12
; Sequence 12, Application US/08313288B
; Patent No. 5750502
; GENERAL INFORMATION:
; APPLICANT: Jessell, Thomas M. and Avihu Klar
; TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
; TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
```

```
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,288B
; FILING DATE: January 5, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 40028-A-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0526
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 802 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-313-288B-12

Query Match          74.5%; Score 38; DB 1; Length 802;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PWTAM 8
    |||||
Db 754 PWTAM 758

RESULT 11
PCT-US93-03164-12
; Sequence 12, Application PC/TUS9303164
; GENERAL INFORMATION:
; APPLICANT: Jessell, Thomas M
; APPLICANT: Klar, Avihu
; TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
; TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/03164
; FILING DATE: 19930402
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
```

REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40028
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 802 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-03164-12

Query Match 74.5%; Score 38; DB 1; Length 807;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PWTAW 8
|||||
DB 754 PWTAW 758

RESULT 12
US-07-862-021B-10
Sequence 10, Application US/07862021B
Patent No. 5279966
GENERAL INFORMATION:
APPLICANT: Jessell, Thomas M
APPLICANT: Klar, Avihu
TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/862,021B
FILING DATE: 19920405
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40028
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 807 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-862-021B-10

Query Match 74.5%; Score 38; DB 1; Length 807;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PWTAW 8
|||||

DB 759 PWTAW 763

RESULT 13
US-08-313-288B-10
Sequence 10, Application US/08313288B
Patent No. 5750502
GENERAL INFORMATION:
APPLICANT: Jessell, Thomas M. and Avihu Klar
TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,288B
FILING DATE: January 5, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40028-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 807 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-313-288B-10

Query Match 74.5%; Score 38; DB 1; Length 807;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PWTAW 8
|||||
DB 759 PWTAW 763

RESULT 14
PCT-US93-03164-10
Sequence 10, Application PC/TUS9303164
GENERAL INFORMATION:
APPLICANT: Jessell, Thomas M
APPLICANT: Klar, Avihu
TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/03164
FILING DATE: 19930402
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40028
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 807 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-03164-10

Query Match 74.5%; Score 38; DB 5; Length 807;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PWTAW 8
|||||
DB 759 PWTAW 763

RESULT 15
US-08-334-179A-6
Sequence 6, Application US/08334179A
Patent No. 6306622
GENERAL INFORMATION:
APPLICANT: ROSENBAUM, JAN S.
APPLICANT: NOHNO, TSUTOMU
TITLE OF INVENTION: CDNA ENCODING A BMP TYPE II RECEPTOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: THE PROCTER AND GAMBLE COMPANY
STREET: 11810 EAST MIAMI RIVER ROAD
CITY: ROSS
STATE: OH
COUNTRY: US
ZIP: 45061
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.30, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/334,179A
FILING DATE: 04-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CORSTANJE, BRAHM J.
REGISTRATION NUMBER: 34,804
REFERENCE/DOCKET NUMBER: 5473
TELECOMMUNICATION INFORMATION:
TELEPHONE: 513-627-2858
TELEFAX: 513-627-0260
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 150 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-334-179A-6

Query Match 70.6%; Score 36; DB 4; Length 150;
Best Local Similarity 71.4%; Pred. No. 55;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RVPWTAW 8
|||||
DB 10 RVPWLPW 16

Search completed: August 15, 2002, 11:49:35
Job time: 276 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 11:46:14 ; Search time 35.29 Seconds
(without alignments)
21.783 Million cell updates/sec

Title: US-09-613-092a-5_COPY_3_10

Perfect score: 51

Sequence: 1 SRVPMWTAW 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR-71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	76.5	335	2	H72420 oligopeptide ABC t
2	39	76.5	497	2	C49850 protochlorophyllid
3	38	74.5	162	2	T48152 hypothetical prote
4	38	74.5	441	2	G83212 hypothetical prote
5	38	74.5	454	2	G86284 F9L1.4 protein - A
6	38	74.5	483	2	T06712 probable cytochrom
7	38	74.5	489	2	T06715 probable cytochrom
8	38	74.5	616	2	I38155 DNA-binding regula
9	38	74.5	773	2	C84554 hypothetical prote
10	38	74.5	803	2	A47723 F-spondin precursor
11	38	74.5	807	2	A38152 membrane alanyl am
12	38	74.5	870	1	DPECN F-spondin - rat
13	38	74.5	870	2	G90755 aminopeptidase N [
14	38	74.5	870	2	E85619 F608.20 [imported]
15	37	72.5	309	2	E85656 probable cytochrom
16	37	72.5	490	2	T06714 genome polyprotein
17	37	72.5	2290	1	GNNYE capsid polypeptide
18	37	72.5	2292	2	S75961 hypothetical prote
19	36	70.6	316	2	H55975 probable pyruvate
20	36	70.6	323	2	A39877 autocrine motility
21	36	70.6	328	2	T37734 SUR4 family protei
22	36	70.6	351	2	S63197 hypothetical prote
23	36	70.6	397	2	A49349 succinoglycan bios
24	36	70.6	437	2	T47831 hypothetical prote
25	36	70.6	490	2	T06711 probable cytochrom
26	36	70.6	541	2	A87595 amine oxidase, fla
27	36	70.6	658	2	A33598 endoglucanase 3 (E
28	36	70.6	823	2	T02812 probable membrane
29	36	70.6	823	2	T02812

30	36	70.6	851	2	T47495 hypothetical prote
31	36	70.6	1038	2	I38935 bone morphogenetic
32	36	70.6	1038	2	JC5527 bone morphogenetic
33	36	70.6	1524	2	G84721 hypothetical prote
34	36	70.6	1750	2	G84649 hypothetical prote
35	35	68.6	133	2	JQ0150 hypothetical 13k p
36	35	68.6	122	2	AF0447 probable phage-rel
37	35	68.6	182	2	T24511 hypothetical prote
38	35	68.6	262	2	T52310 L113 protein [limp
39	35	68.6	277	2	A46241 interferon respons
40	35	68.6	280	2	C70023 retinol dehydrogen
41	35	68.6	303	1	QOECRT L(+)-tartrate dehy
42	35	68.6	303	2	H91121 L-tartrate dehydra
43	35	68.6	303	2	G85966 L-tartrate dehydra
44	35	68.6	312	2	C71243 hypothetical prote
45	35	68.6	313	2	C75208 sugar transport sy

ALIGNMENTS

RESULT 1
H72420 oligopeptide ABC transporter, permease protein - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: H72420
R:Neilon, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A:Reference number: A72200; MUID:99287316
A:Accession: H72420
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-335 <ARN>
A:Cross-References: GB:AE001694; GB:AE000512; NID:g4980558; PIDN:AA035166.1; PID:g498
C:Genetics:
A:Experimental source: strain MSB8
C:Superfamily: oligopeptide permease protein opps
Query Match 76.5%; Score 39; DB 2; Length 335;
Best Local Similarity 83.3%; Pred. No. 42;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 VPWTAW 8
DB 109 LPWTAW 114
RESULT 2
C49850 protochlorophyllide reductase (EC 1.3.1.33) 52.5k chain - Rhodobacter capsulatus
N:Alternate names: chlorin reductase subunit bchx
C:Species: Rhodobacter capsulatus
C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 17-Mar-2000
C:Accession: C49850; S17824
R:Burke, D.H.; Alberti, M.; Hearst, J.E.
J. Bacteriol. 175, 2407-2413, 1993
A:Title: The Rhodobacter capsulatus chlorin reductase-encoding locus, bchA, consists
A:Reference number: A49850; MUID:93224464
A:Accession: C49850
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-497 <BUR>
A:Cross-References: EMBL:211165; NID:g46097; PIDN:CAA77549.1; PID:g46132
A:Experimental source: strain SB1003
C:Genetics:
A:Note: Sequence extracted from NCBI backbone (NCBIN:129230, NCBIPI:129233)
A:Gene: bchx

C:Superfamily: protochlorophyllide reductase chain chlB
C:Keywords: oxidoreductase; transmembrane protein

Query Match 76.5%: Score 39; DB 2; Length 497;
Best Local Similarity 71.4%: Pred. No. 61;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 2 RPWTAW 8
Db 356 RTPMSAW 362

RESULT 3
T48152
hypothetical protein T1008.10 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 21-Jul-2000
C:Accession: T48152
R:Bevan, M.; Pohl, T.; Welzenegger, T.; Bancroft, I.; Mewes, H.W.; Lemcke, K.; Mayer, K.
submitted to the Protein Sequence Database, March 2000
A:Reference number: Z24486
A:Accession: T48152
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-162 <BEV>
A:Cross-references: EMBL:AL161746
A:Experimental source: cultivar Columbia; BAC clone T1008
C:Genetics:
A:Map position: 5
A:Introns: 40/2; 138/3
A:Note: T1008.10
C:Superfamily: conserved hypothetical protein ybhB

Query Match 74.5%: Score 38; DB 2; Length 162;
Best Local Similarity 83.3%: Pred. No. 30;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 VPWTAW 8
Db 67 VPWTW 72

RESULT 4
G83212
hypothetical protein PA3464 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: G83212
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: AB2950; MUID:20437337
A:Accession: G83212
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-441 <STO>
A:Cross-references: GB:AE004767; GB:AE004091; NID:99949604; PIDN:AA606852.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA3464

Query Match 74.5%: Score 38; DB 2; Length 441;
Best Local Similarity 100.0%: Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PWTAW 8
Db 144 PWTAW 148

RESULT 5
G86284

F911.4 protein - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 27-Nov-2001
C:Accession: G86284
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719
A:Accession: G86284
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-454 <STO>
A:Cross-references: GB:AE005172; NID:95103809; PIDN:AAD3639.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

Query Match 74.5%: Score 38; DB 2; Length 454;
Best Local Similarity 100.0%: Pred. No. 81;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PWTAW 8
Db 32 PWTAW 36

RESULT 6
T06712
probable cytochrome P450 T29H1.180 - Arabidopsis thaliana
N:Alternate names: protein T29H1.180
N:Contains: oxidoreductase (EC 1.-.-.-)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 04-Mar-2000
C:Accession: T06712
R:Queller, F.; Choisme, N.; Robert, C.; Brotlier, P.; Wincker, P.; Cattoilco, L.; Art
submitted to the Protein Sequence Database, April 1999
A:Reference number: Z15793
A:Accession: T06712
A:Molecule type: DNA
A:Residues: 1-483 <QUE>
A:Cross-references: EMBL:AL049659
A:Experimental source: cultivar Columbia; BAC clone T29H11
C:Genetics:
A:Map position: 3
A:Introns: 284/3
A:Note: T29H1.180

C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C:Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; monooxygena
F;286-451/Domain: cytochrome P450 homology <CYP>
F;429/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 74.5%: Score 38; DB 2; Length 483;
Best Local Similarity 75.0%: Pred. No. 85;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 SRVPWTAW 8
Db 211 SYVPWLAW 218

RESULT 7

T06715
Probable cytochrome P450 T29H1.210 - Arabidopsis thaliana
N:Alternate names: protein T29H1.210
M:Contains: oxidoreductase (EC 1.-.-.-)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 04-Mar-2000
C:Accession: T06715
R:Querliar, F.; Choisme, N.; Robert, C.; Brotlier, P.; Wincker, P.; Catolico, L.; Artig
submitted to the Protein Sequence Database, April 1999
A:Reference number: 215793
A:Accession: T06715
A:Molecule type: DNA
A:Residues: 1-489 <QUE>
A:Cross-references: EMBL:AL049659
A:Experimental source: cultivar Columbia; BAC clone T29H11
C:Genetics:
A:Map position: 3
A:Introns: 286/3
A:Note: T29H1.210
A:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C:Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; monooxygenase;
F:288-453/Domain: cytochrome P450 homology <CYP>
F:431/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 74.5%; Score 38; DB 2; Length 489;
Best Local Similarity 75.0%; Pred. No. 86;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 SRVPTAW 8
|||
Db 213 SYVPLAW 220

RESULT 8
I38155
DNA-binding regulatory factor X5 - human
N:Alternate names: protein DKFZp586K091.1; RFX5 protein
C:Species: Homo sapiens (man)
C:Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 21-Jul-2000
C:Accession: I38155; T08770
R:Steimle, V.; Durand, B.; Barras, E.; Zufferey, M.; Hadam, M.R.; Mach, B.; Relth, W.
Genes Dev. 9, 1021-1032, 1995
A:Title: A novel DNA-binding regulatory factor is mutated in primary MHC class II defect
A:Reference number: I38155; MUID:95262896
A:Accession: I38155
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-616 <RES>
A:Cross-references: EMBL:X85786; NID:q840788; PIDN:CAAS9771.1; PID:q840789
A:Experimental source: B cell line RAJI
R:Ottewaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A:Reference number: Z16474
A:Accession: T08770
A:Molecule type: mRNA
A:Residues: 183-616 <OTT>
A:Cross-references: EMBL:AL050135
A:Experimental source: adult uterus; clone DKFZp586K091
C:Genetics:
A:Gene: GDB:RFX5
A:Cross-references: GDB:6288464; OMIM:601863
A:Map position: 19p13.3-19p13.3
A:Note: DKFZp586K091.1

Query Match 74.5%; Score 38; DB 2; Length 616;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 SRVPTAW 8
|||
Db 496 SRVPTAW 503

RESULT 9
C84554
Hypothetical protein At2g17610 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: C84554
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vankar, S.E.; Umayam, L.; Tallon,
euss, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: C84554
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-773 <STO>
A:Cross-references: GB:AE002093; NID:q4926870; PIDN:AD32950.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g17610
A:Map position: 2

Query Match 74.5%; Score 38; DB 2; Length 773;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 RVPTAW 8
::|||
Db 290 KIPWVAV 296

RESULT 10
A47723
F-spondin precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 17-Nov-2000
C:Accession: A47723
R:Ruiz I Altaba, A.; Cox, C.; Jessell, T.M.; Klar, A.
Proc. Natl. Acad. Sci. U.S.A. 90, 8268-8272, 1993
A:Title: Ectopic neural expression of a floor plate marker in frog embryos injected w
A:Reference number: A47723; MUID:93376785
A:Accession: A47723
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-803 <RUT>
A:Cross-references: GB:L09123; NID:q409244; PIDN:AAA19105.1; PID:q409245
C:Superfamily: F-spondin; thombospondin type 1 repeat homology <THR2>
F:435-489/Domain: thombospondin type 1 repeat homology <THR2>
F:607-662/Domain: thombospondin type 1 repeat homology <THR1>

Query Match 74.5%; Score 38; DB 2; Length 803;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PWTAW 8
|||||
Db 755 PWTAW 759

RESULT 11
A38152
F-spondin - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
C:Accession: A38152
R:Klar, A.; Baldassare, M.; Jessell, T.M.
Cell 69, 95-110, 1992
A:Title: F-spondin: a gene expressed at high levels in the floor plate encodes a secr
A:Reference number: A38152; MUID:92208952
A:Accession: A38152

A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-807 <RLA>
A:Cross-references: GB:M88469; NID:g204176; PIDN:AAA41174.1; PID:g204177
A:Experimental source: embryo floor plate
A>Note: sequence extracted from NCBI backbone (NCBIN:90877, NCBIP:90878)
C:Superfamily: F-spondin; thrombospondin type 1 repeat homology
F:441-495/Domain: thrombospondin type 1 repeat homology <THR2>
F:500-555/Domain: thrombospondin type 1 repeat homology <THR3>
F:557-611/Domain: thrombospondin type 1 repeat homology <THR4>
F:613-666/Domain: thrombospondin type 1 repeat homology <THR5>
F:667-721/Domain: thrombospondin type 1 repeat homology <THR6>
F:753-807/Domain: thrombospondin type 1 repeat homology <THR6>

Query Match 74.5%; Score 38; DB 2; Length 807;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PWM 8
|||||
Db 759 PWM 763

RESULT 12
DPECN
membrane alanyl aminopeptidase (EC 3.4.11.2) - Escherichia coli
N:Alternate names: alpha-aminoacylpeptidase hydrolase; aminopeptidase N; microsomal aminop
C:Species: Escherichia coli
C>Date: 30-Jun-1988 #sequence_revision 26-Sep-1997 #text_change 01-Feb-2002
C:Accession: C64833; A27164; A91561; A91163; I57748; A25058; A29045
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Ferna, N.T.; Burland, V.; Riley, M.; Co
.A.: Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: C64833
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-870 <BLAT>
A:Cross-references: GB:AE000195; GB:U00096; NID:g1787156; PIDN:MAC74018.1; PID:g1787163;
A:Experimental source: strain K-12, substrain MG1655
R:Fogolino, M.; Garbi, S.; Lazdunski, A.
Gene 49, 303-309, 1986
A:Title: Nucleotide sequence of the pepN gene encoding aminopeptidase N of Escherichia
A:Reference number: A27164; MUID:87192020
A:Accession: A27164
A:Molecule type: DNA
A:Residues: 1-870 <FOG>
A:Cross-references: GB:M15676; NID:g147143; PIDN:AAA24318.1; PID:g147144
R:McCann, M.T.; Gabe, J.D.
Gene 48, 145-153, 1986
A:Title: The nucleotide sequence of the pepN gene and its over-expression in Escherichia
A:Reference number: A91561; MUID:87163509
A:Accession: A91561
A:Molecule type: DNA
A:Residues: 1-642 'R', 644-870 <MCC>
R:Bally, M.; Foglino, M.; Bruschl, M.; Murgier, M.; Lazdunski, A.
Eur. J. Biochem. 155, 565-569, 1986
A:Title: Nucleotide sequence of the promoter and amino-terminal encoding region of the
A:Reference number: A91163; MUID:86164315
A:Accession: A91163
A:Molecule type: DNA
A:Residues: 1-176 <BA1>
A:Cross-references: GB:X03709; NID:g42354; PIDN:CAA27336.1; PID:g42356
A:Accession: B91163
A:Molecule type: protein
A:Residues: 1-21 <BA2>
R:McCann, M.T.; Gabe, J.D.
Mol. Gen. Genet. 204, 148-152, 1986
A:Title: Sequence of the promoter and 5' coding region of pepN, and the amino-terminus
A:Reference number: I57748; MUID:86310300
A:Accession: I57748

A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-75, 'D', 77-242 <RES>
A:Cross-references: EMBL:X04020; NID:g42352; PIDN:CAA27647.1; PID:g42353
C:Comment: This enzyme is active in the cytoplasm and is probably bound to the inner
C:Comment: This enzyme hydrolyzes L-amino acid beta-naphthylamides.
C:Genetics:
A:Gene: pepN
A:Map position: 21 min
C:Function:
A:Description: releases N-terminal amino acid residues from polypeptides and proteins
A>Note: requires zinc for proteolytic activity
C:Superfamily: microsomal aminopeptidase
C:Keywords: aminopeptidase; membrane protein; metalloproteinase; zinc
F:297,301,320/Binding site: zinc, catalytic (His, His, Glu) #status predicted
F:381/Active site: Tyr #status predicted

Query Match 74.5%; Score 38; DB 1; Length 870;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PWM 8
|||||
Db 70 PWM 74

RESULT 13
G90755
aminopeptidase N [imported] - Escherichia coli (strain O157:H7, substrain RIMD 050995
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C:Accession: G90755
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g
A:Reference number: A9629; MUID:21156231; PMID:11258796
A:Accession: G90755
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-870 <NAV>
A:Cross-references: GB:BA000007; PIDN:BA034438.1; PID:g13360474; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECS1015
C:Superfamily: microsomal aminopeptidase

Query Match 74.5%; Score 38; DB 2; Length 870;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PWM 8
|||||
Db 70 PWM 74

RESULT 14
E85619
aminopeptidase N [imported] - Escherichia coli (strain O157:H7, substrain EDJ933)
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: E85619
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
Miller, L.; Grobbeck, E.J.; Davis, N.W.; Llim, A.; DiMantanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: E85619
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-870 <STO>

A:Cross-references: GB:AE005174; NID:g12514107; PIDN:AG55417.1; GSPDB:GN00145; UWGP:212
 A:Experimental source: strain 0157:H7, substrain EDL933
 C:Genetics:
 A:Gene: pepN
 C:Superfamily: microsomal aminopeptidase

Query Match 74.5%; Score 38; DB 2; Length 870;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PWTAW 8
 |||||
 DB 70 PWTAW 74

RESULT 15

E96566
 F6D8.20 [Imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: E96566
 R:Rheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 Ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luros, J.S.; Malt, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719
 A:Accession: E96566
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-309 <STO>
 A:Cross-references: GB:AE005173; NID:g5903047; PIDN:AAD55606.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: F6D8.20
 A:Map position: 1

Query Match 72.5%; Score 37; DB 2; Length 309;
 Best Local Similarity 83.3%; Pred. No. 80;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 VPWTAW 8
 |||||
 DB 29 VPWTAW 34

Search completed: August 15, 2002, 11:50:17
 Job time: 243 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 11:49:40 ; Search time 18.61 seconds

(without alignments)
16.645 Million cell updates/sec

Title: US-09-613-092a-5_COPY_3_10

Perfect score: 51

Sequence: 1 SRVPMWTAW 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	ID	Description
1	39	76.5	497	1	BCHY_RHOCA
2	39	76.5	1189	1	HAIR_HUMAN
3	38	74.5	483	1	C71N_ARATH
4	38	74.5	489	1	C71Q_ARATH
5	38	74.5	616	1	REF5_HUMAN
6	38	74.5	803	1	ESPO_XENLA
7	38	74.5	807	1	FSPQ_RAT
8	38	74.5	869	1	AMPN_ECOLI
9	37	72.5	490	1	C71P_ARATH
10	37	72.5	2290	1	POLG_EMCV
11	36	70.6	316	1	EXOV_RHME
12	36	70.6	323	1	AMFR_HUMAN
13	36	70.6	351	1	YNYL_YEAST
14	36	70.6	395	1	SYT8_MOUSE
15	36	70.6	650	1	C71M_ARATH
16	36	70.6	498	1	GUN3_FIBSU
17	36	70.6	1038	1	BMR2_MOUSE
18	36	70.6	1038	1	BMR2_MOUSE
19	35	68.6	280	1	YUS2_BACSU
20	35	68.6	303	1	TTDA_ECOLI
21	35	68.6	708	1	CAO2_CANTR
22	35	68.6	1074	1	SM5A_HUMAN
23	35	68.6	1077	1	SM5A_MOUSE
24	35	68.6	1120	1	RPOM_SCHPO
25	35	68.6	1180	1	TRK2_MOUSE
26	34	66.7	119	1	VPX_STIVAI
27	34	66.7	119	1	VPX_STIVAI
28	34	66.7	119	1	VPX_STIVAI
29	34	66.7	184	1	MPL_MPLV
30	34	66.7	280	1	SOL3_YEAST
31	34	66.7	350	1	YN04_YEAST
32	34	66.7	426	1	PIRC_THEAO
33	34	66.7	470	1	MTR_NEUCR

34	34	66.7	541	1	BBL1_SCHCO	P78741 schizoplyll
35	34	66.7	581	1	CHLE_RABIT	P21927 oryctolagus
36	34	66.7	595	1	SNX9_HUMAN	O915X1 homo sapien
37	34	66.7	602	1	CHLE_HUMAN	P06276 homo sapien
38	34	66.7	603	1	CHLE_MOUSE	Q00311 mus musculu
39	34	66.7	625	1	TPOR_MOUSE	Q08351 mus musculu
40	34	66.7	775	1	MGD1_MOUSE	O99YH6 mus musculu
41	34	66.7	775	1	MGD1_RAT	O99573 rattus norv
42	34	66.7	778	1	MGD1_HUMAN	O915V3 homo sapien
43	34	66.7	990	1	TNP7_ECOLI	P13694 escherichia
44	34	66.7	1385	1	RRPO_P1AVY	Q07518 plantago as
45	34	66.7	1473	1	NAL1_HUMAN	O9C000 homo sapien

ALIGNMENTS

RESULT	ID	BCHY_RHOCA	STANDARD	PRT	497 AA
1	AC	P26178:			
DT	DT	01-MAY-1992 (Rel. 22, Created)			
DT	DT	01-MAY-1992 (Rel. 22, Last sequence update)			
DT	DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	DE	Chlorophyllide reductase 52.5 kDa chain (EC 1.18.1.-) (Chlorin reductase).			
GN	GN	BCHY.			
OS	OS	Rhodobacter capsulatus (Rhodospseudomonas capsulata).			
OC	OC	Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group; Rhodobacter.			
OX	OX	NCBI_TaxID=1061;			
RN	RN	[1]			
RP	RP	SEQUENCE FROM N.A.			
RC	RC	STRAIN=SB1003;			
RX	RX	MEDLINE=93224464; PubMed=8468299;			
RA	RA	Burke D.H., Alberti M., Hearst J.E.;			
RT	RT	"The Rhodobacter capsulatus chlorin reductase-encoding locus, bcha, consists of three genes, bchy, bchy, and bchz.";			
RL	RL	J. Bacteriol. 175:2407-2413(1993).			
CC	CC	-1- FUNCTION: CONVERTS CHLOROPHYLLS (CHL) INTO BACTERIOCHLOROPHYLLS (BCHL) BY REDUCING RING B OF THE TETRAPIROLE.			
CC	CC	-1- PATHWAY: Light-independent bacteriochlorophyll biosynthesis.			
CC	CC	-1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).			
CC	CC	-1- SIMILARITY: BELONGS TO THE BCHN / CHLN FAMILY.			
CC	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	CC	-----			
DR	DR	EMBL, Z11165; CAA7549.1; -.			
DR	DR	PIR, S17824; S17824.			
DR	DR	PIR, C49850; C49850.			
KW	KW	Oxidoreductase; Photosynthesis; Bacteriochlorophyll biosynthesis;			
KW	KW	Transmembrane.			
FT	FT	TRANSMEM 65 82 POTENTIAL.			
FT	FT	TRANSMEM 126 142 POTENTIAL.			
FT	FT	TRANSMEM 216 233 POTENTIAL.			
SO	SO	SEQUENCE 497 AA; 52618 MW; 99369F0EA91A4209 CRC64;			

Query Match 76.5%; Score 39; DB 1; Length 497;
Best Local Similarity 71.4%; Pred. No. 21;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 RVPMTAW 8
DB 356 RTPWSAW 362

```

RESULT 2
HAIR_HUMAN STANDARD: PRT; 1189 AA.
ID HAIR_HUMAN
AC Q43593; Q9NPE1;
DT 15-JUL-1999 (Rel. 38, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Hairless protein.
GN HR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (LONG ISOFORM), AND VARIANT ALUNC ALA-1022.
RX MEDLINE=9811413; PubMed=9445480;
RA Ahmad W., ul Haque M.F., Brancolini V., Tsou H.C., ul Haque S.,
RA Lam H., Alta V.M., Owen J., Deblaquiere M., Frank J.,
RA Cserhalml-Friedman P.B., Leask A., McGrath J.A., Peacocke M.,
RA Ahmad M., Ott J., Cristiano A.M.;
RT "Alopecia universalis associated with a mutation in the human hairless
RT gene";
RL Science 279:720-724(1998).
RN [2]
RP SEQUENCE FROM N.A. (LONG ISOFORM), REVISIONS TO 572 AND 774, AND
RP TISSUE SPECIFICITY.
RC TISSUE-Peripheral blood leukocytes, and Skin fibroblast;
RX MEDLINE=99162400; PubMed=10051399;
RA Ahmad W., Zlotogorski A., Panteleyev A.A., Lam H., Ahmad M.,
RA ul Haque M.F., Abdallah H.M., Dragan L., Cristiano A.M.;
RT "Genomic organization of the human hairless gene (HR) and
RT identification of a mutation underlying congenital atrichia in an Arab
RT Palestinian family.";
RL Genomics 56:141-148(1999).
RN [3]
RP SEQUENCE FROM N.A., VARIANT ALUNC ASP-1136, TISSUE SPECIFICITY, AND
RP ALTERNATIVE SPLICING.
RC TISSUE-Peripheral blood leukocytes, Brain, and Fetal brain;
RX MEDLINE=98409496; PubMed=9736769;
RA Cichon S., Anker M., Vogt I.R., Rohleder H., Putzstuck M., Hillemer A.,
RA Farooq S.A., Al-Dhafiri K.S., Ahmad M., Haque S., Rletschel M.,
RA Propping P., Kruse R., Noethen M.M.;
RT "Cloning, genomic organization, alternative transcripts and mutational
RT analysis of the gene responsible for autosomal recessive universal
RT congenital alopecia.";
RL Hum. Mol. Genet. 7:1671-1679(1998).
RN [4]
RP VARIANT APL GLN-620.
RX MEDLINE=98431781; PubMed=9758627;
RA Ahmad W., Irvine A.D., Lam H., Buckley C., Bingham E.A.,
RA Panteleyev A.A., Ahmad M., McGrath J.A., Cristiano A.M.;
RT "A missense mutation in the zinc-finger domain of the human hairless
RT gene underlies congenital atrichia in a family of Irish travellers.";
RL Am. J. Hum. Genet. 63:984-991(1998).
CC -1- FUNCTION: MAY ACT AS A TRANSCRIPTION FACTOR THAT COULD ACT ON TO
CC REGULATE ONE OF THE PHASES OF HAIR GROWTH.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- ALTERNATIVE PRODUCTS: At least 2 isoforms: a long form (shown
CC here) and a short form; are produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: Strongest expression of both isoforms is seen
CC in the small intestine, weaker expression in brain and colon, and
CC trace expression is found in liver, pancreas, spleen, thymus,
CC stomach, salivary gland, appendix and trachea. Long isoform is
CC always the most abundant. Long isoform is exclusively expressed at
CC low levels in kidney and testis and short isoform exclusively at
CC high levels in the skin.
CC -1- DISEASE: DEFECTS IN HR ARE THE CAUSE OF ALOPECIA UNIVERSALIS
CC (ALUNC), A RARE AUTOSOMAL RECESSIVE FORM OF HAIR LOSS. IT IS
CC CHARACTERIZED BY HAIR FOLICLES WITHOUT HAIR.
CC -1- DISEASE: DEFECTS IN HR ARE THE CAUSE OF ATRICHA WITH PAPULAR
CC LESIONS (APL) (ALSO KNOWN AS CONGENITAL ATRICHA). THIS AUTOSOMAL
CC RECESSIVE DISEASE IS CHARACTERIZED BY PAPULAR LESIONS OVER MOST
CC OF THE BODY AND ALMOST COMPLETE ABSENCE OF HAIR.

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CC -----
DR EMBL; AF039196; AAC32258.2; -;
DR EMBL; AJ277249; CAB87577.2; -;
DR EMBL; AJ277250; CAB87577.2; JOINED.
DR EMBL; AJ277251; CAB87577.2; JOINED.
DR EMBL; AJ277252; CAB87577.2; JOINED.
DR EMBL; AJ277253; CAB87577.2; JOINED.
DR EMBL; AJ400825; CAB87577.2; JOINED.
DR EMBL; AJ400826; CAB87577.2; JOINED.
DR EMBL; AJ400827; CAB87577.2; JOINED.
DR EMBL; AJ400828; CAB87577.2; JOINED.
DR EMBL; AJ400829; CAB87577.2; JOINED.
DR EMBL; AJ400830; CAB87577.2; JOINED.
DR EMBL; AJ400831; CAB87577.2; JOINED.
DR EMBL; AJ400832; CAB87577.2; JOINED.
DR EMBL; AJ400833; CAB87577.2; JOINED.
DR EMBL; AJ400834; CAB87577.2; JOINED.
DR EMBL; AJ400835; CAB87577.2; JOINED.
DR EMBL; AJ400836; CAB87577.2; JOINED.
DR EMBL; AJ400837; CAB87577.2; JOINED.
DR EMBL; AJ277165; CAB86602.1; -;
DR MIM; 602302; -;
DR MIM; 203655; -;
DR MIM; 209500; -;
DR InterPro; IPR003347; JmjC.
DR Pfam; PF02373; jmjC; 1.
KW Zinc-finger; DNA-binding; Nuclear protein; Transcription regulation;
KW Metal-binding; Alternative splicing; Disease mutation.
FT ZN-FING 600 625
FT VARSPLIC 1072 1126
FT VARIANT 620 620
FT VARIANT 1022 1022
FT VARIANT 1136 1136
FT VARIANT 1136 1136
FT CONFLICT 337 337
FT CONFLICT 446 446
FT CONFLICT 584 584
SQ SEQUENCE 1189 AA; 127509 MW; 5E244858716EB5DF CRC64;
OY 3 VPWTAW 8
DB 274 VPWTSW 279
Query Match 76.5%; Score 39; DB 1; Length 1189;
Best Local Similarity 83.3%; Pred. No. 47;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA:
RX MEDLINE-21016720: PubMed-11130713:
RA Salanoubat M., Lemcke K., Rieger M., Ansoerge W., Unsel'd M.,
RA Farman B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
RA Delany M., Bouty M., Griwell L.A., Mache R., Pulgdenesch P.,
RA De Simone V., Choise N., Artiguenave F., Robert C., Brotier P.,
RA Winkler P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Schefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppi S., Simionati B.,
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordstiek G.,
RA Relchelt J., Scharte M., Schoen O., Barges M., Terol J., Climent J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwelder B., Duchemin D.,
RA Cooke R., Lande M., Berger-Liauro C., Purnelle B., Masuy D.,
RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA Montfort A., Argirou A., Flores M., Liguori R., Vitale D.,
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts A., Uterback T., Fujii C.Y., Shea T.P.,
RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Pal G., Miltischer J., Sellers P., Gill J.E., Feldblum T.V.,
RA Preuss D., Lin X., Niernan W.C., Salzberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Idesawa K., Kawashina K., Kishida Y.,
RA Kiyokawa S., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shino S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.,
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
thaliana."
RA Nature 408:820-822(2000).
RT -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC -----
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CC -----
DR EMBL: AL049659; CAB41168.1; -.
DR InterPro: IPR001128; Cyt_P450.
DR Pfam: PF00067; P450; 1.
DR PRINTS: PR00385; P450.
DR PROSITE: PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Transmembrane; Heme; Multigene family.
FT BINDING 429 429 HEME (BY SIMILARITY).
FT TRANSMEM 1 21 POTENTIAL.
SQ SEQUENCE 483 AA; 54761 MW; 4CB55E1F4AC436C7 CRC64;

Query Match 74.5%; Score 38; DB 1; Length 483;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 SRVPTW 8
DB 213 STYPMILAW 218

RESULT 4
C710.ARATH STANDARD; PRT; 489 AA.
AC Q9STK7;
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DE Cytochrome P450 71A26 (EC 1.14.-.-).
GN CYP71A26 OR AT3G48270 OR T29H1.210.
OS Arabidopsis thaliana (Mouse-ear cress).

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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA:
RX MEDLINE-21016720: PubMed-11130713:
RA Salanoubat M., Lemcke K., Rieger M., Ansoerge W., Unsel'd M.,
RA Farman B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
RA Delany M., Bouty M., Griwell L.A., Mache R., Pulgdenesch P.,
RA De Simone V., Choise N., Artiguenave F., Robert C., Brotier P.,
RA Winkler P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Schefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppi S., Simionati B.,
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordstiek G.,
RA Relchelt J., Scharte M., Schoen O., Barges M., Terol J., Climent J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwelder B., Duchemin D.,
RA Cooke R., Lande M., Berger-Liauro C., Purnelle B., Masuy D.,
RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA Montfort A., Argirou A., Flores M., Liguori R., Vitale D.,
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts A., Uterback T., Fujii C.Y., Shea T.P.,
RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Pal G., Miltischer J., Sellers P., Gill J.E., Feldblum T.V.,
RA Preuss D., Lin X., Niernan W.C., Salzberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Idesawa K., Kawashina K., Kishida Y.,
RA Kiyokawa S., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shino S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.,
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
thaliana."
RA Nature 408:820-822(2000).
RT -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC -----
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CC -----
DR EMBL: AL049659; CAB41171.1; -.
DR InterPro: IPR001128; Cyt_P450.
DR Pfam: PF00067; P450; 1.
DR PRINTS: PR00385; P450.
DR PROSITE: PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Transmembrane; Heme; Multigene family.
FT BINDING 431 431 HEME (BY SIMILARITY).
FT TRANSMEM 1 21 POTENTIAL.
SQ SEQUENCE 489 AA; 55832 MW; 224FC596FB3BA75 CRC64;

Query Match 74.5%; Score 38; DB 1; Length 489;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 SRVPTW 8
DB 213 STYPMILAW 220

RESULT 5
REFS_HUMAN STANDARD; PRT; 616 AA.
AC P48382;
DT 01-FEB-1996 (Rel. 33; Created)
DT 01-FEB-1996 (Rel. 33; Last sequence update)

```

DT 16-OCT-2001 (Rel. 40, last annotation update)
 DE DNA-binding protein RFX5 (Regulatory factor X subunit 5).
 GN RFX5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95262896; PubMed=7744245;
 RA Steime V., Durand B., Barras E., Zufferey M., Hadam M.R.,
 Mach B., Reich M.;
 RT "A novel DNA-binding regulatory factor is mutated in primary MHC
 class II deficiency (bare lymphocyte syndrome).";
 RL Genes Dev. 9:1021-1032(1995).
 RL [2]
 RP PARTIAL SEQUENCE.
 RC TISSUE=Lymphoblast;
 RX MEDLINE=99170284; PubMed=10072068;
 RA Nagatjan U.M., Louis-Pence P., Desandro A., Nilsen R., Bushey A.,
 Boss J.M.;
 RT "RFX-B is the gene responsible for the most common cause of the bare
 lymphocyte syndrome, an MHC class II immunodeficiency.";
 RL Immunity 10:153-162(1999).
 RN [3]
 RP ERRATUM.
 RA Nagatjan U.M., Louis-Pence P., Desandro A., Nilsen R., Bushey A.,
 Boss J.M.;
 RL Immunity 10:399-399(1999).
 RN [4]
 RP CHARACTERIZATION.
 RX MEDLINE=20242030; PubMed=10779326;
 RA Villard J., Peretti M., Masternak K., Barras E., Caretti G.,
 Mantovani R., Reich M.;
 RT "A functionally essential domain of RFX5 mediates activation of major
 histocompatibility complex class II promoters by promoting
 cooperative binding between RFX and NF-Y.";
 RL Mol. Cell Biol. 20:3364-3376(2000)
 CC -1- FUNCTION: ACTIVATES TRANSCRIPTION FROM CLASS II MHC PROMOTERS.
 CC RCOGNIZES X-BOXES. MEDIATES COOPERATIVE BINDING BETWEEN RFX AND
 CC NF-Y. RFX BINDS THE X1 BOX OF MHC-II PROMOTERS.
 CC -1- SUBUNIT: RFX CONSISTS OF AT LEAST THREE DIFFERENT SUBUNITS. RFXAP,
 CC RFX5 AND RFX-B/REXANK; WITH EACH SUBUNIT REPRESENTING A SEPARATE
 CC COMPLEMENTATION GROUP. RFX FORMS COOPERATIVE DNA BINDING COMPLEXES
 CC WITH X2B2 AND CBF/NF-Y. RFX ASSOCIATES WITH CITTA TO FORM AN
 CC ACTIVE TRANSCRIPTIONAL COMPLEX.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- TISSUE SPECIFICITY: UBIQUITOUS.
 CC -1- DOMAIN: THE N-TERMINUS IS REQUIRED FOR ITS ASSOCIATION WITH RFXANK
 CC AND RFXAP, FOR ASSEMBLY OF THE RFX COMPLEX, AND FOR BINDING OF
 CC THIS COMPLEX TO ITS X BOX TARGET SITE IN THE MHC-II PROMOTER. THE
 CC C-TERMINUS MEDIATES COOPERATIVE BINDING BETWEEN THE RFX COMPLEX
 CC AND NF-Y.
 CC -1- PTM: PHOSPHORYLATED.
 CC -1- DISEASE: DEFECTS IN RFX5 ARE A CAUSE OF HEREDITARY MHC CLASS II
 CC DEFICIENCY (ALSO KNOWN AS BARE LYMPHOCYTE SYNDROME (BLS) OR HLA
 CC CLASS II DEFICIENT COMBINED IMMUNODEFICIENCY); A FORM OF SEVERE
 CC COMBINED IMMUNODEFICIENCY DISEASE (SCID). RFX5 IS LINKED WITH
 CC BLS COMPLEMENTATION GROUPS C.
 CC -1- SIMILARITY: BELONGS TO THE RFX FAMILY.
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 CC -----
 DR EMBL; X85786; CA59771.1; -;
 DR TRANSFAC; T01672; -;
 DR MIM; 601863; -;
 DR MIM; 209920; -;

DR InterPro: IPR003150; RFX-DNA-binding.
 DR Pfam; PF02257; RFX-DNA-binding; 1.
 KW DNA-binding; Transcription regulation; Activator; Nuclear protein;
 KW SCID; Phosphorylation.
 FT DNA_BIND 92 168 POTENTIAL.
 SO SEQUENCE 616 AA; 65322 MW; 5EBB33C677BB717F CRC64;

 Query Match 74.5%; Score 38; DB 1; Length 616;
 Best Local Similarity 62.5%; Pred. No. 37;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

 QY 1 SRVPTW 8
 Db 496 SRLPWTW 503

 RESULT 6
 FSPO_XENLA STANDARD; PRT; 803 AA.
 ID FSPO_XENLA
 AC P35447;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUN-1999 (Rel. 38, Last annotation update)
 DE F-spodin precursor.
 OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 CC Anophelinae; Xenopus.
 NX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP TISSUE=Embryo;
 RX MEDLINE=93376785; PubMed=8367492;
 RA Ruiz i Altaba A., Cox C., Jessell T.M., Klar A.;
 RT "Ectopic neural expression of a floor plate marker in frog embryos
 RT injected with the midline transcription factor Pintallavis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:8268-8272(1993).
 CC -1- FUNCTION: PROMOTES THE ATTACHMENT OF SPINAL CORD AND SENSORY
 CC NEURON CELLS AND THE OUTGROWTH OF NEURITES IN VITRO. MAY
 CC CONTRIBUTE TO THE GROWTH AND GUIDANCE OF AXONS IN BOTH THE SPINAL
 CC CORD AND THE PNS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN THE FLOOR PLATE.
 CC -1- SIMILARITY: CONTAINS 6 TSP TYPE-1 DOMAINS.
 CC -----
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 CC -----
 DR EMBL; L09123; AA19105.1; -;
 DR PIR; A47723; A47723.
 DR InterPro; IPR002861; Reeler.
 DR InterPro; IPR000884; TSP1.
 DR Pfam; PF02014; Reeler; 1.
 DR Pfam; PF00090; tsp.1; 6.
 DR SMART; SM00209; TSP1; 6.
 DR PROSITE; PSS0092; TSP1; 6.
 KW Glycoprotein; Signal; Repeat; Cell adhesion.
 FT SIGNAL 1 23
 FT CHAIN 24 803 POTENTIAL.
 FT DOMAIN 437 488 F-SPONDIN.
 FT DOMAIN 496 548 TSP TYPE-1 1.
 FT DOMAIN 553 604 TSP TYPE-1 3.
 FT DOMAIN 609 661 TSP TYPE-1 4.
 FT DOMAIN 665 716 TSP TYPE-1 5.
 FT DOMAIN 751 803 TSP TYPE-1 6.
 FT CARBOHYD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 677 677 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 803 AA: 90702 MW: D3A54E329548AED9 CRC64;

Query Match 74.5%; Score 38; DB 1; Length 803;

Best Local Similarity 100.0%; Pred. No. 48;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PWTAW 8
 |||||
 DB 755 PWTAW 759

RESULT 7
 FSPD_RAT STANDARD: PRT: 807 AA.
 AC P35446:
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE F-spodin precursor.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryonic floor plate;
 RX MEDLINE=92208952; PubMed=1555244;
 RA Klar A., Baldassare M., Jessell T.M.;
 RT "F-spodin: a gene expressed at high levels in the floor plate
 RT encodes a secreted protein that promotes neural cell adhesion and
 RT neurite extension.";
 RL Cell 69:95-110(1992).
 CC -1- FUNCTION: PROMOTES THE ATTACHMENT OF SPINAL CORD AND SENSORY
 CC NEURON CELLS AND THE OUTGROWTH OF NEURITES IN VITRO. MAY
 CC CONTRIBUTE TO THE GROWTH AND GUIDANCE OF AXONS IN BOTH THE SPINAL
 CC CORD AND THE PNS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN THE FLOOR PLATE.
 CC -1- SIMILARITY: CONTAINS 6 TSP TYPE-1 DOMAINS.
 CC -----
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 CC -----
 CC EMBL: M88469; AAA41174.1; -
 DR PIR: A38152; A38152.
 DR InterPro: IPR002861; Reeler.
 DR InterPro: IPR000884; TSP1.
 DR Pfam: PF02014; Reeler_1.
 DR Pfam: PF00090; TSP_1; 6.
 DR SMART: SM00209; TSP1; 6.
 DR PROSITE: PS50092; TSP1; 5.
 KM Glycoprotein; Signal: Repeat; Cell adhesion.
 FT SIGNAL 1 28
 FT CHAIN 29 807
 FT DOMAIN 443 494 TSP TYPE-1 1.
 FT DOMAIN 502 554 TSP TYPE-1 2.
 FT DOMAIN 559 610 TSP TYPE-1 3.
 FT DOMAIN 615 665 TSP TYPE-1 4.
 FT DOMAIN 669 720 TSP TYPE-1 5.
 FT DOMAIN 755 807 TSP TYPE-1 6.
 FT CARBOHYD 214 681
 FT CARBOHYD 681 681
 SEQUENCE 807 AA: 90773 MW: 309525F9EAFEA9A CRC64;

Query Match 74.5%; Score 38; DB 1; Length 807;
 Best Local Similarity 100.0%; Pred. No. 48;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PWTAW 8
 |||||
 DB 759 PWTAW 763

RESULT 8
 AMPN_ECOLI STANDARD: PRT: 869 AA.
 ID AMPN_ECOLI
 AC P04825;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Aminopeptidase N (EC 3.4.11.2) (Alpha-aminocysteine hydrolase).
 GN PEPP OR B0932.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87192020; PubMed=2436977;
 RA Fogliano M., Garbi S., Lazdunski A.;
 RT "Nucleotide sequence of the pepN gene encoding aminopeptidase N of
 RT Escherichia coli.";
 RL Gene 49:303-309(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE=87163509; PubMed=3549459;
 RA McCaman M.T., Gabe J.D.;
 RT "The nucleotide sequence of the pepN gene and its over-expression in
 RT Escherichia coli.";
 RL Gene 48:145-153(1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12; MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 MAU B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE=97061202; PubMed=8905232;
 RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
 RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K.,
 RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
 RA Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
 RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
 RA Yano M., Horiuchi T.;
 RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
 RT corresponding to the 12.7-28.0 min region on the linkage map.";
 RL DNA Res. 3:137-155(1996).
 RN [5]
 RP SEQUENCE OF 1-241 FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE=86310300; PubMed=3018440;
 RA McCaman M.T., Gabe J.D.;
 RT "Sequence of the promoter and 5' coding region of pepN, and the
 RT amino terminus of peptidase N from Escherichia coli K-12.";
 RL Mol. Gen. Genet. 204:148-152(1986).
 RN [6]
 RP SEQUENCE OF 1-176 FROM N.A., AND SEQUENCE OF 1-21.
 RX MEDLINE=86164315; PubMed=2869947;
 RA Bally M., Fogliano M., Bruschi M., Murgier M., Lazdunski A.;
 RT "Nucleotide sequence of the promoter and amino-terminal encoding
 RT region of the Escherichia coli pepN gene.";
 RL Eur. J. Biochem. 155:565-569(1986).

```

CC -1- FUNCTION: AMINOPEPTIDASE N IS INVOLVED IN THE DEGRADATION OF
CC INTRACELLULAR PEPTIDES GENERATED BY PROTEIN BREAKDOWN DURING
CC NORMAL GROWTH AS WELL AS IN RESPONSE TO NUTRIENT STARVATION.
CC -1- COFACTOR: BINDS 1 ZINC ION.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC, BOUND TO THE INNER FACE OF
CC THE CYTOPLASMIC MEMBRANE.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M1.
CC -----
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CC -----
DR EMBL: X04020; CAA27647.1; -
DR EMBL: X03709; CAA27336.1; -
DR EMBL: M15676; AAA24318.1; -
DR EMBL: AE000195; AAC74018.1; -
DR EMBL: D90731; BAA35684.1; -
DR EMBL: D90732; BAA35687.1; -
DR EMBL: M15273; AAA24317.1; -
DR PIR: A29045; DPECN.
DR PIR: A27164; A27164.
DR MEROPS: M01.005; -.
DR Ecogene; EG10696; pepN.
DR InterPro: IPR001930; Zn_MTPeptase.
DR InterPro: IPR000130; Zn_MTPeptase.
DR Pfam: PF01433; Peptidase_M1; 1.
DR PRINTS: PR00756; ALADIPPTASE.
DR PROSITE: PS00142; ZINC_PROTEASE; 1.
KW Hydrolase; Metallopeptidase; Amino-peptidase; Zinc; Membrane;
KW Complete proteome.
FT METAL 296 296 ZINC (CATALYTIC) (BY SIMILARITY).
FT INT_MET 0 0
FT ACT_SITE 297 297 BY SIMILARITY.
FT METAL 300 300 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 319 319 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 380 380 PROTON DONOR (POTENTIAL).
FT CONFLICT 75 75 E -> D (IN REF. 6).
SQ SEQUENCE 869 AA; 98787 MW; 9DED2712669CECA3 CRC64;

Query Match 74.5%; Score 38; DB 1; Length 869;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PWTAW 8
Db 69 PWTAW 73

RESULT 9
C71P_ARATH STANDARD; PRT; 490 AA.
ID C71P_ARATH
AC Q9STK8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytochrome P450 71A25 (EC 1.14.-.-).
GN CYP71A25 OR AT3G48360 OR T29H1.200.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustoids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=21016720; Pubmed=11130713;
RA Sahnounbat M., Lemcke K., Rieger M., Ansoorge W., Unseld M.,
RA Fattmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,

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RA Delseny M., Boutry M., Grivell L.A., Mache R., Puidomenech P.,
RA De Simone V., Choisne N., Artiguenave F., Robert C., Brotlier P.,
RA Wincker P., Catolico L., Weissenbach J., Saurin W., Queller F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Verzi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B.,
RA Conrad A., Hornischer K., Kauer G., Loehmet T.-H., Nordtsiek G.,
RA Reichelt J., Scharte M., Schoen O., Bargues M., Terol J., Climent J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RA Cooke R., Landre A., Berger-Llauro C., Punelle B., Masny D.,
RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Cascuberta E.,
RA Montfort A., Argirrou A., Flores M., Liuzzi R., Vitale D.,
RA Mannhaupt G., Haase D., Schoof H., Rued S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Wals A., Uteback T., Fujii C.Y., Shen T.P.,
RA Creasy T.H., Haas B., Malti R., Wu D., Peterson J., Van Aken S.,
RA Pai G., Miltischer J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Frazer D., Lin X., Nieman W.C., Salzberg S.L., White O., Venter J.C.,
RA Sasamoto S., Kimura T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
RT thaliana."
RL Nature 408:820-822(2000).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC -----
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CC -----
DR EMBL: AL049659; CAB4170.1; -
DR InterPro: IPR001128; Cyt_P450.
DR Pfam: PF00067; P450; 1.
DR PRINTS: PR00385; P450.
DR PROSITE: PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Transmembrane; Heme; Multigene family.
FT TRANSMEM 1 21 POTENTIAL.
FT BINDING 431 431 HEME (BY SIMILARITY).
SQ SEQUENCE 490 AA; 55783 MW; FB97BA80A4C1EA50 CRC64;

Query Match 72.5%; Score 37; DB 1; Length 490;
Best Local Similarity 75.0%; Pred. No. 44;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SRVPTAW 8
Db 212 SRVPTAW 219

RESULT 10
POLG_EMCV STANDARD; PRT; 2290 AA.
ID POLG_EMCV
AC P03304;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Genome polyprotein [Contains: Coat proteins VP1 TO VP4; Core proteins
DE P2A TO P2C, P3A; Genome-linked protein VPg; Picornain 3C
DE (EC 3.4.22.28) (Protease 3C) (P3c); RNA-directed RNA polymerase P2D
DE (EC 2.7.7.48)].
OS Enterovirus; Picornaviridae; Picornavirales; no DNA stage; Picornaviridae;
OS Cardiovirus.
OX NCBI_TaxID=12104;
RN [1]

```

RP SEQUENCE FROM N.A.
RX MEDLINE=84169586; PubMed=6324136;
RA Palmenberg A.C., Kirby E.M., Janda M.R., Drake N.L., Duke G.M.,
RA Portratz K.F., Collett M.S.;
RT "The nucleotide and deduced amino acid sequences of the
RL encephalomyocarditis viral polypeptide coding region.";
CC Nucleic Acids Res. 12:2969-2985(1984).
CC -1- FUNCTION: PC POLYPEPTIDE IS A PROTEASE THAT CLEAVES AT CERTAIN
CC O/G SITES IN THE POLYPEPTIDE. IT MAY BE A CYSTEINE PROTEASE.
CC -1- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAEDRAL UNITS,
CC EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC VP3, AND VP4.
CC -1- PTM: SPECIFIC ENZYMAIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
CC -----
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CC -----
DR EMBL; X00463; CAA25152.1; -.
DR PIR; A03906; GNNE.
DR HSSP; P12296; 2MEV.
DR MEROPS; C03.009; -.
DR MEROPS; U29.001; -.
DR InterPro; IPR000605; RNA_helicase.
DR InterPro; IPR001205; RNA_pol_P3D.
DR InterPro; IPR001676; Riv.
DR Pfam; PF00073; Ihv; 3.
DR Pfam; PF00680; RNA_dep_RNA_pol; 1.
DR Pfam; PF00910; RNA_helicase; 1.
KM Polyprotein: Coat protein: Core protein: Transferase:
KM RNA-directed RNA polymerase: Hydrolyase; Thiol protease; Myristate.
FT PROPEP 1 67 LEADER PEPTIDE.
FT CHAIN 68 136 COAT PROTEIN VP4 (RHQ).
FT CHAIN 137 391 COAT PROTEIN VP2 (BETA).
FT CHAIN 392 622 COAT PROTEIN VP3 (GAMMA).
FT CHAIN 623 910 COAT PROTEIN VP1 (ALPHA).
FT CHAIN 911 1056 CORE PROTEIN P2A (G).
FT CHAIN 1057 1192 CORE PROTEIN P2B (I).
FT CHAIN 1193 1517 CORE PROTEIN P2C (F).
FT CHAIN 1518 1605 CORE PROTEIN P3A.
FT CHAIN 1606 1625 GENOME-LINKED PROTEIN VP6 (H).
FT CHAIN 1626 1830 PICORNAIN 3C (P22).
FT CHAIN 1831 2290 RNA-DIRECTED RNA POLYMERASE P3D (E).
FT LIPID 68 MYRISTATE (BY SIMILARITY).
FT ACT_SITE 1784 1784 PROTEASE (POTENTIAL).
FT ACT_SITE 1802 1802 PROTEASE (POTENTIAL).
SQ SEQUENCE 2290 AA; 255756 MW; 26BC81BB7CF68CB5 CRC64;

Query Match 72.5%; Score 37; DB 1; Length 2290;
Best Local Similarity 62.5%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 SRVPTAW 8
DB 964 SRAPNMPW 971

RESULT 11
EXOV_RHIME
ID EXOV_RHIME STANDARD; PRT; 316 AA.
AC P33701.
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DE Succinoglycan biosynthesis protein exov.
GN EXOV OR R81072 OR S8B20949.
OS Rhizobium meliloti (Sinorhizobium meliloti).

OG Plasmid p5ymb (megaplasmid 2).
CC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
CC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=94042869; PubMed=8226645;
RA Glucksmann M.A., Reuber T.L., Walker G.C.;
RT "Family of glycosyl transferases needed for the synthesis of
RT succinoglycan by Rhizobium meliloti.";
RL J. Bacteriol. 175:7033-7044(1993).
RN
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=94042870; PubMed=8226646;
RA Glucksmann M.A., Reuber T.L., Walker G.C.;
RT "Genes needed for the modification, polymerization, export, and
RT processing of succinoglycan by Rhizobium meliloti: a model for
RT succinoglycan biosynthesis.";
RL J. Bacteriol. 175:7045-7055(1993).
RN
RP SEQUENCE FROM N.A.
RC STRAIN=RCR2011 / S047;
RX MEDLINE=94162682; PubMed=8118055;
RA Becker A., Kleckmann A., Kuester H., Keller W., Arnold W.,
RA Puehler A.;
RT "Analysis of the Rhizobium meliloti genes exov, exov, exow, exot and
RT exoi involved in exopolysaccharide biosynthesis and nodule invasion:
RT exov and exow probably encode glucosyltransferases.";
RL Mol. Plant Microbe Interact. 6:735-744(1993).
RN
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396508; PubMed=11481431;
RA Flann T.M., Weidner S., Wong K., Buhmester J., Chain P.,
RA Vorhoefer F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
RA Golding B., Puehler A.;
RT "The complete sequence of the 1,683-kb pSymb megaplasmid from the N2-
RT fixing endosymbiont Sinorhizobium meliloti.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
RN
RP -1- PATHWAY: EXOPOLYSACCHARIDE BIOSYNTHESIS.
CC -----
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CC -----
DR EMBL; L20758; AAA16052.1; ALT_INT.
DR EMBL; Z22646; CAA80360.1; -.
DR EMBL; AL603645; CAC49472.1; -.
DR PIR; A49349; A49349.
KW Exopolysaccharide synthesis; Plasmid; Complete proteome.
SQ SEQUENCE 316 AA; 35321 MW; 9BA45C6E7D763171 CRC64;

Query Match 70.6%; Score 36; DB 1; Length 316;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 RVPWTA 7
DB 181 RVPWTA 186

RESULT 12
AMFR_HUMAN
ID AMFR_HUMAN STANDARD; PRT; 323 AA.
AC P26442.
DT 01-AUG-1992 (Rel. 23, Created)

```

DT 01-AUG-1992 (Rel. 23, last sequence update)
DE 16-OCT-2001 (Rel. 40, last annotation update)
DE Autocrine motility factor receptor precursor (AMF receptor) (GP78).
GN AMF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91302382; PubMed=1649192;
RA Matarabe H., Carmi P., Hogan V., Raz T., Silletti S., Nabi I.R.,
RA Raz A.;
RT "Purification of human tumor cell autocrine motility factor and
RT molecular cloning of its receptor.";
RL J. Biol. Chem. 266:13442-13448(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Placenta;
RX MEDLINE=95352090; PubMed=7626106;
RA Huang B., Xie Y., Raz A.;
RT "Identification of an upstream region that controls the transcription
RT of the human autocrine motility factor receptor.";
RL Biochem. Biophys. Res. Commun. 212:727-742(1995).
CC -1- FUNCTION: SPECIFIC RECEPTOR FOR THE AUTOCRINE MOTILITY FACTOR.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- PTM: PHOSPHORYLATED IN THE PRESENCE OF AMF.
CC -1- PTM: O-GLYCOSYLATED.
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CC -----
DR EMBL; M63175; AAA3671.1; -.
DR EMBL; L35233; AAA9362.1; -.
DR PIR; A39877; A39877.
DR MIM; 603243; -.
KW Receptor; Glycoprotein; Phosphorylation; Signal; Transmembrane.
FT SIGNAL 1 17
FT CHAIN 18 323 POTENTIAL.
FT DOMAIN 18 110 AUTOCRINE MOTILITY FACTOR RECEPTOR.
FT TRANSMEM 111 137 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 138 323 POTENTIAL.
FT CARBOHYD 24 24 CYTOPLASMIC (POTENTIAL).
FT MOD RES 194 194 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 323 AA; 34325 MW; 0A7AF4DCF90A8700 CRC64;

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Query Match 70.6%; Score 36; DB 1; Length 323;
Best Local Similarity 75.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 SRVPTWAM 8
I I I I I
Db 149 SGVDWTAM 156

RESULT 13
YXN1_YEAST STANDARD; PRT; 351 AA.
AC P53860;
DT 01-OCT-1996 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Hypothetical 40.7 kDa protein in CSL4-ORE2 intergenic region.
GN YNL231C OR N1158.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Funghi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

```

OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97051596; PubMed=8896273;
RA Pandolfo D., de Antoni A., Lanfranchi G., Valle G.;
RT "The DNA sequence of cosmid 14-5 from chromosome XIV reveals 21 open
RT reading frames including a novel gene encoding a globin-like
RT domain.";
RL Yeast 12:1071-1076(1996).
CC -1- SIMILARITY: BELONGS TO THE SEC14 CYTOSOLIC FACTOR FAMILY.
CC -----
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CC -----
DR EMBL; Z69381; CAA9367.1; -.
DR EMBL; Z71507; CAA96136.1; -.
DR SGD; S0005175; YNL231C.
DR InterPro; IPR001251; CRAL_TRIO.
DR Pfam; PF00650; CRAL_TRIO; 1.
DR SMART; SM00516; SEC14; 1.
KW Hypothetical protein.
SQ SEQUENCE 351 AA; 40714 MW; 24C5B3262016F037 CRC64;

```

Query Match 70.6%; Score 36; DB 1; Length 351;
Best Local Similarity 50.0%; Pred. No. 47;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 SRVPTWAM 8
I I I I I
Db 243 TNPWTAM 250

RESULT 14
SYT8_MOUSE STANDARD; PRT; 395 AA.
AC Q9R0N6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Synaptotagmin VIII (SytyIII).
GN SYT8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX SRRAIN=ICR; TISSUE=Cerebellum;
RX MEDLINE=20002669; PubMed=10531343;
RA Fukuda M., Kanno E., Mikoshiba K.;
RT "Conserved N-terminal cysteine motif is essential for homo- and
RT heterodimer formation of synaptotagmins III, V, VI, and X.";
RL J. Biol. Chem. 274:31421-31427(1999).
CC -1- FUNCTION: MAY BE INVOLVED IN CA2+-DEPENDENT EXOCYTOSIS OF
CC SECRETORY VESICLES THROUGH CA2+ AND PHOSPHOLIPID BINDING TO THE C2
CC DOMAIN OR MAY SERVE AS CA2+ SENSORS IN THE PROCESS OF VESICULAR
CC TRAFFICKING AND EXOCYTOSIS (BY SIMILARITY).
CC -1- SUBUNIT: Homodimer. Can also forms heterodimer (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. SYNAPTIC
CC VESICLES (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE SYNAPTOTAGMIN FAMILY.
CC -----
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 CC -----
 DR EMBL: AB026805; BAAB5777.1; -.
 DR HSSP: P21707; IRSY.
 DR MGD: MGI:1859867; SYL8.
 DR InterPro: IPR000008; C2.
 DR InterPro: IPR002149; LRT.
 DR InterPro: IPR001565; Synaptotagmin.
 DR Pfam: PF00168; C2; 2.
 DR PRINTS: PR00399; SYNAPTOTAGMN.
 DR SMART: SM00239; C2; 2.
 DR PROSITE: PS00499; C2_DOMAIN_1; FALSE_NEG.
 DR PROSITE: PS00004; C2_DOMAIN_2; 2.
 KW Transmembrane; Repeat; Synapse.
 FT DOMAIN 1 44 VESICULAR (POTENTIAL).
 FT TRANSMEM 45 65 POTENTIAL.
 FT DOMAIN 66 395 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 115 213 C2_DOMAIN_1.
 FT DOMAIN 243 342 C2_DOMAIN_2.
 SQ SEQUENCE 395 AA; 44093 MW; 10E833FA8C454A3B CRC64;

Query Match 70.6%; Score 36; DB 1; Length 395;
 Best Local Similarity 50.0%; Pred. No. 52;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 SVVPTAW 8
 : : : : :
 Db 36 TRIPWRW 43

RESULT 15
 C71M_ARATH STANDARD; PRT; 490 AA.
 AC Q9STL1;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cytochrome P450 71A22 (EC 1.14.-.-).
 GN CYP71A22 OR AT3G48330 OR T29H11.170.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RX MEDLINE=21016720; PubMed=11130713;
 RA Salanoubat M., Lemcke K., Rieger M., Ansgorge W., Unseld M.,
 RA Fartmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
 RA Deiseny M., Boutry M., Griwell L.A., Maché R., Puigdomenech P.,
 RA De Simone V., Choisne N., Arliguenave F., Robert C., Brottier P.,
 RA Wincker P., Cattivello L., Weissenbach J., Saurin W., Quetier F.,
 RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
 RA Mumbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
 RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
 RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,
 RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordiek G.,
 RA Reichelt J., Scharfe M., Schoen O., Barges M., Terol J., Climent J.,
 RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
 RA Cooke R., Laurie M., Berger-Llauro C., Purnelle B., Masuy D.,
 RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
 RA Monfort A., Argitlou A., Flores M., Liguori R., Vitale D.,
 RA Mannhaupt G., Haese D., Schoof H., Rood S., Zaccaria P., Mewes H.-W.,
 RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
 RA Rooney T., Rizzo M., Walts A., Uterback T., Fujii C.Y., Shea T.P.,
 RA Creasy T.H., Haas B., Malt R., Wu D., Peterson J., Van Aken S.,
 RA Pal G., Milišcher J., Sellers P., Gill J.E., Feldlyum T.V.,
 RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
 RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,

RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
 RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakayama A., Nakazaki N., Shino S., Takeuchi C., Wada T.,
 RA Watanabe A., Yamada M., Yasuda M., Yabuta S.;
 RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
 thaliana.";
 RL Nature 408:820-822(2000).
 CC -I SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
 CC -----
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 DR EMBL: AL049659; CAB41167.1; -.
 DR InterPro: IPR001128; CYL_P450.
 DR Pfam: PF00067; P450; 1.
 DR PRINTS: PR00385; P450.
 DR PROSITE: PS00086; CYTOCHROME_P450; 1.
 KW Oxidoreductase; Monooxygenase; Transmembrane; Heme; Multigene family.
 FT TRANSMEM 2 22 POTENTIAL.
 FT BINDING 432 432 HEME (BY SIMILARITY).
 SQ SEQUENCE 490 AA; 55998 MW; 64C96AF349CA5672 CRC64;

Query Match 70.6%; Score 36; DB 1; Length 490;
 Best Local Similarity 83.3%; Pred. No. 63;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 VPTAW 8
 : : : : :
 Db 216 VPTAW 221

Search completed: August 15, 2002, 11:58:16
 Job time: 516 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 11:49:05 ; Search time 58.57 Seconds
(without alignments)
23.629 Million cell updates/sec

Title: US-09-613-092a-5_COPY_3_10
Perfect score: 51
Sequence: 1 SRVPMWTAW 8

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp-archaea:*
2: sp-bacteria:*
3: sp-fungi:*
4: sp-human:*
5: sp-invertebrate:*
6: sp-mammal:*
7: sp-mhc:*
8: sp-organelle:*
9: sp-phage:*
10: sp-plant:*
11: sp-rodent:*
12: sp-virus:*
13: sp-vertebrate:*
14: sp-unclassified:*
15: sp-rvirus:*
16: sp-bacteriap:*
17: sp-archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	87.4	81	5	Q9VBC3
2	41	80.4	164	10	Q9FS18
3	39	76.5	335	16	Q9WXS7
4	39	76.5	668	2	Q9ALX8
5	39	76.5	797	16	Q98P32
6	39	76.5	800	4	Q96H33
7	38	74.5	147	11	Q61427
8	38	74.5	151	11	Q9DA47
9	38	74.5	162	11	Q9M042
10	38	74.5	271	11	Q9CTW8
11	38	74.5	297	10	Q9FTE7
12	38	74.5	434	4	Q9UG77
13	38	74.5	441	16	Q9HYE2
14	38	74.5	454	10	Q9X159
15	38	74.5	595	11	Q91VH2
16	38	74.5	624	4	Q94862

17	38	74.5	773	10	Q9SHP2	Q9shp2 arabidopsis
18	38	74.5	802	13	Q9W770	Q9w770 gallus gall
19	38	74.5	807	4	Q9HC86	Q9hc86 homo sapien
20	38	74.5	807	6	Q9GLX9	Q9glx9 bos taurus
21	37	72.5	309	10	Q9SSR0	Q9ssr0 arabidopsis
22	37	72.5	415	2	Q93728	Q93728 mycobacteri
23	37	72.5	602	3	Q9P8C3	Q9p8c3 acromonium
24	37	72.5	2292	12	Q66765	Q66765 encephalomy
25	37	72.5	2292	12	Q66850	Q66850 encephalomy
26	36	70.6	97	4	Q9H235	Q9h235 homo sapien
27	36	70.6	241	13	Q9DDW2	Q9ddw2 tuva rudrip
28	36	70.6	247	16	Q92R85	Q92r85 rhizobium m
29	36	70.6	291	16	P74129	P74129 synchocyst
30	36	70.6	328	3	Q9UR34	Q9ur34 schizosach
31	36	70.6	335	6	Q97916	Q97916 bos taurus
32	36	70.6	437	10	Q9M1D6	Q9m1d6 arabidopsis
33	36	70.6	530	4	Q13161	Q13161 homo sapien
34	36	70.6	541	16	Q9A4N7	Q9a4n7 caulobacter
35	36	70.6	657	2	Q59446	Q59446 fibrobacter
36	36	70.6	669	2	Q59445	Q59445 fibrobacter
37	36	70.6	823	5	Q25343	Q25343 leishmania
38	36	70.6	851	10	Q9M1F2	Q9m1f2 arabidopsis
39	36	70.6	870	10	Q96376	Q96376 clarkia bre
40	36	70.6	871	10	Q92PM5	Q92pm5 clarkia con
41	36	70.6	1524	10	Q9S1Q5	Q9s1q5 arabidopsis
42	36	70.6	1750	10	Q9SKJ4	Q9skj4 arabidopsis
43	35	68.6	109	4	Q9GZT3	Q9gzt3 homo sapien
44	35	68.6	182	5	Q22231	Q22231 caenothabdi
45	35	68.6	254	10	Q9LTR7	Q9ltr7 arabidopsis

ALIGNMENTS

RESULT	ID	Q9VBC3	PRELIMINARY:	PRT:	81 AA.
1	Q9VBC3	09VBC3			
	AC	09VBC3			
	DT	01-MAY-2000 (TREMBLrel. 13, Created)			
	DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
	DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
	DE	CG14244 PROTEIN.			
	GN	CG14244			
	OS	Drosophila melanogaster (Fruit fly).			
	OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
	OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
	OC	Ephydroidea; Drosophilidae; Drosophila.			
	OX	NCBI_TaxID=7227;			
	RM	[1]			
	RP	SEQUENCE FROM N.A.			
	RC	STRAIN-BERKELEY;			
	RX	MEDLINE-20196006; PubMed-10731132;			
	RA	Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,			
	RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,			
	RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,			
	RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,			
	RA	Brandon R.C., Rogers Y.H.C., Blazer R.G., Champe M., Pfeiffer B.D.,			
	RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,			
	RA	Abriil J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,			
	RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,			
	RA	Beeson K.Y., Benos P.V., Bertan B.P., Bhandari D., Bolshakov S.,			
	RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,			
	RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,			
	RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,			
	RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,			
	RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,			
	RA	Dubin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,			
	RA	Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,			
	RA	Glocke A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,			
	RA	Haris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,			
	RA	Hoslin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,			
	RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,			
	RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,			

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclebo J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003757; AAF56619.1; -;
 DR FlyBase: FBgn0040607; CG14244.
 DR InterPro: IPR002557; Chitin_binding.
 DR Pfam: PF01607; Chitin_bind_2; 1.
 SQ SEQUENCE 81 AA; 9185 MW; AF1E54DECEC8CE1 CRC64;

Query Match 82.4%; Score 42; DB 5; Length 81;
 Best Local Similarity 100.0%; Pred. No. 5.8;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 VFWTAW 8
 |||||
 Db 58 VFWTAW 63

RESULT 2
 Q9FS18 PRELIMINARY; PRT; 164 AA.
 ID Q9FS18
 AC Q9FS18;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE COLD-REGULATED PROTEIN.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticaceae; Hordeum.
 OC NCBI_TaxID=4513;
 OX [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=LEAF;
 RC Cattiveili L.;
 RA "Plasid development and plastoquinone redox state control the low
 RT temperature specific accumulation of COR14b protein in barley.";
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ291295; CAC12881.1; -;
 DR HSSP: P12994; 1FTJ.
 SQ SEQUENCE 164 AA; 17613 MW; 1F5A99FF0D59B746 CRC64;

Query Match 80.4%; Score 41; DB 10; Length 164;
 Best Local Similarity 85.7%; Pred. No. 16;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 RVPTAW 8
 |||||
 Db 63 RVPTAW 69

RESULT 3
 ID Q9WX57 PRELIMINARY; PRT; 335 AA.
 AC Q9WX57;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE OLIGOPEPTIDE ABC TRANSPORTER, PERMEASE PROTEIN.
 GN TM0072.
 OS Thermotoga maritima.
 OC Bacteria; Thermotogales; Thermotoga.
 OX NCBI_TaxID=2336;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MSB / DSM 3109;
 RX MEDLINE=99287316; Pubmed=10360571;
 RA Nelson K.E., Clayton R.A., Gill S.R., Gwin M.L., Dodson R.J.,
 RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
 RA McDonald L., Utterback T.R., Malek J.A., Liner K.D., Garrett M.W.,
 RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
 RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
 RT "Evidence for lateral gene transfer between Archaea and Bacteria from
 genome sequence of *Thermotoga maritima*.";
 RL Nature 391:323-329(1999).
 DR EMBL: AE001694; AAD35166.1; -;
 DR TIGR: TM0072; -;
 DR InterPro: IPR000515; BPD_transp.
 DR Pfam: PF00528; BPD_transp; 1.
 KM Complete proteome.
 SQ SEQUENCE 335 AA; 38222 MW; 653D1AA484DC9FF3 CRC64;

Query Match 76.5%; Score 39; DB 16; Length 335;
 Best Local Similarity 83.3%; Pred. No. 68;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 VFWTAW 8
 |||||
 Db 109 LPWTAW 114

RESULT 4
 Q9ALX8 PRELIMINARY; PRT; 668 AA.
 ID Q9ALX8
 AC Q9ALX8;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE HYDROGENASE-4 COMPONENT B.
 OS Burkholderia pseudomallei (Pseudomonas pseudomallei).
 OC Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
 OC Burkholderia.
 OC NCBI_TaxID=28450;
 OX [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=G9313;
 RA Steiner B., Meyer R., Bowen M., Morrill W.;
 RT "Random sequencing of Burkholderia pseudomallei strain G9313 for
 RT clinical PCR development.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: NADH + UBIDIONE = NAD(+) + UBIDINOL.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 DR EMBL: AF335723; AAK06855.1; -;
 DR InterPro: IPR003439; ABC_transport.
 DR InterPro: IPR003918; NADhub_oxidoreductase.
 DR InterPro: IPR003916; NADhub_oxidoreductase.
 DR InterPro: IPR001750; Oxidored_q1.
 DR Pfam: PF00361; Oxidored_q1; 1.
 DR PRINTS: PRO1434; NADHDGNASE5.
 DR PRINTS: PRO1437; NTOXDRTASE4.
 DR PROSITE: PS00211; ABC_TRANSPORTER; UNKNOWN_1.
 KM NAD: Oxidoreductase; Transmembrane.
 SQ SEQUENCE 668 AA; 71822 MW; 2F016ACB950DD519 CRC64;

Query Match 76.5%; Score 39; DB 2; Length 668;
 Best Local Similarity 83.3%; Pred. No. 13e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 VPWTAW 8
:|||||
DB 382 MPWTAW 387

RESULT 5
Q98P32
ID 098P32 PRELIMINARY; PRT; 797 AA.
AC 098P32:
DT 01-OCT-2001 (TREMBLrel. 18, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE FORMATE DEHYDROGENASE.
GN ML9633.
OS Rhizobium loti (Mesorhizobium loti).
OC Plasmid pMLb.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MAFF303099;
RX MEDLINE-21082930; PubMed-11214968;
RA Kaneo T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Matanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL: AP003017; BAB54823.1; -;
DR InterPro: IPR001467; MolYbdopterin.
DR Pfam: PF00384; molybdopterin; 2.
DR Plasmid; Complete proteome.
FT NON_TER 1
SQ SEQUENCE 797 AA; 87533 MW; CA69E6373093B0FE CRC64;

Query Match 76.5%; Score 39; DB 16; Length 797;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 SRVPWTAW 8
:|||||
DB 599 TKVPWDAM 606

RESULT 6
Q96H33
ID 096H33 PRELIMINARY; PRT; 800 AA.
AC 096H33:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE UNKNOWN (PROTEIN FOR IMAGE:3050359) (FRAGMENT).
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-MELANOMA;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: BC008946; AAH08946.1; -;
FT NON_TER 1
SQ SEQUENCE 800 AA; 85125 MW; 708926A0A67085E6 CRC64;

Query Match 76.5%; Score 39; DB 4; Length 800;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 VPWTAW 8
:|||||
DB 80 VPWTSM 85

RESULT 7
O61427
ID 061427 PRELIMINARY; PRT; 147 AA.
AC 061427:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ALPHA 1 TYPE I COLLAGEN (FRAGMENT).
GN COL1A1 OR COL1A1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6; TISSUE=LIVER;
RX MEDLINE-94344105; PubMed-8065328;
RA Rhodes K., Rippe R.A., Umezawa A., Nehls M., Brenner D.A., Breindl M.;
RT "DNA methylation represses the murine alpha 1(I) collagen promoter by
RT an indirect mechanism";
RL Mol. Cell. Biol. 14:5950-5960(1994).
DR EMBL: X54876; CAA38657.1; -;
DR MGD; MGI:88467; Col1a1.
DR InterPro: IPR001007; VWFc.
DR Pfam: PF00093; vwc; 1.
DR SMART: SM00214; VWC; 1.
DR PROSITE: PS01208; VWFc; 1.
DR Collagen.
FT NON_TER 147
SQ SEQUENCE 147 AA; 16652 MW; 9263BP0A91B4307D CRC64;

Query Match 74.5%; Score 38; DB 11; Length 147;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PWTAW 8
:|||||
DB 125 PWTAW 129

RESULT 8
Q9DA47
ID 09DA47 PRELIMINARY; PRT; 151 AA.
AC 09DA47:
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE 4933425020RIK PROTEIN.
GN 4933425020RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6J; TISSUE-TESTIS;
RX MEDLINE-21085660; PubMed-11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischer W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

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RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wnshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK006188; BAB24448.1; -;
DR MGD: MGI:1914016; 4933425020Rik.
SQ SEQUENCE 151 AA; 17201 MW; 4B0658DD62565EFD CRC64;

Query Match
Best Local Similarity 74.5%; Score 38; DB 11; Length 151;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 VPWTAW 8
    |||:|
Db 21 VPMSAW 26

RESULT 9
Q9NM042 PRELIMINARY; PRT; 162 AA.
ID Q9NM042;
AC Q9NM042;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HPPOTHEICAL 17.8 KDA PROTEIN.
GN T1008-10.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Lemve M., Pohl T., Weizenegger T., Bancroft I., Mewes H.W., Rudd S.,
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA ED Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL161746; CAB81913.1; -;
DR HSSP: P77366; 1FUX.
KW Hypothetical protein.
SQ SEQUENCE 162 AA; 17823 MW; B34C3E450B61AD59 CRC64;

Query Match
Best Local Similarity 74.5%; Score 38; DB 10; Length 162;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 VPWTAW 8
    |||:|
Db 67 VPMTVM 72

RESULT 10
Q9CTW8 PRELIMINARY; PRT; 271 AA.
ID Q9CTW8;
AC Q9CTW8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE 4930565F05RIK PROTEIN (FRAGMENT).
GN 4930565F05RIK.
OS Mus musculus (Mouse).

```

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TESTIS;
RX MEDLINE=21083660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirnl L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Mashio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wnshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK019785; BAB31852.1; -;
DR MGD: MGI:1924880; 4930565F05Rik.
FT NON_TER 1
SQ SEQUENCE 271 AA; 29278 MW; 3654CD2B7224A24 CRC64;

Query Match
Best Local Similarity 74.5%; Score 38; DB 11; Length 271;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PWTAW 8
    |||:|
Db 209 PWTAW 213

RESULT 11
Q9PTE7 PRELIMINARY; PRT; 297 AA.
ID Q9PTE7;
AC Q9PTE7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE P0698A04.4 PROTEIN (P0494A10.20 PROTEIN).
GN P0698A04.4 OR P0494A10.20.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Euphorbiaceae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponebare(GA3) genomic DNA, chromosome 1, PAC
clone:P0698A04.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponebare(GA3) genomic DNA, chromosome 1, PAC
clone:P0698A04.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP002541; BAB55480.1; -;
DR InterPro: IPR004277; PSS.

```

DR Pfam: PF03034; PSS: 1.
SQ SEQUENCE 297 AA; 34429 MW; E1730EFC71208E09 CRC64;

Query Match 74.5%; Score 38; DB 10; Length 297;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PWTAW 8
|||||
DB 32 PWTAW 36

RESULT 12
09UG77

ID 09UG77; PRELIMINARY; PRT; 434 AA.

AC 09UG77; 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE HYPOTHEICAL 45.1 KDA PROTEIN (FRAGMENT).
GN DKFZP586K091.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=UTERUS;
RA Oltenswelder B., Obermayer B., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL050135; CAB43285.1; -.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 434 AA; 45064 MW; FF4BA8CA93693B0 CRC64;

Query Match 74.5%; Score 38; DB 4; Length 434;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 SRPWTAW 8
|||||
DB 314 SRPWTAW 321

RESULT 13
09HYE2 PRELIMINARY; PRT; 441 AA.

AC 09HYE2; 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE HYPOTHEICAL PROTEIN PA3464.
GN PA3464.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Storer C.K., Pham X.-Q.T., Ervin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltz L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.A., Coulter S.N., Folger K.R., Kas A., LaBis K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
opportunistic pathogen."
RL Nature 406:959-964 (2000).
DR EMBL; AE004767; AAG06852.1; -.

KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 441 AA; 49000 MW; 4923F37C2A044DA2 CRC64;

Query Match 74.5%; Score 38; DB 16; Length 441;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PWTAW 8
|||||
DB 144 PWTAW 148

RESULT 14
09XI59

ID 09XI59; PRELIMINARY; PRT; 454 AA.

AC 09XI59; 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE F9L1.4 PROTEIN.
GN F9L1.4.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Vysotskaya V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
RA Lee J., Liu A., Li J., Kremenetskaia I., Lucos J., Gonzalez A.,
RA Altaji H., Araujo R., Brooks S., Buehler E., Chao O., Conn L.,
RA Conway A.B., Dunn P., Hansen N., Huizer L., Khan S., Kim C., Palm C.,
RA Rowley D., Shinn P., Walker M., Davis R.W., Ecker J.R.,
RA Federpspiel N.A., Theologis A.;
RT "Arabidopsis thaliana chromosome 1 BAC F9L1 sequence."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC007591; AAD39639.1; -.
DR InterPro: IPR004277; PSS.
DR Pfam: PF03034; PSS: 1.
SQ SEQUENCE 454 AA; 52610 MW; 1EDC8AA5A418BA44 CRC64;

Query Match 74.5%; Score 38; DB 10; Length 454;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PWTAW 8
|||||
DB 32 PWTAW 36

RESULT 15
09IVH2

ID 09IVH2; PRELIMINARY; PRT; 595 AA.

AC 09IVH2; 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE SIMILAR TO SORTING NEXIN 9.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BREAST TUMOR;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC014814; AAH14814.1; -.
SQ SEQUENCE 595 AA; 66545 MW; 3D5568476F2D816D CRC64;

Query Match 74.5%; Score 38; DB 11; Length 595;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 PWTAW 8
|1111
Db 107 PWTAW 111

Search completed: August 15, 2002, 11:57:51
Job time: 526 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 11:49:02 ; Search time 73.67 Seconds
(without alignments)
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Title: US-09-613-092a-7_COPY_3_10
Perfect score: 45
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 747574

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	15	20	AAV30353
2	40	88.9	15	20	AAV30354
3	36	80.0	328	22	AA41174
4	35	77.8	115	22	ABG25336
5	35	77.8	663	22	AB64497
6	34.5	76.7	287	20	AAV38511
7	34.5	76.7	304	20	AAV38512
8	34	75.6	70	22	AAU49814
9	34	75.6	156	22	AA875292
10	34	75.6	156	22	AA875293
11	34	75.6	217	22	ABB65332

12	34	75.6	243	22	ABB58399
13	34	75.6	273	22	ABG18986
14	34	75.6	280	22	ABG10923
15	34	75.6	282	22	ABG10922
16	34	75.6	303	22	ABG04502
17	34	75.6	351	20	AAV59757
18	33	73.3	68	22	AAU50169
19	33	73.3	95	22	ABG24721
20	33	73.3	155	18	AAW10569
21	33	73.3	155	18	AAW23587
22	33	73.3	246	22	AAU42864
23	33	73.3	580	20	AAV34665
24	33	73.3	1055	22	AAV39198
25	32	71.1	35	21	AA825737
26	32	71.1	52	22	AAU50373
27	32	71.1	53	22	AAU57016
28	32	71.1	53	22	AAU67050
29	32	71.1	65	22	AAU52989
30	32	71.1	84	22	AAU52388
31	32	71.1	85	21	AAV96825
32	32	71.1	125	22	AAO02969
33	32	71.1	134	21	AA616146
34	32	71.1	141	22	ABG10757
35	32	71.1	143	21	AA616145
36	32	71.1	175	21	AA616144
37	32	71.1	184	22	ABG68567
38	32	71.1	193	21	AA629225
39	32	71.1	196	22	AA895630
40	32	71.1	202	21	AA629224
41	32	71.1	202	21	AAV96820
42	32	71.1	222	21	AA629223
43	32	71.1	267	21	AA825731
44	32	71.1	295	21	AA619761
45	32	71.1	295	21	AA648834

ALIGNMENTS

RESULT 1
ID AAV30353 standard; Peptide: 15 AA.
XX
AC AAV30353:
XX
DT 09-NOV-1999 (first entry)
XX
DE Epitope derived from pneumococcal surface adhesion A protein.
XX
DE
XX
KW Pneumococcal surface adhesion A protein; Psaa; monoclonal antibody;
KW vaccine; Streptococcus pneumoniae Infection.
XX
OS Streptococcus pneumoniae.
XX
PN W09945121-A1.
XX
PD 10-SEP-1999.
XX
PF 26-FEB-1999; 99WO-US04326.
XX
PR 02-MAR-1998; 98US-0076565.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Ades EW, Calzone GM, Sampson JS, Tharpe JA, Westerink MAJ;
PI Zeller JL;
DR WPI; 1999-540849/45.
XX
PT New peptides corresponding to Streptococcus pneumoniae Psaa, used
PT for treating or preventing Streptococcus pneumoniae infection in a
PT subject

PS Claim 6; Page 43; 58pp; English.
 XX
 CC AAY30351-54 represent immunogenic peptides which are derived from
 CC a pneumococcal surface adhesion A protein (PsaA). The specification
 CC describes monoclonal antibodies which bind epitopes of the PsaA protein
 CC (e.g. present sequence). The peptides can be used in vaccines to prevent
 CC Streptococcus pneumoniae infections. The antibodies of the invention
 CC can also be used to detect S. pneumoniae in a sample or individual.
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 45; DB 20; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.035;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRFVHRP 8
 |||||
 DB 3 rrfvhrp 10

RESULT 2

AAY30354
 ID AAY30354 standard; Peptide; 15 AA.

XX
 AC AAY30354;

DT 09-NOV-1999 (first entry)

DE Epitope derived from pneumococcal surface adhesion A protein.

XX
 KW Pneumococcal surface adhesion A protein; PsaA; monoclonal antibody;
 KW vaccine; Streptococcus pneumoniae infection.

XX OS Streptococcus pneumoniae.

XX PN WO9945121-A1.

XX PD 10-SEP-1999.

XX PF 26-FEB-1999; 99WO-US04326.

XX PR 02-MAR-1998; 98US-0076565.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Ades EW, Carlone GM, Sampson JS, Tharpe JA, Westerlink MAJ;
 PI Zeiler JL;

XX DR WPI; 1999-540849/45.

XX PT New peptides corresponding to Streptococcus pneumoniae PsaA, used
 PT for treating or preventing Streptococcus pneumoniae infection in a
 PT subject

XX PS Claim 6; Page 43; 58pp; English.

XX CC AAY30351-54 represent immunogenic peptides which are derived from
 CC a pneumococcal surface adhesion A protein (PsaA). The specification
 CC describes monoclonal antibodies which bind epitopes of the PsaA protein
 CC (e.g. present sequence). The peptides can be used in vaccines to prevent
 CC Streptococcus pneumoniae infections. The antibodies of the invention
 CC can also be used to detect S. pneumoniae in a sample or individual.
 XX

SQ Sequence 15 AA;

Query Match 88.9%; Score 40; DB 20; Length 15;
 Best Local Similarity 87.5%; Pred. No. 0.32;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RRFVHRP 8
 |||||

DB 3 rrfvhrp 10

RESULT 3

AAM41174
 ID AAM41174 standard; Protein; 328 AA.

XX
 AC AAM41174;

DT 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 6105.

XX
 KW Human; nocotropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW Leukaemia.

XX OS Homo sapiens.

XX PN WO200153312-A1.

XX PD 26-JUL-2001.

XX PE 26-DEC-2000; 2000WO-US34263.

XX PR 21-JAN-2000; 2000US-0488725.

XX PR 25-APR-2000; 2000US-0552317.

XX PR 09-JUL-2000; 2000US-0598042.

XX PR 19-JUL-2000; 2000US-0620312.

XX PR 03-AUG-2000; 2000US-0653450.

XX PR 14-SEP-2000; 2000US-0662191.

XX PR 19-OCT-2000; 2000US-0693036.

XX PR 29-NOV-2000; 2000US-0727344.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;

XX DR WPI; 2001-442253/47.

XX DR N-PSDB; AAI60330.

XX PT Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -

XX PS Example 2; SEQ ID NO 6105; 10078pp; English.

XX CC The invention relates to human nucleic acids (AA157798-AA161369) and
 CC the encoded polypeptides (AAM38642-AAM42213) with nocotropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 XX

SQ Sequence 328 AA;

Query Match 80.0%; Score 36; DB 22; Length 328;
 Best Local Similarity 75.0%; Pred. No. 38;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RRFVRRP 8
:|||||
Db 12 grfchrrp 19

RESULT 4
ID ABG25336
ABG25336 standard; Protein: 115 AA.
XX
AC ABG25336;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #25327.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PE 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Dermanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS89523.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID NO 55695; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridization probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 115 AA;

Query Match 77.8%; Score 35; DB 22; Length 115;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 FVHRRP 8
:|||||
Db 107 fvhrrp 112

RESULT 5
ID ABB64497
ABB64497 standard; Protein: 663 AA.
XX
AC ABB64497;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 20283.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PE 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR N-PSDB; ABL08600.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Disclosure; SEQ ID NO 20283; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL01840-ABL16175), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 663 AA;

Query Match 77.8%; Score 35; DB 22; Length 663;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RRFVRRP 8
:|||||
Db 369 krfvrrp 376

RESULT 6
ID AAY38511
AAY38511 standard; Protein: 287 AA.
XX
AC AAY38511;
XX

DT	08-OCT-1999	(first entry)
XX		
DE	Neisseria gonorrhoeae antigen encoded by partial ORF5.	
XX		
KW	Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine; treatment; Neisseria infection; meningitis; septicaemia; gonorrhea.	
XX		
OS	Neisseria gonorrhoeae.	
PN	W09924578-A2.	
XX		
PD	20-MAY-1999.	
XX		
PF	09-OCT-1998; 98WO-1B0165.	
XX		
PR	01-SEP-1998; 98GB-0019016.	
PR	06-NOV-1997; 97GB-0023516.	
PR	14-NOV-1997; 97GB-0024190.	
PR	18-NOV-1997; 97GB-0024386.	
PR	27-NOV-1997; 97GB-0025158.	
PR	10-DEC-1997; 97GB-0026147.	
PR	14-JAN-1998; 98GB-0000759.	
XX		
PA	(CHIR-) CHIRON SPA.	
XX		
PI	Grandi G, Maignani V, Pizza M, Rapuoli R, Scarlato V;	
XX		
DR	WPI, 1999-327407/27.	
XX		
PT	Proteins from Neisseria meningitidis and N. gonorrhoeae useful for diagnosis, treatment and prevention of infection	
XX		
PS	Claim 4; Page 71; 524pp; English.	
XX		
CC	Amino acid sequences AAY38499-Y38944 represent Neisseria meningitidis and N. gonorrhoeae antigenic proteins. They are encoded by open reading frames (ORFs) AA211972-212358. The antigenic proteins, their fragments, their nucleic acids and antibodies are used for diagnosis, prevention (as vaccines) or treatment of Neisseria infections, such as meningitis, septicaemia and gonorrhea. Both organisms are closely related. Fragments of the nucleic acids are useful as hybridisation probes and antisense reagents.	
CC		
CC		
XX	Sequence 287 AA;	
SO		
Query Match	76.7%; Score 34.5; DB 20; Length 287;	
Best Local Similarity	88.9%; Pred. No. 64;	
Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 1;		
QY	1 RRF-VHRRP 8	
Db	251 rrfavhrp 259	
RESULT 7.		
ID	AAY38512	
XX	AAY38512 standard; Protein: 304 AA.	
AC	AAY38512;	
XX		
DT	08-OCT-1999 (first entry)	
XX		
DE	Neisseria gonorrhoeae antigenic protein encoded by ORF5.	
KW	Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine; treatment; Neisseria infection; meningitis; septicaemia; gonorrhea.	
XX		
OS	Neisseria gonorrhoeae.	
PN	W09924578-A2.	
XX		
PD	20-MAY-1999.	

[illegible]

PI Skeiky YAM, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX
DR WPI: 2001-616774/71.
XX N-PDOB: AAS59545.
XX
PT Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris -
XX
PS Example 1: SEQ ID No 11009; 1069pp; English.
XX
XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA).
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at [ftp.wipo.int/pub/published_pcl_sequences](http://wipo.int/pub/published_pcl_sequences).
XX
SQ Sequence 70 AA:

Query Match 75.6%; Score 34; DB 22; Length 70;
Best Local Similarity 75.0%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRFVHRPP 8
Db 58 rrwshrrp 65
11:11111
58 rrwshrrp 65

RESULT 9
ID AAB75292 standard; Protein: 156 AA.
AAB75292:
XX
AC AAB75292:
XX
DT 03-APR-2001 (first entry)
XX
DE Gene 6 human secreted protein homologous amino acid sequence #111.
XX
XX Human; immunosuppressive; antiarthritic; antirheumatic; nootropic;
KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
KW neuroprotective; antibacterial; virucide; fungicide; opthalmological;
KW vulnery; autoimmune disease; hyperproliferative disorder; cancer;
KW cardiovascular disorder; cerebrovascular disorder; infection;
KW nervous system disorder; ocular disorder; chemotaxis; food additive;
KW secreted protein.
XX
XX Homo sapiens.
XX
PN WO200077021-A1.
XX
PD 21-DEC-2000.
XX
PF 01-JUN-2000; 2000WO-US15135.
XX
PR 11-JUN-1999; 99US-0138632.
XX

PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX
PI Rosen CA, Ruben SM, Komatsoulis GA;
XX
DR WPI: 2001-071257/08.
XX
XX Nucleic acid molecules encoding human secreted proteins, used in
PT preventing, treating or ameliorating a disorder, e.g. Alzheimer's and
PT Parkinson's diseases and cancers -
XX
XX
PS Disclosure; Page 18-19; 530pp; English.
XX
XX This invention relates to polynucleotide sequences AAF63789 - AAF63836
CC which encode human secreted proteins AAB75260 - AAB75287. Included in the
CC invention are protein sequences AAB75288 - AAB75341 which are fragments
CC of the secreted proteins and amino acid sequences with which these
CC fragments share homology. Examples of the activities of the proteins and
CC polynucleotides and the activities of their agonists and antagonists
CC include, immunosuppressive; antiarthritic; antirheumatic;
CC antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
CC neuroprotective; antibacterial; virucide; fungicide;
CC opthalmological; and vulnery activity. The protein and polynucleotide
CC sequences, their agonists and antagonists may be useful for treating,
CC preventing and diagnosing diseases and disorders such as autoimmune
CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders
CC e.g. neoplasms of the breast or liver, cardiovascular disorders
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischemia,
CC angioneuromas, nervous system disorders e.g. Alzheimer's disease,
CC infections caused by bacteria, viruses and fungi and ocular disorders
CC e.g. corneal infection. The polypeptides can also be used to aid wound
CC healing and epithelial cell proliferation, to prevent skin aging due to
CC sunburn, to maintain organs before transplantation, for supporting cell
CC culture of primary tissues, to regenerate tissues and in chemotaxis. The
CC polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities. Included in the invention are
CC oligonucleotides AAF63780 - AAF63788 and peptide AAB75239 which are used
CC in the identification and characterisation of the DNA and protein
CC sequences of the invention.
XX
SQ Sequence 156 AA:

Query Match 75.6%; Score 34; DB 22; Length 156;
Best Local Similarity 75.0%; Pred. No. 44;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRFVHRPP 8
Db 24 rffvhrkp 31
111111
24 rffvhrkp 31

RESULT 10
ID AAB75293 standard; Protein: 156 AA.
AAB75293:
XX
AC AAB75293:
XX
DT 03-APR-2001 (first entry)
XX
DE Human secreted protein sequence encoded by gene 6 SEQ ID NO:112.
XX
XX Human; immunosuppressive; antiarthritic; antirheumatic; nootropic;
KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
KW neuroprotective; antibacterial; virucide; fungicide; opthalmological;
KW vulnery; autoimmune disease; hyperproliferative disorder; cancer;
KW cardiovascular disorder; cerebrovascular disorder; infection;
KW nervous system disorder; ocular disorder; chemotaxis; food additive;
KW secreted protein.
XX
XX Homo sapiens.
XX
PN WO200077021-A1.
XX

XX 21-DEC-2000.
 PD 01-JUN-2000; 2000WO-US15135.
 PF 11-JUN-1999; 99US-0138632.
 PR (HUMA-) HUMAN GENOME SCI INC.
 PA (ROSE/) ROSEN C A.
 XX Rosen CA, Ruben SM, Komatsoulis GA;
 PI WPI: 2001-071257/08.
 DR N-PSDB; AAF63794.
 XX Nucleic acid molecules encoding human secreted proteins, used in
 PT preventing, treating or ameliorating a disorder, e.g. Alzheimer's and
 PT Parkinson's diseases and cancers -
 PS Disclosure; Page 18-19; 530pp; English.
 XX This invention relates to polynucleotide sequences AAF63789 - AAF63836
 CC which encode human secreted proteins AAB75260 - AAB75287. Included in the
 CC invention are protein sequences AAB75288 - AAB75341 which are fragments
 CC of the secreted proteins and amino acid sequences with which these
 CC fragments share homology. Examples of the activities of the proteins and
 CC polynucleotides and the activities of their agonists and antagonists
 CC include: immunosuppressive; antiarthritic; antihemetic;
 CC antiproliferative; cytostatic; cardiatic; vasotropic; cerebroprotective;
 CC neurotrophic; neuroprotective; antibacterial; virocidic; fungicide;
 CC ophthalmological; and vulnerary activity. The protein and polynucleotide
 CC sequences, their agonists and antagonists may be useful for treating,
 CC preventing and diagnosing diseases and disorders such as autoimmune
 CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders
 CC e.g. neoplasms of the breast or liver, cardiovascular disorders
 CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
 CC angiogenesis, nervous system disorders e.g. Alzheimer's disease,
 CC infections caused by bacteria, viruses and fungi and ocular disorders
 CC e.g. corneal infection. The polypeptides can also be used to aid wound
 CC healing and epithelial cell proliferation, to prevent skin aging due to
 CC sunburn, to maintain organs before transplantation, for supporting cell
 CC culture of primary tissues, to regenerate tissues and in chemotaxis. The
 CC polypeptides can also be used as a food additive or preservative to
 CC increase or decrease storage capabilities. Included in the invention are
 CC oligonucleotides AAF63780 - AAF63788 and peptide AAB75239 which are used
 CC in the identification and characterisation of the DNA and protein
 CC sequences of the invention.
 CC
 SQ Sequence 156 AA;
 Query Match 75.6%; Score 34; DB 22; Length 156;
 Best Local Similarity 75.0%; Pred. No. 44;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RRFVRRP 8
 DB 24 RRFVRRP 31
 RESULT 11
 ABB65332
 ID ABB65332 standard; Protein; 217 AA.
 XX ABB65332;
 AC ABB65332;
 XX 26-MAR-2002 (first entry)
 DT Drosophila melanogaster polypeptide SEQ ID NO 22788.
 XX Drosophila melanogaster polypeptide SEQ ID NO 22788.
 DE Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX

OS Drosophila melanogaster.
 XX WO200171042-A2.
 PN 27-SEP-2001.
 XX 23-MAR-2001; 2001WO-US09231.
 PF 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX (PEKE) PE CORP NY.
 PA Venter JC, Adams M, Li PMD, Myers EW;
 PI WPI: 2001-656860/75.
 DR N-PSDB; ABL09435.
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 PS Disclosure; SEQ ID NO 22788; 21pp + Sequence Listing; English.
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (AAB57737-ABR2072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 SQ Sequence 217 AA;
 Query Match 75.6%; Score 34; DB 22; Length 217;
 Best Local Similarity 87.5%; Pred. No. 61;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RRFVRRP 8
 DB 123 RRFVRRP 130
 RESULT 12
 ABB58399
 ID ABB58399 standard; Protein; 243 AA.
 XX ABB58399;
 AC ABB58399;
 XX 26-MAR-2002 (first entry)
 DT Drosophila melanogaster polypeptide SEQ ID NO 1989.
 XX Drosophila melanogaster polypeptide SEQ ID NO 1989.
 DE Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX Drosophila melanogaster.
 OS WO200171042-A2.
 XX WO200171042-A2.
 PN 27-SEP-2001.
 PD 23-MAR-2001; 2001WO-US09231.
 PF 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX (PEKE) PE CORP NY.
 PA

XX Venter JC, Adams M, Li PWD, Myers EW;
PI
XX WPI: 2001-6556860/75.
DR N-PSDB; ABL02502.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Disclosure; SEQ ID NO 1989; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABB57737-ABB72072).
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 243 AA;

Query Match 75.6%; Score 34; DB 22; Length 243;
Best Local Similarity 75.0%; Pred. No. 68;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 RRFVHRRP 8
| |||: ||
Db 104 rffvhrkp 111

RESULT 13
ABG18986
ID ABG18986 standard; Protein; 273 AA.
XX
AC ABG18986;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #18977.
XX
KW Human: chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
DR N-PSDB; AAS83173.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID No 49345; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 273 AA;

Query Match 75.6%; Score 34; DB 22; Length 273;
Best Local Similarity 75.0%; Pred. No. 76;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 RRFVHRRP 8
| |||: ||
Db 125 rffvhrkp 132

RESULT 14
ABG10923
ID ABG10923 standard; Protein; 280 AA.
XX
AC ABG10923;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #10914.
XX
KW Human: chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
DR N-PSDB; AAS75110.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID No 41282; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
SQ Sequence 280 AA;
XX

Query Match 75.6%; Score 34; DB 22; Length 280;
Best Local Similarity 75.0%; Pred. No. 78;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 RRFVHRPP 8
| | | | : | |
Db 125 rffvhrkp 132

RESULT 15
ABG10922
ID ABG10922 standard; Protein; 282 AA.
XX
AC ABG10922;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #10913.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
OS
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
DR N-PSDB; AAS75109.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID NO 41281; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and

CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
SQ Sequence 282 AA;
XX

Query Match 75.6%; Score 34; DB 22; Length 282;
Best Local Similarity 75.0%; Pred. No. 79;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 RRFVHRPP 8
| | | | : | |
Db 104 rffvhrkp 111

Search completed: August 15, 2002, 11:49:03
Job time: 559 sec

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OM protein - protein search, using sw model

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(without alignments)
7.203 Million cell updates/sec

Title: US-09-613-092a-7_COPY_3_10
Perfect score: 45
Sequence: 1 RRFVHRP 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	75.6	244	2	US-08-933-750C-23
2	34	75.6	244	4	US-09-234-613-23
3	33	73.3	155	2	US-08-670-186-2
4	31	68.9	282	2	US-08-997-080-134
5	31	68.9	282	2	US-08-997-362-134
6	31	68.9	282	4	US-09-095-855-134
7	31	68.9	282	4	US-09-324-542-134
8	31	68.9	297	2	US-08-997-080-177
9	31	68.9	297	2	US-08-997-362-177
10	31	68.9	297	4	US-09-095-855-177
11	31	68.9	297	4	US-09-324-542-177
12	31	68.9	315	3	US-08-558-135-5
13	31	68.9	455	2	US-08-997-080-121
14	31	68.9	455	2	US-08-997-362-121
15	31	68.9	455	4	US-09-095-855-121
16	31	68.9	455	4	US-09-324-542-121
17	31	68.9	471	2	US-08-997-080-172
18	31	68.9	471	2	US-08-997-362-172
19	31	68.9	471	4	US-09-095-855-172
20	31	68.9	471	4	US-09-324-542-172
21	31	68.9	591	2	US-08-889-402-1
22	31	68.9	605	2	US-08-889-402-2
23	31	68.9	2890	4	US-09-413-814-67
24	31	68.9	3200	2	US-08-477-451-8
25	31	68.9	3798	3	US-09-335-409-6
26	31	68.9	3798	4	US-09-368-102-6
27	31	68.9	3798	4	US-09-567-969-6

28	31	68.9	3798	4	US-09-568-480-6	Sequence 6, Appl1
29	31	68.9	3798	4	US-09-568-486-6	Sequence 6, Appl1
30	31	68.9	3798	4	US-09-568-472-6	Sequence 6, Appl1
31	30	66.7	278	2	US-08-701-191A-39	Sequence 39, Appl
32	30	66.7	304	2	US-08-701-191A-30	Sequence 30, Appl
33	30	66.7	392	4	US-09-147-926-2	Sequence 2, Appl1
34	30	66.7	530	5	PCT-US95-08493-2	Sequence 2, Appl1
35	30	66.7	860	5	PCT-US95-08493-19	Sequence 19, Appl1
36	30	66.7	868	1	US-08-374-834-1	Sequence 1, Appl1
37	30	66.7	868	2	US-08-644-271-1	Sequence 1, Appl1
38	30	66.7	868	5	PCT-US95-08493-21	Sequence 21, Appl1
39	30	66.7	869	1	US-08-374-834-16	Sequence 16, Appl
40	30	66.7	869	2	US-08-644-271-29	Sequence 29, Appl
41	30	66.7	946	5	PCT-US95-08493-13	Sequence 13, Appl
42	30	66.7	1052	3	US-08-863-118-1	Sequence 1, Appl1
43	30	66.7	1052	3	US-08-863-118-2	Sequence 2, Appl1
44	30	66.7	1052	4	US-09-377-310-2	Sequence 2, Appl1
45	30	66.7	1053	3	US-08-863-118-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-08-933-750C-23
: Sequence 23, Application US/08933750C
: Patent No. 5932442
: GENERAL INFORMATION:
: APPLICANT: Lal, Preeti
: APPLICANT: Hillman, Jennifer L.
: APPLICANT: Bandman, Olga
: APPLICANT: Shah, Purvi
: APPLICANT: Au-Young, Janice
: APPLICANT: Yue, Henry
: APPLICANT: Guegler, Karl J.
: APPLICANT: Corley, Neil C.
: TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
: NUMBER OF SEQUENCES: 98
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Incyte Pharmaceuticals, Inc.
: STREET: 3174 Porter Drive
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94304
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/933,750C
: FILING DATE: September 23, 1997
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Billings, Lucy J.
: REGISTRATION NUMBER: 36,749
: REFERENCE/DOCKET NUMBER: PF-0356 US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-855-0555
: TELEFAX: 415-845-4166
: TELEX:
: INFORMATION FOR SEQ ID NO: 23:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 244 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: IMMEDIATE SOURCE:
: LIBRARY: SPLNNOT04

CLONE: 1561587
US-08-933-750C-23

Query Match
Best Local Similarity 75.6%; Score 34; DB 2; Length 244;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRFVHRP 8
Db 105 RRFVHRP 112

RESULT 2

US-09-234-613-23
; Sequence 23, Application US/09234613
; Patent No. 6132973
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Bandman, Olga
; APPLICANT: Shah, Purvi
; APPLICANT: Au-Young, Janice
; APPLICANT: Yue, Henry
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,613
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,750
; FILING DATE: September 23, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0356 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 244 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SPLNOT04
; CLONE: 1561587
; US-09-234-613-23

Query Match
Best Local Similarity 75.6%; Score 34; DB 4; Length 244;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 RRFVHRP 8
1 |||:|

Db 105 RRFVHRP 112

RESULT 3

US-08-670-186-2
; Sequence 2, Application US/08670186
; Patent No. 585343
; GENERAL INFORMATION:
; APPLICANT: SUN, SAMUEL S.M.
; APPLICANT: XIONG, LIWEN
; APPLICANT: HU, ZHONG
; APPLICANT: CHEN, HANG
; TITLE OF INVENTION: RECOMBINANT SWEET PROTEIN MABINLIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FORSTER
; STREET: 2000 PENNSYLVANIA AVE NW, STE. 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/670,186
; FILING DATE: 21-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MORASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 23461-20007.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 822-0168
; TELEX: 90-4030 MRSNFORSMH
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 155 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-670-186-2

Query Match
Best Local Similarity 73.3%; Score 33; DB 2; Length 155;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRFVHRP 7
Db 54 RRFVHRP 60

RESULT 4

US-08-997-080-134
; Sequence 134, Application US/08997080
; Patent No. 5968524
; GENERAL INFORMATION:
; APPLICANT: WATSON, JAMES D.
; APPLICANT: TAN, PAUL L.J.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997.080
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 282 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-997-080-134

Query Match 68.9%; Score 31; DB 2; Length 282;
Best Local Similarity 71.4%; Pred. No. 98;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 REVHRP 8
Db 267 RLVHRKP 273

RESULT 5
US-08-997-362-134
Sequence 134, Application US/08997362
Patent No. 5985287
GENERAL INFORMATION:
APPLICANT: Tan, Paul
APPLICANT: Hiwama, Jun
APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot
APPLICANT: Scott, Linda
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997.362
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873.970
FILING DATE: June 12, 1997
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705.347
FILING DATE: August 29, 1996

ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1002c2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 282 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-997-362-134

Query Match 68.9%; Score 31; DB 2; Length 282;
Best Local Similarity 71.4%; Pred. No. 98;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 REVHRP 8
Db 267 RLVHRKP 273

RESULT 6
US-09-095-855-134
Sequence 134, Application US/09095855
Patent No. 6160093
GENERAL INFORMATION:
APPLICANT: Tan, Paul
APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: Compounds and Methods for
Treatment and Diagnosis of Mycobacterial Infections
NUMBER OF SEQUENCES: 208
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095.855
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/705.347
FILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/873.970
FILING DATE: 12-JUN-1997
APPLICATION NUMBER: 08/997.362
FILING DATE: 23-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1002c3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 282 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-095-855-134

Query Match 68.9%; Score 31; DB 4; Length 282;
Best Local Similarity 71.4%; Pred. No. 98;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RYVHRP 8
DB 267 RLVHRP 273

RESULT 7
US-09-324-542-134
Sequence 134, Application US/09324542
Patent No. 6328978
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L.J.
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: Methods and Compounds for the Treatment
FILE REFERENCE: 11000.1007c1
CURRENT APPLICATION NUMBER: US/09/324,542
CURRENT FILING DATE: 1999-06-02
EARLIER APPLICATION NUMBER: US 08/997,080
EARLIER FILING DATE: 1997-12-23
NUMBER OF SEQ ID NOS: 194
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 134
LENGTH: 282
TYPE: PRP
ORGANISM: Mycobacterium vaccae
FEATURE:
NAME/KEY: UNSURE
LOCATION: (145)...(145)
NAME/KEY: UNSURE
LOCATION: (151)...(151)
US-09-324-542-134

Query Match 68.9%; Score 31; DB 4; Length 282;
Best Local Similarity 71.4%; Pred. No. 98;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RYVHRP 8
DB 267 RLVHRP 273

RESULT 8
US-08-997-080-177
Sequence 177, Application US/08997080
Patent No. 5968524
GENERAL INFORMATION:
APPLICANT: WATSON, JAMES D.
APPLICANT: TAN, PAUL L.J.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,080
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 177:
SEQUENCE CHARACTERISTICS:
LENGTH: 297 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-997-080-177

Query Match 68.9%; Score 31; DB 2; Length 297;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RYVHRP 8
DB 267 RLVHRP 273

RESULT 9
US-08-997-362-177
Sequence 177, Application US/08997362
Patent No. 5985287
GENERAL INFORMATION:
APPLICANT: Tan, Paul
APPLICANT: Hiyyama, Jun
APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot
APPLICANT: Scott, Linda
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,362
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970
FILING DATE: June 12, 1997
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
FILING DATE: August 29, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007

REFERENCE/DOCKET NUMBER: 11000.1002c2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 177:
SEQUENCE CHARACTERISTICS:
LENGTH: 297 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-997-362-177

Query Match
Best Local Similarity 68.9%; Score 31; DB 2; Length 297;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 REVHRRP 8
Db 267 RLVHRRP 273

RESULT 10
US-09-095-855-177
Sequence 177, Application US/09095855
Patent No. 6160093
GENERAL INFORMATION:
APPLICANT: Tan, Paul
APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: Compounds and Methods for
TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
NUMBER OF SEQUENCES: 208
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,855
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/705,347
FILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/873,970
FILING DATE: 12-JUN-1997
APPLICATION NUMBER: 08/997,362
FILING DATE: 23-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1002c3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 177:
SEQUENCE CHARACTERISTICS:
LENGTH: 297 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-095-855-177

Query Match
Best Local Similarity 68.9%; Score 31; DB 4; Length 297;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 REVHRRP 8
Db 267 RLVHRRP 273

RESULT 11
US-09-324-542-177
Sequence 177, Application US/09324542
Patent No. 6328978
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L.J.
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: Methods and Compounds for the Treatment
of Immunologically-Mediated Skin Disorders
FILE REFERENCE: 11000.1007c1
CURRENT APPLICATION NUMBER: US/09/324,542
CURRENT FILING DATE: 1999-06-02
EARLIER APPLICATION NUMBER: US 08/997,080
EARLIER FILING DATE: 1997-12-23
NUMBER OF SEQ ID NOS: 194
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 177
LENGTH: 297
TYPE: PRT
ORGANISM: Mycobacterium vaccae
FEATURE:
NAME/KEY: UNSURE
LOCATION: (145)...(145)
NAME/KEY: UNSURE
LOCATION: (151)...(151)
US-09-324-542-177

Query Match
Best Local Similarity 68.9%; Score 31; DB 4; Length 297;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 REVHRRP 8
Db 267 RLVHRRP 273

RESULT 12
US-08-558-135-5
Sequence 5, Application US/08558135
Patent No. 6090631
GENERAL INFORMATION:
APPLICANT: Catterall, William A.
APPLICANT: Sheng, Zu-Hang
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/558,135

FILING DATE: 13-NOV-1995
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.602C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 315 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-558*135-5

Query Match 68.9%; Score 31; DB 3; Length 315;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRVHRRP 8
Db 242 RRVHRRP 249

RESULT 13
US-08-997-080-121
Sequence 121, Application US/08997080
Patent No. 5968524
GENERAL INFORMATION:
APPLICANT: WATSON, JAMES D.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,080
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 455 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-997-080-121

Query Match 68.9%; Score 31; DB 2; Length 455;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RRVHRRP 8
Db 440 RRVHRRP 446

RESULT 14
US-08-997-362-121
Sequence 121, Application US/08997362
Patent No. 5985287
GENERAL INFORMATION:
APPLICANT: Tan, Paul
APPLICANT: Hiyama, Jun
APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot
APPLICANT: Scott, Linda
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,362
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970
FILING DATE: June 12, 1997
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
FILING DATE: August 29, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1002c2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 455 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-997-362-121

Query Match 68.9%; Score 31; DB 2; Length 455;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RRVHRRP 8
Db 440 RRVHRRP 446

RESULT 15
US-09-095-855-121

; Sequence 121, Application US/09095855
; Patent No. 6160093
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Compounds and Methods for
; TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections
; NUMBER OF SEQUENCES: 208
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,855
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/705,347
; FILING DATE: 29-AUG-1996
; APPLICATION NUMBER: 08/873,970
; FILING DATE: 12-JUN-1997
; APPLICATION NUMBER: 08/997,362
; FILING DATE: 23-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 121:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 455 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-095-855-121

Query Match 68.9%; Score 31; DB 4; Length 455;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 RFVHRP 8
| | | | |
Db 440 RLVHRKP 446

Search completed: August 15, 2002, 11:49:36
Job time: 277 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 11:50:18 ; Search time 35.29 Seconds
(Without alignments)
21.783 Million cell updates/sec

Title: US-09-613-092a-7_COPY_3_10
Perfect score: 45
Sequence: 1 RRFVHRR 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	38	84.4	434	2 F75425	tRNA nucleotidyltr
2	35	77.8	72	2 T12874	hypothetical prote
3	35	77.8	246	2 AG2988	competence protein
4	35	77.8	291	2 A99295	compeptence protein
5	35	77.8	403	2 B70961	probable esterase
6	34	75.6	80	2 G81065	hypothetical prote
7	34	75.6	248	2 S30194	ribosomal protein
8	33	73.3	33	2 S28842	mablinin II chain
9	33	73.3	118	2 T35747	hypothetical prote
10	33	73.3	155	2 UC5379	mablinin II precu
11	33	73.3	246	2 T47398	hypothetical prote
12	33	73.3	301	2 AC0266	oligopeptide trans
13	33	73.3	345	1 S36607	protein kinase (EC
14	33	73.3	496	2 T50146	probable era/thbf
15	33	73.3	548	2 T30369	DNA ligase-like pr
16	33	73.3	577	2 F72122	hypothetical prote
17	33	73.3	577	2 C86499	hypothetical prote
18	33	73.3	722	2 C88397	protein H04J21.3 f
19	33	73.3	786	2 T49414	related to ahmpl p
20	32	71.1	138	2 H72534	hypothetical prote
21	32	71.1	140	2 E83381	probable ring-clea
22	32	71.1	202	2 T01601	probable PREG1-lik
23	32	71.1	290	2 AH3448	xhc protein (assi
24	32	71.1	295	2 F70936	hypothetical prote
25	32	71.1	370	2 T46150	protein kinase ATN
26	32	71.1	382	2 AE0681	probable ABC trans
27	32	71.1	451	2 A70539	hypothetical prote
28	32	71.1	527	2 T37055	probable oxidoredu
29	32	71.1	776	2 T29064	hyaluronate lyase

30	32	71.1	1263	2 T15496	hypothetical prote
31	32	71.1	1527	1 RNZMB2	DNA-directed RNA p
32	32	71.1	1792	2 T13939	myosin V - fruit f
33	31	68.9	193	2 A82705	oligotribonuclease
34	31	68.9	194	2 A87333	hypothetical prote
35	31	68.9	202	2 B86447	hypothetical prote
36	31	68.9	238	2 T47386	hypothetical prote
37	31	68.9	320	2 B90325	conserved hypobhet
38	31	68.9	360	2 A85016	hypothetical prote
39	31	68.9	382	2 H83672	hypothetical prote
40	31	68.9	428	2 A89900	conserved hypobhet
41	31	68.9	444	2 T01721	hypothetical prote
42	31	68.9	444	2 T15907	hypothetical prote
43	31	68.9	446	2 S46802	hypothetical prote
44	31	68.9	557	2 A55933	hypothetical prote
45	31	68.9	634	2 JC2376	paxillin - human dnak-type molecula

ALIGNMENTS

RESULT 1
F75425
tRNA nucleotidyltransferase/poly A polymerase family protein - Deinococcus radioduran
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 18-Aug-2000
C:Accession: F75425
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
S.; Shen, M.; Vamathevan, J.V.; Lam, P.; McDonald, L.; Ulterback, T.; Zalewski, C.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896
A:Accession: F75425
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-434 <WHI>
A:Cross-references: GB:AE001968; GB:AE000513; NID:96458930; PIDN:AAF10763.1; PID:9645
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR1191
A:Map position: 1
C:Superfamily: Escherichia coli tRNA adenylyltransferase

Query Match 84.4% Score 38; DB 2; Length 434;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RRFVHRR 7
|||||||
Db 322 RRFVHRR 328

RESULT 2
T12874
hypothetical protein yocN - Bacillus subtilis phage SPBc2
C:Species: Bacillus subtilis phage SPBc2
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 15-Oct-1999
R:Iazarevic, V.; Duesterhoeft, A.; Soldo, B.; Hilbert, H.; Maue, C.; Karamata, D.
submitted to the EMBL Data Library, August 1997
A:Description: The complete nucleotide sequence of the Bacillus subtilis spBc2 pro
A:Reference number: Z17583
A:Accession: T12874
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-72 <LAZ>
A:Cross-references: EMBL:AF020713; NID:93025478; PID:93025588; PIDN:AA013083.1
R:Kunst, F.; Ogasawara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Azavedo, V.; Ber
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emerson, P.T.; Eutlian, K.D.; Errington, J.; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi, A.; Gallier, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koester, P.; Konungstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mueel, Y., M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon, A.;Authors: Schleich, S.; Schreter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot, akuch, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Whitters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K. A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*. A:Reference number: A69580; MID:198044033 A:Accession: F69920 A:Status: nucleic acid sequence not shown; translation not shown A:Molecule type: DNA A:Residues: 1-72 <KUN> A:Cross-references: GB:299114; GB:AL009126; NID:g2634230; PIDN:CAB13949.1; PID:el185529; A:Experimental source: strain 168 C:Genetics: A:Gene: yocN A:Gene: yocN A:Note: yocN

Query Match 77.8%; Score 35; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 FRRVHRR 8
|||||
Db 60 FRRVHRR 65

RESULT 3
AG2988
Competence protein F [imported] - *Agrobacterium tumefaciens* (strain C58, Dupont)
C:Species: *Agrobacterium tumefaciens*
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
C:Accession: AG2988
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I. erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McEl
; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W. A:Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58. A:Reference number: AB2577; PMID:11743193 A:Accession: AG2988 A:Status: preliminary A:Molecule type: DNA A:Residues: 1-246 <KUR> A:Cross-references: GB:AE008609; PIDN:AAL44325.1; PID:g17741916; GSPDB:GNO0187 A:Experimental source: strain C58 (Dupont) C:Genetics: A:Gene: comF A:Map position: linear chromosome C:Superfamily: transformation competence-related protein comF

Query Match 77.8%; Score 35; DB 2; Length 246;
Best Local Similarity 85.7%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RRRVHRR 7
|||||
Db 135 RRRVHRR 141

RESULT 4
A99295
Competence protein F (AF124757) [imported] - *Agrobacterium tumefaciens* (strain C58, Cere C:Species: *Agrobacterium tumefaciens*
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
C:Accession: A99295

R;Goodier, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Gold A.; Liu, F.; Mollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium A:Reference number: A97359; PMID:11743194*

A:Accession: A99295
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-291 <KUR>
A:Cross-references: GB:AE007870; PIDN:AAK89883.1; PID:g15159828; GSPDB:GNO0170 C:Genetics: A:Gene: AGR_L_2633 A:Map position: linear chromosome

Query Match 77.8%; Score 35; DB 2; Length 291;
Best Local Similarity 85.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RRRVHRR 7
|||||
Db 180 RRRVHRR 186

RESULT 5
B70961
probable esterase - *Mycobacterium tuberculosis* (strain H37RV)
C:Species: *Mycobacterium tuberculosis*
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: B70961
R:Coile, S.T.; Brosch, R.; Parish, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon ; Connor, R.; Davies, R.; Devlin, K.; Fellwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A:Authors: Seares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A:Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete geno A:Reference number: A70500; MID:98295987 A:Accession: B70961 A:Status: preliminary; nucleic acid sequence not shown; translation not shown A:Molecule type: DNA A:Residues: 1-403 <COL> A:Cross-references: GB:292669; GB:AL123456; NID:g3242271; PIDN:CAB07015.1; PID:g18715 A:Experimental source: strain H37RV C:Genetics: A:Gene: lipC C:Superfamily: *Mycobacterium tuberculosis* probable esterase

Query Match 77.8%; Score 35; DB 2; Length 403;
Best Local Similarity 85.7%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RRRVHRR 7
|||||
Db 125 RRRVHRR 131

RESULT 6
G81065
hypothetical protein NMB1589 [imported] - *Neisseria meningitidis* (strain MC58 serogro C:Species: *Neisseria meningitidis*
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: G81065
R:Teitelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scalapato, V.; Maignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A:Authors: Grandt, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A:Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58. A:Reference number: A81000; MID:20175755 A:Accession: G81065 A:Status: preliminary A:Molecule type: DNA

A:Residues: 1-80 <TEF>
A:Cross-references: GB:AE002509; GB:AE002098; NID:g7226832; PID:AAE41942.1; PID:g722683
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB1569

Query Match 75.6%; Score 34; DB 2; Length 80;
Best Local Similarity 85.7%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RRFVHRR 7
Db 63 RQFVHRR 69

RESULT 7
S30194
ribosomal protein S6, cytosolic - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jul-2000
C:Accession: S30194; A47240
R:Spencer, T.A.; Mackie, G.A.
Biochim. Biophys. Acta 1172, 332-334, 1993
A:Title: The nucleotide sequence of a cloned cDNA encoding ribosomal protein S6 from Drc
A:Reference number: S30194; MUID:93192329
A:Accession: S30194
A:Molecule type: mRNA
A:Residues: 1-248 <SPE>
A:Cross-references: EMBL:L07881; NID:g158335; PID:AAA28871.1; PID:g158336
R:Watson, K.L.; Konrad, K.D.; Woods, D.F.; Bryant, P.J.
Proc. Natl. Acad. Sci. U.S.A. 89, 11302-11306, 1992
A:Title: Drosophila homolog of the human S6 ribosomal protein is required for tumor supp
A:Reference number: A47240; MUID:93087515
A:Accession: A47240
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-248 <MAT>
A:Cross-references: GB:L01658; NID:g3540130; PID:AAAC34306.1; PID:g158338
A:Note: sequence extracted from NCBI backbone (NCBIR:119775)
C:Genetics:
A:Gene: FlyBase:RPS6
A:Cross-references: FlyBase:FBgn0004922
C:Superfamily: rat ribosomal protein S6
C:Keywords: protein biosynthesis; ribosome

Query Match 75.6%; Score 34; DB 2; Length 248;
Best Local Similarity 87.5%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RRFVHRR 8
Db 154 RRFVHRR 161

RESULT 8
S28842
mabinlin II chain A - Yunnan caper
C:Species: Capparis masakal (Yunnan caper)
C>Date: 22-Jan-1994 #sequence_revision 27-Oct-1995 #text_change 25-Oct-1996
C:Accession: S28842
R:Li, X.; Maeda, S.; Hu, Z.; Aluchi, T.; Nakaya, K.; Kurihara, Y.
Eur. J. Biochem. 211, 281-287, 1993
A:Title: Purification, complete amino acid sequence and structural characterization of t
A:Reference number: S28842; MUID:93145958
A:Accession: S28842
A:Molecule type: protein
A:Residues: 1-33 <LID>
C:Superfamily: wheat alpha-amylase inhibitor
C:Keywords: sweet taste

Query Match 73.3%; Score 33; DB 2; Length 33;
Best Local Similarity 71.4%; Pred. No. 7.2;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RRFVHRR 7
Db 19 QRFVHRR 25

RESULT 9
T35747
hypothetical protein SC7H2.16c - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C:Accession: T35747
R:Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream,
submitted to the EMBL Data Library, August 1999
A:Reference number: 221598
A:Accession: T35747
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-118 <SAU>
A:Cross-references: EMBL:AL109732; PID:GAB52058.1; GSPDB:GN00070; SCODEB:SC7H2.16c
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCODEB:SC7H2.16c

Query Match 73.3%; Score 33; DB 2; Length 118;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 RRFVHRR 8
Db 53 RFLVHRR 60

RESULT 10
JC5379
mabinlin II precursor - Yunnan caper
C:Species: Capparis masakal (Yunnan caper)
C>Date: 02-Jun-1997 #sequence_revision 12-Sep-1997 #text_change 20-Jun-2000
C:Accession: JC5379; PC4316
R:Nirasawa, S.; Masuda, Y.; Nakaya, K.; Kurihara, Y.
Gene 181, 225-227, 1996
A:Title: Cloning and sequencing of a cDNA encoding a heat-stable sweet protein, mabln
A:Reference number: JC5379; MUID:97128796
A:Accession: JC5379
A:Molecule type: mRNA
A:Residues: 1-155 <NIR1>
A:Cross-references: DDBJ:D83997; NID:g1817545; PID:BAI2204.1; PID:g1817546
A:Accession: PC4316
A:Molecule type: protein
A:Residues: 36-41; 149-154 <NIR2>
A:Experimental source: seed
C:Superfamily: wheat alpha-amylase inhibitor
C:Keywords: sweet taste
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-35/Domain: amino-terminal propeptide #status predicted <PRO>
F:36-68/83-154/Product: mabinlin II #status experimental <MAT>
F:36-68/Domain: mabinlin II A chain #status experimental <CHA>
F:69-83/Domain: mabinlin linker peptide #status predicted <LNK>
F:83-154/Domain: mabinlin II B chain #status experimental <CHR>

Query Match 73.3%; Score 33; DB 2; Length 155;
Best Local Similarity 71.4%; Pred. No. 32;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RRFVHRR 7
Db 54 QRFVHRR 60

RESULT 11
T47398
hypothetical protein T18D12.130 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: T47398
R:Massenet, O.; Clabault, G.; Quigley, F.; Mache, R.; Mewes, H.W.; Lemcke, K.; Mayer, K.
submitted to the Protein Sequence Database, March 2000
A:Reference number: Z24464
A:Accession: T47398
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-246 <MAS>
A:Cross-references: EMBL:AL138644
A:Experimental source: cultivar Columbia; BAC clone T18D12
C:Genetics:
A:Map position: 3
A:Introns: 48/2: 73/1; 145/1; 189/1
A>Note: T18D12.130

Query Match 73.3%; Score 33; DB 2; Length 246;
Best Local Similarity 85.7%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RRFVHRR 8
DB 208 RFDHRRP 214

RESULT 12
AC0266
oligopeptide transport system permease protein oppc [imported] - Yersinia pestis (strain
C:Species: Yersinia pestis
C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C:Accession: AC0266
R:Parhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AC0266
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-301 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC90991.1; PID:g15980186; GSPDB:GN00175
C:Genetics:
A:Gene: oppc
C:Superfamily: oligopeptide permease protein oppb

Query Match 73.3%; Score 33; DB 2; Length 301;
Best Local Similarity 85.7%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRFVHRR 7
DB 30 RRFVHNR 36

RESULT 13
S36607
protein kinase (EC 2.7.1.37) crk2 [similarity] - Trypanosoma brucei
C:Species: Trypanosoma brucei
C>Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 16-Jun-2000
C:Accession: S36607
R:Smith, G.; Motttram, J.
submitted to the EMBL Data Library, August 1993
A:Description: A family of CDC2-related kinases in Trypanosoma brucei.
A:Reference number: S36607
A:Accession: S36607

A:Molecule type: DNA
A:Residues: 1-345 <SMI>
A:Cross-references: EMBL:X74598; NID:g9397161; PIDN:CAA52676.1; PID:g9397162
A:Experimental source: strain Istat
C:Genetics:
A:Gene: crk2
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; phosphotransferase
F:44-297/Domain: protein kinase homology <KIN>
F:52-60/Region: protein kinase ATP-binding motif
F:75,93,168,170/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 73.3%; Score 33; DB 1; Length 345;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRFVHR 6
DB 162 RRFVHR 167

RESULT 14
T50146
probable era/thof family GTP-binding protein [imported] - fission yeast (Schizosaccha
C:Species: Schizosaccharomyces pombe
C>Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000
C:Accession: T50146
R:Hamlin, N.; Churcher, C.M.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, November 1999
A:Reference number: Z25043
A:Accession: T50146
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-496 <RAM>
A:Cross-references: EMBL:AL132798; PIDN:CAB60697.1; GSPDB:GN00066; SPDB:SPAC222.05c
A:Experimental source: strain 972h(-); cosmid c222
C:Genetics:
A:Gene: SPDB:SPAC222.05c
A:Map position: 1
A:Introns: 50/3
C:Superfamily: thiophen / furan oxidation protein; translation elongation factor Tu h

Query Match 73.3%; Score 33; DB 2; Length 496;
Best Local Similarity 75.0%; Pred. No. 98;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRFVHRR 8
DB 17 RRFVHQIP 24

RESULT 15
T30369
DNA ligase-like protein - Lymantria dispar nuclear polyhedrosis virus
C:Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jul-2000
C:Accession: T30369
R:Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; R
Virology 253, 17-34, 1999
A:Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantri
A:Reference number: Z20836; MUID:99124785
A:Accession: T30369
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-548 <KUZ>
A:Cross-references: EMBL:AF081810; NID:g3822234; PIDN:AAC70207.1; PID:g3822256
C:Superfamily: vaccinia virus DNA ligase

Query Match 73.3%; Score 33; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 11e+02;

Matches	6;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	RRVYHR	6						
Db	333	RRVYHR	338						

Search completed: August 15, 2002, 11:50:19
 Job time: 245 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 11:58:17 ; Search time 18.61 Seconds

(Without alignments)
16.645 Million cell updates/sec

Title: US-09-613-092a-7_COPY_3_10
Perfect score: 45
Sequence: 1 RRFVHRP 8

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	34	75.6	248	1	RS6_DROME	P29327 drosophila
2	33	73.3	155	1	ZSS2_CAPPA	P30233 caparis ma
3	33	73.3	345	1	CC22_TRYBB	P54665 trypanosoma
4	33	73.3	496	1	MSS1_SCHPO	Q9ute7 schizosacch
5	32	71.1	140	1	YK24_PSEAE	P23205 pseudomonas
6	32	71.1	263	1	YCY3_ASTLO	P58147 astasia lon
7	32	71.1	451	1	YB28_MYCTU	O06580 mycobacteri
8	32	71.1	1479	1	RM56_MOUSE	Q9qps9 mus musculu
9	32	71.1	1527	1	RPOD_WHEAT	Q9qps9 triticum ae
10	31	68.9	193	1	RPOD_MAIZE	P16025 zea mays (m
11	31	68.9	421	1	ORN_XYLFA	O9qdx2 xyloella fas
12	31	68.9	421	1	WCOM_ADECC	O65952 canine aden
13	31	68.9	421	1	WCOM_ADECC	O96685 canine aden
14	31	68.9	446	1	YHG4_YEAST	P38757 saccharomyc
15	31	68.9	557	1	PAXI_HUMAN	P49023 homo sapien
16	31	68.9	634	1	DNK2_SYNP7	P50021 synechococc
17	31	68.9	898	1	NIA_BETVE	P27783 betula vert
18	31	68.9	1513	1	RPOD_ORYSA	P12093 oryza sativ
19	31	68.9	1997	1	OTOF_HUMAN	O9nc10 homo sapien
20	31	68.9	1997	1	OTOF_HUMAN	O9nc10 homo sapien
21	31	68.9	2067	1	BIMB_EMENT	P35611 mus musculu
22	31	68.9	2424	1	CCAA_RABIT	Q91442 emericella
23	31	68.9	2424	1	CCAA_RABIT	P27884 oryctolagus
24	31	66.7	125	1	YN25_CAEEL	P34584 caenorhabdi
25	30	66.7	176	1	EM2_RAT	P23943 rattus norv
26	30	66.7	269	1	RF42_SALTY	P26473 salmonella
27	30	66.7	302	1	OPPC_ECOLI	P77664 escherichia
28	30	66.7	342	1	AOX_HANAN	P08006 salmoneilla
29	30	66.7	349	1	AFEL_ECOLI	Q00912 hansecula a
30	30	66.7	541	1	BRL1_SCHOL	P71295 escherichia
31	30	66.7	637	1	PRIM_LACIA	P78741 schizosphyll
32	30	66.7	704	1	GLGB_YEAST	O04505 lactococcus
33	30	66.7	757	1	HT16_HYDAT	P33775 saccharomyc
						P53356 hydra atten

34	30	66.7	1052	1	FAK1_HUMAN	O05397 homo sapien
35	30	66.7	1052	1	FAK1_MOUSE	P34152 mus musculu
36	30	66.7	1053	1	FAK1_CHICK	O00944 gallus gall
37	30	66.7	1055	1	FAK1_RAT	O35346 rattus norv
38	30	66.7	1063	1	PDRL_YEAST	O35346 rattus norv
39	30	66.7	1068	1	FAK1_XENLA	P12383 saccharomyc
40	30	66.7	1071	1	TR1_THEAC	Q91738 xenopus lae
41	29	64.4	205	1	RS2_AERPE	P96086 thermoplasma
42	29	64.4	217	1	RL3_MYCHO	O9ybh4 aeropyrum p
43	29	64.4	217	1	RL3_MYCHO	O06044 mycobacteri
44	29	64.4	217	1	RL3_MYCHO	P30762 mycobacteri
45	29	64.4	370	1	MDS1_YEAST	P5049 mycobacteri
						P38615 saccharomyc

ALIGNMENTS

RESULT	ID	RS6_DROME	STANDARD	PRT	248 AA.
AC	P29327	094993; Q9W3N4			
DT	01-DEC-1992	(Rel. 24, Created)			
DT	01-DEC-1992	(Rel. 24, Last sequence update)			
DT	16-OCT-2001	(Rel. 40, Last annotation update)			
DE	40S ribosomal protein S6.				
GN	RP56 OR L(1)A1R8 OR HEN OR CG10944.				
OS	Drosophila melanogaster (fruit fly).				
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;				
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;				
OC	Ephydroidea; Drosophilidae; Drosophila.				
OX	NCBI_TaxID=7227;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=93087515; PubMed=1454811;				
RA	Watson K.L., Konrad K.D., Woods D.F., Bryant P.J.;				
RT	"Drosophila homolog of the human S6 ribosomal protein is required for				
RT	tumor suppression in the hematopoietic system.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 89:11302-11306(1992).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=93192329; PubMed=8448211;				
RA	Spencer T.A., Mackie G.A.;				
RT	"The nucleotide sequence of a cloned cDNA encoding ribosomal protein				
RT	S6 from Drosophila melanogaster.";				
RL	Biochim. Biophys. Acta 1172:332-334(1993).				
RN	[3]				
RP	SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.				
RX	MEDLINE=94018587; PubMed=8412647;				
RA	Stewart M.J., Denell R.;				
RT	"The Drosophila ribosomal protein S6 gene includes a 3' triplication				
RT	that arose by unequal crossing-over.";				
RL	Mol. Biol. Evol. 10:1041-1047(1993).				
RN	[4]				
RP	SEQUENCE FROM N.A. (ISOFORM A).				
RC	STRAIN-BERKELEY;				
RX	MEDLINE=20196006; PubMed=10731132;				
RA	Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,				
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,				
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,				
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,				
RA	Brandon R.C., Rogers Y.-H.C., Blazek R.G., Chang M., Pfeiffer B.D.,				
RA	Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mkilios G.L.G.,				
RA	Abriil J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,				
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,				
RA	Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,				
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,				
RA	Butlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,				
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,				
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,				
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,				
RA	Dudin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,				
RA	Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,				
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,				

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Malshtina N.V., Mobarry C., Morris J., Moshirefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spralling A.C., Stapleton M., Strong R., Sun E.,
 RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*." ;
 RL Science 287:2185-2195(2000).
 CC -1- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN CONTROLLING CELL GROWTH
 AND PROLIFERATION THROUGH THE SELECTIVE TRANSLATION OF PARTICULAR
 CLASSES OF MRNA.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B/C; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- PTM: RIBOSOMAL PROTEIN S6 IS THE MAJOR SUBSTRATE OF PROTEIN
 CC KINASES IN EUKARYOTE RIBOSOMES. THE PHOSPHORYLATION IS STIMULATED
 CC BY GROWTH FACTORS, TUMOR PROMOTING AGENTS, AND MITOGENS. IT IS
 CC DEPHOSPHORYLATED AT GROWTH ARREST.
 CC -1- SIMILARITY: BELONGS TO THE S6E FAMILY OF RIBOSOMAL PROTEINS.
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 CC -----
 DR EMBL: L01658; AAC34306.1; -
 DR EMBL: L07881; AAA28871.1; -
 DR EMBL: L02074; AAB05982.1; -
 DR EMBL: L02074; AAB05983.1; -
 DR EMBL: L02074; AAB05984.1; -
 DR EMBL: L02075; AAB05985.1; -
 DR EMBL: AE003442; AAF46288.1; ALT_SEQ.
 DR PIR: A47240; A47240.
 DR PIR: S30194; S30194.
 DR FlyBase: FBgn0004822; Rps6.
 DR InterPro: IPR001377; Ribosomal_S6e.
 DR Pfam: PF01092; Ribosomal_S6e; 1.
 DR ProDom: PD003460; Ribosomal_S6e; 1.
 DR PROSITE: PS00578; RIBOSOMAL_S6e; 1.
 KW Ribosomal protein; Phosphorylation; Alternative splicing.
 FT VARSPLIC 73 200
 FT LKGEKDIGLDTITPRLDGPRKAKIKLNLVSKEDYR
 FT RFVRRRLPAKDNKATSKAPKIQRLITPVVLQKRRRLAL
 FT KKKRQ -> LRLKLIHSCFHPNCNCKVRYKRYTEAN
 FT VSLATLVLKNNPSPCRLGPNVSNISKLIYCEEDDEVIP
 FT VKLORRHKRRONATKEAIAEYVKIKLIVKKEKSKANRGYV
 FT TTRKPSVSGSK (IN ISOFORM B).
 FT VARSPLIC 201 248
 FT MISSING (IN ISOFORM B).
 FT SEQUENCE 248 AA; 28407 MW; 4E781737C33B3B6D CRC64;

RESULT 2
 2SS2_CAPMA STANDARD; PRT; 155 AA.
 ID 2SS2_CAPMA
 AC P30233; Q04774;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Mabinlin II precursor (MAB II) (Sweet protein).
 OS Capparis mabalinii (Mablinang).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Capparidaceae;
 OC NCBI_TaxID=13395;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Seed;
 RX MEDLINE=97128796; PubMed=8973336;
 RA Nirasawa S., Masuda Y., Nakaya K., Kurihara Y.,
 RT "Cloning and sequencing of a cDNA encoding a heat-stable sweet
 RT protein, mabinlin II." ;
 RL Gene 181:225-227(1996).
 RN [2]
 RP SEQUENCE OF 36-68 AND 83-154.
 RC TISSUE=Seed;
 RX MEDLINE=93145958; PubMed=8425538;
 RA Liu X., Maeda S., Hu Z., Aiuchi T., Kurihara Y.,
 RT "Purification, complete amino acid sequence and structural
 RT characterization of the heat-stable sweet protein, mabinlin II." ;
 RL Eur. J. Biochem. 211:281-287(1993).
 RN [3]
 RP PARTIAL SEQUENCE, AND DISULFIDE BONDS.
 RX MEDLINE=94002261; PubMed=839391;
 RA Nirasawa S., Liu X., Nishino T., Kurihara Y.,
 RT "Disulfide bridge structure of the heat-stable sweet protein mabinlin
 RT II." ;
 RL Biochim. Biophys. Acta 1202:277-280(1993).
 CC -1- FUNCTION: HEAT STABLE 2S SEED STORAGE PROTEIN HAVING SWEETNESS-
 CC INDUCING ACTIVITY.
 CC -1- SUBUNIT: HETERODIMER OF A SMALL A AND A LARGE B CHAIN LINKED BY
 CC DISULFIDE BONDS.
 CC -1- SIMILARITY: BELONGS TO THE 2S SEED STORAGE ALBUMINS FAMILY.
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 CC -----
 DR EMBL: D83997; BAA12204.1; -
 DR Mendel: 14634; Capma; 1175; 14634.
 DR InterPro: IPR003612; AAI.
 DR InterPro: IPR000617; Napin.
 DR Pfam: PF01631; Seedstore_2S; 1.
 DR PRINTS: PR00496; NAPIN.
 DR ProDom: PD002498; Napin; 1.
 DR SMART: SM00499; AAI; 1.
 KW Seed storage protein; Albumin; Signal; Sweet-taste.
 FT SIGNAL 1 20
 FT POTENTIAL.
 FT PROPEP 21 35
 FT CHAIN 36 68
 FT PROPEP 69 82
 FT CHAIN 83 154
 FT PROPEP 155 155
 FT DISULFID 40 103
 FT DISULFID 53 92
 FT DISULFID 93 141
 FT DISULFID 105 149
 FT MOD_RES 36 36
 FT MOD_RES 83 83
 PYRROLIDONE CARBOXYLIC ACID.
 PYRROLIDONE CARBOXYLIC ACID.

Query Match 75.6%; Score 34; DB 1; Length 248;
 Best Local Similarity 87.5%; Pred. No. 8.5;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RRFVRRRP 8
 |||||
 Db 154 RRFVRRRP 161

FT CONFLICT 148 148 A -> T (IN REF. 1).
FT CONFLICT 153 153 A -> T (IN REF. 1).
SQ SEQUENCE 155 AA; 18089 MM; 72E885DEDC2D46A CRC64;

Query Match 73.3%; Score 33; DB 1; Length 155;
Best Local Similarity 71.4%; Pred. No. 8.4;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRFVHRR 7
Db 54 QRFTHRR 60

RESULT 3
CC22_TRYBB STANDARD; PRT; 345 AA.
ID CC22_TRYBB
AC P54665;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-1999 (Rel. 38, Last annotation update)
DE Cell division control protein 2 homolog 2 (EC 2.7.1.-).
GN CRK2.
OS Trypanosoma brucei brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ISTAT;
RX MEDLINE=96009893; PubMed=7557404;
RA Mottiram J., Smith G.;
RT "A family of trypanosome cdc2-related protein kinases."
RL Gene 162.147-153(1995).
CC -1- FUNCTION: PROBABLY INVOLVED IN THE CONTROL OF THE CELL CYCLE.
CC -1- ENZYME REGULATION: PHOSPHORYLATION AT SER-56 OR TYR-57 INACTIVATES THE ENZYME (BY SIMILARITY).
CC -1- SUBUNIT: FORMS A STABLE BUT NON-COVALENT COMPLEX WITH A REGULATORY SUBUNIT AND WITH A CYCLIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -1- CDDX/CDDX SUBFAMILY.

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CC
DR EMBL: X74598; CA52676.1; -.
DR HSSP: P24941; ICKP.
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR002290; Ser_thr_Pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
KW DOMAIN 46 328 PROTEIN KINASE.
FT NP_BIND 52 60 ATP (BY SIMILARITY).
FT BINDING 75 75 ATP (BY SIMILARITY).
FT ACI_SITE 168 168 BY SIMILARITY.
FT MOD_RES 56 56 PHOSPHORYLATION (BY SIMILARITY).
FT MOD_RES 57 57 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 345 AA; 39238 MM; 6E4E88D2571931B8 CRC64;

Query Match 73.3%; Score 33; DB 1; Length 345;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRFVHR 6
Db 162 RRFVHR 167

RESULT 4
MSS1_SCHPO STANDARD; PRT; 496 AA.
ID MSS1_SCHPO
AC Q9PTE7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE GTPase MSS1 homolog, mitochondrial precursor.
GN SPAC222.05C.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Hamlin N., Churcher C.M., McDougall R.C., Rajandream M.A.,
RA Barrell B.G.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Mitochondrial.
CC -1- SIMILARITY: BELONGS TO THE ERA/TRME FAMILY OF GTP-BINDING PROTEINS. TRME SUBFAMILY.

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CC
DR EMBL: AL132798; CAB60697.1; -.
DR InterPro: IPR002917; MMR_HSR1.
DR Pfam: PF01926; MMR_HSR1; 1.
KW tRNA processing; Mitochondrion; GTP-binding; Transit peptide.
FT TRASNST 1 ? MITOCHONDRION (POTENTIAL).
FT CHAIN ? 496 GTPASE MSS1 HOMOLOG.
FT NP_BIND 246 253 GTP (POTENTIAL).
SQ SEQUENCE 496 AA; 55315 MM; 092F7E1E1CDD8002 CRC64;

Query Match 73.3%; Score 33; DB 1; Length 496;
Best Local Similarity 75.0%; Pred. No. 27;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RRFVHRR 8
Db 17 RRFVHQP 24

RESULT 5
YK24_PSEAE STANDARD; PRT; 140 AA.
ID YK24_PSEAE
AC P23205; Q91290;
DT 01-NOV-1991 (Rel. 20, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein PA2024.
GN PA2024.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAOI;
RX MEDLINE=20437337; PubMed=10984043;

RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Binkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garner R.L., Goltz L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sajer M.H., Hancock R.E.W., Lory S., Olson M.V.,
 RT "Complete genome sequence of *Pseudomonas aeruginosa* PAO1, an
 RT opportunistic pathogen.";
 RL Nature 406:959-964(2000).
 RP SEQUENCE OF 1-28 FROM N.A.
 RC STRAIN-PA08:
 RX MEDLINE-91194546; PubMed-1849605;
 RA "Perry A.C.F., Ni Bhriain N., Brown N.L., Rouch D.A.,
 RT Molecular characterization of the gor gene encoding glutathione
 RT reductase from *Pseudomonas aeruginosa*: determinants of substrate
 RT specificity among pyridine nucleotide-disulphide oxidoreductases.";
 RL Mol. Microbiol. 5:163-171(1991).
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 CC -----
 DR EMBL: AE004629; AAG05412.1; -
 DR EMBL: X54201; CAA38121.1; -
 DR PIR: S15235; S15235.
 DR InterPro: IPR000325; Glyoxalase_1.
 DR Pfam: PF00903; Glyoxalase_1.
 SW Hypothetical protein; Complete proteome.
 SK SEQUENCE 140 AA; 15373 MW; 26221B19B832BF38 CRC64;

Query Match 71.1%; Score 32; DB 1; Length 140;
 Best Local Similarity 71.4%; Pred. No. 12;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 REVHRRP 8
 | :|||
 Db 29 RVHRRP 35

RESULT 6
 YCY3_ASTLO STANDARD; PRT; 263 AA.
 AC P58147:
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical 32.5 kDa protein in rpl14-rpl12 intergenic region
 DE (ORF263).
 OS *Astasia longa* (Euglenophyceae algae).
 OG Chloroplast.
 OC Eukaryota; Euglenozoa; Euglenida; Euglenales; Astasia.
 OX NCBI-TaxID=3037;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CCAP 1204-17A;
 RX MEDLINE-21080522; PubMed-11212895;
 RA Gockel G., Hachtel W.,
 RT "Complete gene map of the plastid genome of the nonphotosynthetic
 RT euglenoid flagellate *Astasia longa*.";
 RL Protist 151:347-351(2000).
 CC -1- SIMILARITY: BELONGS TO THE A.LONGA ORF167/ORF288 FAMILY.
 CC -----
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 CC -----
 DR EMBL: AJ294725; CAC24603.1; -
 KW Hypothetical protein; Chloroplast.
 SQ SEQUENCE 263 AA; 32473 MW; 3508B02DB49CB4E6 CRC64;

Query Match 71.1%; Score 32; DB 1; Length 263;
 Best Local Similarity 50.0%; Pred. No. 22;
 Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 REVHRRP 8
 | :|||
 Db 17 RRVYRRP 24

RESULT 7
 YB28_MYCTU STANDARD; PRT; 451 AA.
 AC 006580:
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Hypothetical 49.3 kDa protein RV1128c.
 GN RV1128C OR MT1160 OR MTCY2268.17C.
 OS *Mycobacterium tuberculosis*.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacteriaceae; *Mycobacterium*.
 OX NCBI-TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RX MEDLINE-98295987; PubMed-9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holtroyd S.,
 RA Hornby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.,
 RT "Deciphering the biology of *Mycobacterium tuberculosis* from the
 RT complete genome sequence.";
 RL Nature 393:537-544(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwin M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Esmolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gali J., Mikula A.,
 RA Bishai W.,
 RT "Whole genome comparison of *Mycobacterium tuberculosis* clinical and
 RT laboratory strains.";
 RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE RV1128C/1588C/1702C/1945/3466
 CC FAMILY.
 CC -----
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 CC -----
 DR EMBL: Z95585; CAB09039.1; -
 DR EMBL: AE006995; AAK45417.1; -
 DR TIGR: MT1160; -
 DR Tuberculist: RV1128c; -
 DR InterPro: IPR003870; DUF222.
 DR InterPro: IPR003615; HNH_nuc.

DR Pfam: PF02720; DUF222; 1.
 DR SMART: SM00507; HNHc; 1.
 KM Hypothetical protein: Complete proteome.
 FT CONFLICT 270 270 E->G (IN REF. 2).
 FT CONFLICT 421 451 MISSING (IN REF. 2).
 SQ SEQUENCE 451 AA: 49274 MW: 4697745EC5E148CDD CRC64;

Query Match
 Best Local Similarity 71.1%; Score 32; DB 1; Length 451;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 RRFVRRP 8
 Db 134 RAYFRLP 141

RESULT 8
 RMS6_MOUSE STANDARD; PRT; 551 AA.
 AC 09EP89;
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Mitochondrial 39S ribosomal protein L56 (MRP-L56) (Serine beta
 lactamase-like protein LACTB).
 GN LACTB OR LACTL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV, AND BALB/C;
 RX PubMed=11707067;
 RA Smith T.S., Southan C., Ellington K., Campbell D., Tew D.G.,
 RA Debouck C.;
 RT "Identification, genomic organization, and mRNA expression of LACTB,
 RT encoding a serine beta-lactamase-like protein with an amino-terminal
 RT transmembrane domain.";
 RL Genomics 78:12-14(2001).
 CC -1- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
 CC -1- TISSUE SPECIFICITY: Expressed predominantly in liver.
 CC -1- SIMILARITY: BELONGS TO THE L56E FAMILY OF RIBOSOMAL PROTEINS.
 CC
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 CC
 CC EMBL: AF317900; AAC37910.1;
 DR EMBL: AF317901; AAC37911.1;
 DR MGD; MGI:1933395; Lactl.
 KM Ribosomal protein: Mitochondrion.
 SQ SEQUENCE 551 AA: 60705 MW: 816C1EB94B1D6009 CRC64;

Query Match
 Best Local Similarity 71.1%; Score 32; DB 1; Length 551;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 RRFVRRP 8
 Db 24 RRGARRP 31

RESULT 9
 RPOD_WHEAT STANDARD; PRT; 1479 AA.
 AC 09XP59;

DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE DNA-directed RNA polymerase beta" chain (EC 2.7.7.6).
 GN RPOC2.
 OS Triticum aestivum (wheat).
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticaceae; Triticum.
 OX NCBI_TaxID=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. CHINESE SPRING;
 RA Matsuno K., Tsunewaki K., Ohnishi Y.;
 RA Terachi T., Utsugi S., Murata M., Mori N., Takumi S., Ito K.,
 RA Gojobori T., Murai R., Murai K., Matsuno K., Ohnishi Y., Tajiri H.,
 RA Tsunewaki K.;
 RT "Chinese spring wheat (Triticum aestivum L.) chloroplast genome:
 RT complete sequence and contig clones";
 RL Plant Mol. Biol. Rep. 18:243-253(2000).
 CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
 CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
 CC SUBSTRATES.
 CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
 CC (RNA)(N).
 CC -1- SUBUNIT: IN CHLOROPLAST THE RNA POLYMERASE IS COMPOSED OF FOUR
 CC SUBUNITS: ALPHA, BETA, BETA', AND BETA".
 CC
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 CC
 CC EMBL: AB027572; BAB78042.1;
 DR EMBL: AB042240; BAB47026.1;
 DR InterPro: IPR000722; RNA_POL_A.
 DR Pfam: PF00623; RNA_POL_A; 1.
 KM Transferrase; Transcription; DNA-directed RNA polymerase; Chloroplast.
 SQ SEQUENCE 1479 AA: 170043 MW: 4DFB5363CB516FB2 CRC64;

Query Match
 Best Local Similarity 71.1%; Score 32; DB 1; Length 1479;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 RRFVRRP 8
 Db 1429 QKFWHRSP 1436

RESULT 10
 RPOD_MAIZE STANDARD; PRT; 1527 AA.
 AC P16025;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE DNA-directed RNA polymerase beta" chain (EC 2.7.7.6).
 GN RPOC2.
 OS Zea mays (Maize).
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
 OC Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90340289; PubMed=2381419;
 RA Iglol G.L., Meinke A., Doery I., Koessel H.;
 RT "Nucleotide sequence of the maize chloroplast rpo B/C1/C2 operon:
 RT comparison between the derived protein primary structures from
 RT various organisms with respect to functional domains.";
 RL Mol. Gen. Genet. 221:379-394(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90175001; PubMed=2308853;
 RA Iglol G.L., Meinke A., Doery I., Koessel H.;
 RT "Nucleotide and derived amino acid sequence of rps2 from maize
 RT chloroplasts.";
 RL Nucleic Acids Res. 18:663-663(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95395841; PubMed=7666415;
 RA Maier R.M., Neckermann K., Iglol G.L., Koessel H.;
 RT "Complete sequence of the maize chloroplast genome: gene content,
 RT hotspots of divergence and fine tuning of genetic information by
 RT transcript editing.";
 RL J. Mol. Biol. 251:614-628(1995).
 RN [4]
 RP SEQUENCE OF 1-52 FROM N.A.
 RX MEDLINE=90160360; PubMed=2304916;
 RA Hu J., Bogorad L.;
 RT "Maize chloroplast RNA polymerase: the 180-, 120-, and 38-kilodalton
 RT polypeptides are encoded in chloroplast genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:1531-1535(1990).
 RN [5]
 RP SEQUENCE OF 1316-1527 FROM N.A.
 RC STRAIN=CV. FR9CMS X RF37; TISSUE=Leaf;
 RX MEDLINE=90272437; PubMed=2140888;
 RA Stahl D., Rodemeier S., Subramanian A.R., Bogorad L.;
 RT "Nucleotide sequence of a 3.46 kb region of maize chloroplast DNA
 RT containing the gene cluster rpoC2-rps2-atpI-atpH.";
 RL Nucleic Acids Res. 18:3073-3074(1990).
 CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
 CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
 CC SUBSTRATES.
 CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
 CC [RNA](N).
 CC -1- SUBUNIT: IN CHLOROPLAST THE RNA POLYMERASE IS COMPOSED OF FOUR
 CC SUBUNITS: ALPHA, BETA, BETA', AND BETA".
 CC -----
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 CC -----
 CC EMBL: X17318; CAA35197.1; -
 CC EMBL: M31208; AA84489.1; -
 CC EMBL: X86563; CAA60278.1; -
 CC EMBL: X52270; CAA36511.1; -
 CC PIR: S08248; RN2MB2.
 CC PIR: A34846; A34846.
 CC MaizeDB: 69586; -
 CC Mendel: 5021; ZEMMA:rpoC2.1.
 CC InterPro: IPR000722; RNA_POL_A.
 CC Pfam: PF00623; RNA_POL_A.1.
 CC Transferrase: Transcription; DNA-directed RNA polymerase; Chloroplast.
 CC CONFLICT 25 25 R -> S (IN REF. 4).
 CC FT ACT SITE 1527 AA; 176082 MW; 98BEA0C3165A8C3D CRC64;
 CC SEQUENCE

Query Match 71.1%; Score 32; DB 1; Length 1527;

Best Local Similarity 62.5%; Pred. No. 1.3e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 OY 1 RRFVRRP 8
 DB 1466 QKRVHSP 1473
 RESULT 11
 ORN_XYLFA
 ID ORN_XYLFA STANDARD; PRT; 193 AA.
 AC 09PDx2,
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Oligoribonuclease (EC 3.1.-.-).
 GN ORN OR XF1257
 OS Xylella fastidiosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
 OC Xylella.
 OX NCBI_TaxID=2371;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=9A5C;
 RX MEDLINE=20365717; PubMed=10910347;
 RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
 RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
 RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
 RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carreir H.,
 RA Colauto N.B., Colombo C., Costa F.P., Costa M.C.R., Costa-Neto C.M.,
 RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
 RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
 RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
 RA Garner M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
 RA Ho P.L., Hohnsels J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
 RA Krieger J.E., Kurmae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
 RA Machado M.A., Martins A.M.B.N., Madeira H.M.F., Martino C.L.,
 RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
 RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
 RA Moon D.H., Nagai M., Nascimento A.L.T.O., Netto L.E.S.,
 RA Nhani A., Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
 RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris J.B.,
 RA Peixoto B.R., Pereira G.A.G., Pereira H.A., Jr., Pesquero J.B.,
 RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
 RA de Rosa V.E., Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
 RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A., Jr.,
 RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
 RA de Souza A.P., Terenzi M.F., Trufil D., Tsai S.M., Tsuchioka H.H.,
 RA Vallada H., Van Sluys M.A., Verjovsky-Almeida S., Vettore A.L.,
 RA Zago M.A., Zatz M., Zeldanis J., Setubal J.C.;
 RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
 RL Nature 406:151-159(2000).
 CC -1- FUNCTION: 3'-5' EXORIBONUCLEASE SPECIFIC FOR SMALL
 CC OLIGORIBONUCLEOTIDES (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC -1- SIMILARITY: BELONGS TO THE OLIGORIBONUCLEASE FAMILY.
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 CC -----
 CC EMBL: AE003959; AAP84066.1; -
 CC InterPro: IPR000520; Exonuclease.
 CC Pfam: PF00929; Exonuclease; 1.
 CC SMART: SM00479; EXOIII; 1.
 CC HYDROLASE; Exonuclease; Nuclease; Complete proteome.
 CC FT ACT SITE 135 135 POTENTIAL.
 CC SEQUENCE 193 AA; 21902 MW; 12D2B2C06B26D58C CRC64;

Query Match 68.9%; Score 31; DB 1; Length 193;
 Best Local Similarity 71.4%; Pred. No. 26;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRFVHRR 7
 |||:|:
 Db 119 RRFRLRQ 125

RESULT 12
 VCOM_ADECC

ID VCOM_ADECC STANDARD; PRT; 421 AA.

AC 065952;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DE Minor core protein (Protein V).

GN PV.

OS Canine adenovirus type 1 (strain CLL).

OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.

OX NCBI_TaxID=69150;

RN [1]

RP Campbell J.B., Zhao Y.;

RA Submitted (Aug-1996) to the EMBL/GenBank/DBJ databases.

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CC -----

DR EMBL: U55001; AAB05440.1; -

KW Core protein; Late protein.

SO SEQUENCE 421 AA; 47538 MW; C84536291CDDEFP9 CRC64;

OY 1 RRFVHRR 8
 ||| |||
 Db 67 RRFAPRRP 74

RESULT 13
 VCOM_ADECR

ID VCOM_ADECR STANDARD; PRT; 421 AA.

AC 096685;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE Minor core protein (Protein V).

GN PV.

OS Canine adenovirus type 1 (strain RI261).

OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.

OX NCBI_TaxID=69151;

RN [1]

RP MEDLINE=92725900; Pubmed=9129661;

RA Morrison M.D., Onions D.E., Nicolson L.;

RT "Complete DNA sequence of canine adenovirus type 1.";

RL J. Gen. Virol. 78:873-878(1997).

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CC -----

DR EMBL: Y07760; CAA69063.1; -

KW Core protein; Late protein.

SO SEQUENCE 421 AA; 47649 MW; A5F523E18748211F CRC64;

OY 1 RRFVHRR 8
 ||| |||
 Db 67 RRFAPRRP 74

Query Match 68.9%; Score 31; DB 1; Length 421;
 Best Local Similarity 75.0%; Pred. No. 57;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 14
 YHG4_YEAST

ID YHG4_YEAST STANDARD; PRT; 446 AA.

AC P38757;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 01-FEB-1995 (Rel. 31, Last annotation update)

DE Hypothetical 50.6 kDa protein in RPL14B-CPA1 intergenic region.

GN YHR004C.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

OX NCBI_TaxID=4932;

RN [1]

RP SEQUENCE FROM N.A.

RC SRRAIN-5288C / AB972;

RA MEDLINE=94378003; Pubmed=8091229;

RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,

RA Du Z., Favell A., Fulton L., Gattung S., Geisel C., Kirsten J.,

RA Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,

RA Latreille P., Louis E.J., Macri C., Mardis E., Meneses S., Mouser L.,

RA Nham M., Rifkin L., Riles L., St. Peter H., Trevisan E., Vaughan K.,

RA Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,

RA Vaudin M.;

RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome

RT VIII.";

RL Science 265:2077-2082(1994).

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CC -----

DR EMBL: U10555; AAB68431.1; -

DR PIR: S46802; S46802.

DR SGD: S0001046; NEM1.

DR InterPro: IPR004274; NIF.

DR Pfam: PF03031; NIF; 1.

DR Hypothetical protein; Transmembrane.

KW TRANSMEM 87 103 POTENTIAL.

SO SEQUENCE 446 AA; 50641 MW; 4260748606E17062 CRC64;

OY 3 FVHRRP 8
 |||:|:
 Db 295 FVHKRP 300

Query Match 68.9%; Score 31; DB 1; Length 446;
 Best Local Similarity 66.7%; Pred. No. 60;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

RESULT 15
PAXI_HUMAN STANDARD; PRT; 557 AA.
ID PAXI_HUMAN
AC P49023;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Paxillin.
GN PXN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-95197488; PubMed-7534286;
RA Salgia R., Li J.-L., Lo S.H., Brunkhorst B., Kansas G.S.,
RA Sobhany E.S., Sun Y., Pistick E., Hallik M., Ernst T., Tantiavahi R.,
RA Chen L.B., Griffin J.D.;
RT "Molecular cloning of human paxillin, a focal adhesion protein
RT phosphorylated by P210BCR/ABL."
RT J. Biol. Chem. 270:5039-5047 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Yamagata K., Oda N., Fututa H., Vaxillaire M., Southam L., Boriraj V.,
RA Chen X., Oda Y., Takeda J., Yamada S., Nishigori H., Lebeau M.M.,
RA Lathrop M., Cox R.D., Bell G.I.;
RT "Transcription map of the 5cm region surrounding the hepatocyte
RT nuclear factor-1a/MODY3 gene on chromosome 12."
RT Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CYTOSKELETAL PROTEIN INVOLVED IN ACTIN-MEMBRANE
CC ATTACHMENT AT SITES OF CELL ADHESION TO THE EXTRACELLULAR MATRIX
CC (FOCAL ADHESION). BINDS IN VITRO TO VINCULIN AS WELL AS TO THE SH3
CC DOMAIN OF C-SRC AND, WHEN TYROSINE PHOSPHORYLATED, TO THE SH2
CC DOMAIN OF V-CRK.
CC -!- PTM: EXTENSIVE TYROSINE PHOSPHORYLATION OCCURS DURING INTEGRIN-
CC MEDIATED CELL ADHESION, EMBRYONIC DEVELOPMENT, FIBROBLAST
CC TRANSFORMATION AND FOLLOWING STIMULATION OF CELLS BY MITOGENS.
CC -!- SIMILARITY: CONTAINS 4 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC
CC IONS.
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CC -----
DR EMBL: U14588; AAC50104.1; -
DR EMBL: U87946; AAD00648.1; -
DR EMBL: U87941; AAD00648.1; JOINED.
DR EMBL: U87942; AAD00648.1; JOINED.
DR EMBL: U87943; AAD00648.1; JOINED.
DR EMBL: U87944; AAD00648.1; JOINED.
DR EMBL: U87945; AAD00648.1; JOINED.
DR HSSP: P04006; 1TML.
DR MIM: 602505; -
DR InterPro: IPR001781; LIM.
DR InterPro: IPR001904; Paxillin.
DR Pfam: PF00412; LIM; 4.
DR PRINTS: PR00832; PAXILLIN.
DR ProDom: PD000094; LIM; 4.
DR SMART: SM00132; LIM; 4.
DR PROSITE: PS00478; LIM DOMAIN 1; 4.
DR PROSITE: PS50023; LIM DOMAIN 2; 4.
DR Cytoskeleton; Phosphorylation; LIM domain; Repeat; Metal-binding;
KW ZINC.
FT DOMAIN 46 53 PRO-RICH.
FT MOD_RES 118 118 PHOSPHORYLATION (BY FAK) (BY SIMILARITY).
FT DOMAIN 324 374 LIM 1.
FT DOMAIN 383 433 LIM 2.
FT DOMAIN 442 492 LIM 3.

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```

FT DOMAIN 501 551 LIM 4.
SQ SEQUENCE 557 AA; 60936 MW; B379BED63E8E63A5 CRC64;

```

Query Match

```

Best Local Similarity 57.18; Score 31; DB 1; Length 557;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 RFVHRRP 8
   ||:::|
DB 75 RFIHQDP 81

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Search completed: August 15, 2002, 11:58:17
Job time: 517 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 15, 2002, 11:57:52 ; Search time 58.57 Seconds
(without alignments)
23.629 Million cell updates/sec

Title: US-09-613-092a-7_COPY_3_10
Perfect score: 45
Sequence: 1 RRFVHRP 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SPREMBL_19:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_potent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
1	38	84.4	434	09RV39	Q9RV39 deinococcus
2	38	84.4	929	09LGE7	Q9LGE7 oryza sativ
3	37	82.2	127	09ZLN3	Q9ZLN3 streptomyc
4	35	77.8	72	064123	064123 bacterioph
5	35	77.8	72	031924	031924 bacillus su
6	35	77.8	403	16	P96A02 mycobacteri
7	35	77.8	663	5	Q9VLG3
8	34	75.6	80	09JYH1	Q9JYH1 drosophila
9	34	75.6	183	16	Q9JYH1
10	34	75.6	217	5	Q9JYH1
11	34	75.6	243	5	Q9JYH1
12	34	75.6	244	4	Q9JYH1
13	34	75.6	244	4	Q9JYH1
14	34	75.6	254	5	Q9JYH1
15	34	75.6	322	2	Q9JYH1
16	34	75.6	386	10	Q94G10

17	33	73.3	118	2	Q9S2K1	Q9S2K1 streptomyc
18	33	73.3	241	10	Q9LPB6	Q9LPB6 arabisdops
19	33	73.3	246	10	Q9M234	Q9M234 arabisdops
20	33	73.3	320	5	Q9N867	Q9N867 leishmania
21	33	73.3	548	12	Q9YMW2	Q9YMW2 lymantria d
22	33	73.3	567	16	Q9ZM37	Q9ZM37 rhizobium m
23	33	73.3	577	16	Q9Z9B5	Q9Z9B5 chlamydia p
24	33	73.3	702	2	Q9AD11	Q9AD11 streptomyc
25	33	73.3	722	5	Q9AD11	Q9AD11 streptomyc
26	33	73.3	786	5	Q9P533	Q9P533 caenorhabdi
27	32	71.1	57	2	Q86472	Q86472 neurospora
28	32	71.1	138	2	Q83021	Q83021 rhododactyl
29	32	71.1	168	17	Q9YBN3	Q9YBN3 aeropyrum p
30	32	71.1	145	11	Q9DA47	Q9DA47 mus muscul
31	32	71.1	174	4	Q9P0B9	Q9P0B9 homo sapien
32	32	71.1	202	10	Q80513	Q80513 arabisdops
33	32	71.1	214	16	Q98J73	Q98J73 rhizobium l
34	32	71.1	295	16	Q53514	Q53514 mycobacteri
35	32	71.1	301	5	Q9VYF8	Q9VYF8 drosophila
36	32	71.1	321	10	Q9LVR5	Q9LVR5 arabisdops
37	32	71.1	321	10	Q94B21	Q94B21 arabisdops
38	32	71.1	334	2	Q9AK99	Q9AK99 streptomyc
39	32	71.1	346	4	Q96DV4	Q96DV4 homo sapien
40	32	71.1	369	16	Q9ZNF0	Q9ZNF0 rhizobium m
41	32	71.1	370	10	Q9S7D5	Q9S7D5 arabisdops
42	32	71.1	443	2	Q93S73	Q93S73 myxococcus
43	32	71.1	460	10	Q9AWS1	Q9AWS1 oryza sativ
44	32	71.1	523	10	Q9ANQ9	Q9ANQ9 oryza sativ
45	32	71.1	527	2	Q9S201	Q9S201 streptomyc

ALIGNMENTS

RESULT	ID	Query Match	Score	DB ID	Description
1	Q9RV39	84.4%	38	434	Q9RV39 deinococcus
2	Q9RV39	84.4%	38	929	Q9LGE7 oryza sativ
3	Q9RV39	82.2%	37	127	Q9ZLN3 streptomyc
4	Q9RV39	77.8%	35	72	064123 bacterioph
5	Q9RV39	77.8%	35	72	031924 bacillus su
6	Q9RV39	77.8%	35	403	16 P96A02 mycobacteri
7	Q9RV39	77.8%	35	663	5 Q9VLG3
8	Q9RV39	75.6%	34	80	09JYH1 drosophila
9	Q9RV39	75.6%	34	183	16 Q9JYH1
10	Q9RV39	75.6%	34	217	5 Q9JYH1
11	Q9RV39	75.6%	34	243	5 Q9JYH1
12	Q9RV39	75.6%	34	244	4 Q9JYH1
13	Q9RV39	75.6%	34	244	4 Q9JYH1
14	Q9RV39	75.6%	34	254	5 Q9JYH1
15	Q9RV39	75.6%	34	322	2 Q9JYH1
16	Q9RV39	75.6%	34	386	10 Q94G10

Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRFVHRR 7
|||||

Db 322 RRFVHRR 328

RESULT 2

Q9LGE7 PRELIMINARY; PRT; 929 AA.

AC 09LGE7; 09LGE7;

DT 01-OCT-2000 (TReMBLrel. 15, Created)

DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)

DE P0406H10.1 PROTEIN (P0509B06.3 PROTEIN).

GN P0406H10.1 OR P0509B06.3.

OS Oryza sativa (Rice).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Erihartoideae; Oryzaceae; Oryza.

OC NCBI_TaxID=4530;

RP SEQUENCE FROM N.A.

RC STRAIN=CV. NIPPONBARE;

RA Sasaki T., Matsumoto T., Yamamoto K.;

RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC

clone:P0509B06.";

RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AP002824; BAB07977.1; -

DR InterPro; IPR002794; DUF92.

DR Pfam; PF01940; DUF92; 1.

DR ProDom; PD014594; DUF92; 1.

DR SEQUENCE 929 AA; 100026 MW; FE869AD16F3F6A78 CRC64;

Query Match 84.4%; Score 38; DB 10; Length 929;

Best Local Similarity 87.5%; Pred. No. 31;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRFVHRR 8
|||||

Db 901 RRFVHRR 908

RESULT 3

Q92N73 PRELIMINARY; PRT; 127 AA.

AC 092N73; 092N73;

DT 01-MAY-1999 (TReMBLrel. 10, Created)

DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)

DT 01-MAY-1999 (TReMBLrel. 10, Last annotation update)

DE MEIC1.

GN MEIC1.

OS Streptomyces griseus.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.

OX NCBI_TaxID=1911;

RP SEQUENCE FROM N.A.

RC STRAIN=IFO13350;

RA Ueda K., Beppu T.;

RT "Tyrosinase gene from Streptomyces griseus.";

RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

SO SEQUENCE 127 AA; 13707 MW; 93801073CCAC86CA CRC64;

Query Match 82.2%; Score 37; DB 2; Length 127;

Best Local Similarity 87.5%; Pred. No. 7.2;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRFVHRR 8
|||||

Db 66 RRFVHRR 73

RESULT 4

O64123 PRELIMINARY; PRT; 72 AA.

AC 064123; 064123;

DT 01-AUG-1998 (TReMBLrel. 07, Created)

DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)

DE HYPOTHETICAL 8.4 KDA PROTEIN.

GN YOON.

OS Bacteriophage SPBc2.

OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.

OC NCBI_TaxID=66797;

RP SEQUENCE FROM N.A.

RA Lazarevic V., Duesterhoeft A., Soldo B., Hilbert H., Manuel C.,

RT "The complete nucleotide sequence of the Bacillus subtilis SPBc2

prophage.";

RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF020713; AAC13083.1; -

DR Hypothetical protein.

DR SEQUENCE 72 AA; 8382 MW; 11178AF395985ED8 CRC64;

Query Match 77.8%; Score 35; DB 9; Length 72;

Best Local Similarity 100.0%; Pred. No. 10;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FVHRRP 8
|||||

Db 60 FVHRRP 65

RESULT 5

O31924 PRELIMINARY; PRT; 72 AA.

AC 031924; 031924;

DT 01-JAN-1998 (TReMBLrel. 05, Created)

DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)

DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)

DE YOON PROTEIN.

GN YOON.

OS Bacillus subtilis.

OC Bacteria; Firmicutes; Bacillus/Clostridium group;

OC Bacillus/Staphylococcus group; Bacillus.

OX NCBI_TaxID=1423;

RP SEQUENCE FROM N.A.

RC STRAIN=168;

RX MEDLINE=98044033; PubMed=9384377;

RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

RA Azevedo V., Bertoletti M.G., Bessieres P., Bolotin A., Borchert S.,

RA Borris R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,

RA Brouillet S., Bruschi C.V., Caldwell B., Capiano V., Carter N.M.,

RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,

RA Entian K.D., Errington J., Fabret C., Ferrati E., Foulger D.,

RA Fritz C., Fujita M., Fujita Y., Funa S., Galizzi A., Galleron N.,

RA Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,

RA Giuseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,

RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
 RA Kunita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Nodack M.,
 RA Moore D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Portolillo S., Prescott A.M.,
 RA Pirescan E., Puig P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivoita C., Rocha E., Roche B., Rose M., Sadleir Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 RA Seiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Takakoshi A., Tanaka T., Terpiltra P., Tognoni K.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassartoli A.,
 RA Viari A., Wambler R., Wedler E., Wedler H., Weitzenger T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,
 RT "The complete genome sequence of the gram-positive bacterium *Bacillus*
 RT *subtilis*.";
 RL Nature 390:249-256(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-168;
 RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: 299114; CAB13949.1; -
 KM Complete proteome.
 SQ SEQUENCE 72 AA: 8382 MW: 11178AF395985ED8 CRC64;

Query Match 77.8%; Score 35; DB 16; Length 72;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 FVHRP 8
 |||||
 Db 60 FVHRP 65

RESULT 6
 P96402 PRELIMINARY; PRT; 403 AA.
 AC P96402;
 DT 01-MAY-1997 (TRENBLREL. 03, Created)
 DT 01-MAY-1997 (TRENBLREL. 03, Last sequence update)
 DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
 DE HYDROTHERMAL 44.3 KDA PROTEIN.
 GN LIPC OR RV0220 OR MTCY08D5.15.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RA MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Horsley T., Jagels K., Kiroh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sultson J.E., Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of *Mycobacterium tuberculosis* from the
 RT complete genome sequence.";
 RL Nature 393:537-544(1998).
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLTERASE/LIPASE FAMILY.
 DR EMBL: 292669; CAB07015.1; -
 DR Tuberculit: RV0220; -
 DR InterPro: IPR000379; Est_lip_chiostc_actsite.
 DR PROSITE: PS00122; CARBOXYLTERASE_B.1; 1.

KW Complete proteome; Hydrolase; Hypothetical protein.
 SQ SEQUENCE 403 AA: 44307 MW: 4FBAB5F1DECC563 CRC64;

Query Match 77.8%; Score 35; DB 16; Length 403;
 Best Local Similarity 85.7%; Pred. No. 53;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RRVHRR 7
 |||||
 Db 125 RRVHRR 131

RESULT 7
 O9VLG3 PRELIMINARY; PRT; 663 AA.
 AC O9VLG3;
 DT 01-MAY-2000 (TRENBLREL. 13, Created)
 DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
 DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
 DE CG18088 PROTEIN.
 GN CG18088.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Matel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svrtskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003623; AAF52729.1; -
 DR FlyBase: FBgn0032082; CG18088.
 DR InterPro: IPR004245; DUF2229.
 DR Pfam: PF02995; DUF2229; 1.

SO SEQUENCE ~ 663 AA; 77363 MW; 135B5E43A61591B2 CRC64;

Query Match 77.8%; Score 35; DB 5; Length 663;
Best Local Similarity 75.0%; Pred. No. 86;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RRFVHRR 8
Db 369 KRFVHRR 376

RESULT 8

09JYH1 PRELIMINARY; PRT; 80 AA.
AC 09JYH1;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE HYPOTHETICAL PROTEIN NMB1589.
GN NMB1589.
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / SEROGROUP B;
RA MEDLINE=20175755; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gwin M.L., Deboy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Clecko A., Parksey D.S., Blair E., Ciftci H., Clark E.B.,
RA Cotton M.D., Utechtack T.R., Khouri H., Qin H., Vamathevan J.,
RA Gill J., Scarlato V., Maignani V., Pizsa M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappelli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
MC58.";
RL Science 287:1809-1815(2000).
DR EMBL; AEO02509; AAF41942.1; -.
DR TIGR; NMB1589; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 80 AA; 9395 MW; 8FBC5E79AB29DCEA CRC64;

Query Match 75.6%; Score 34; DB 16; Length 80;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRFVHRR 7
Db 63 KRFVHRR 69

RESULT 9

093PZ8 PRELIMINARY; PRT; 183 AA.
AC 093PZ8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE RSP.
GN RSP.
OS Pseudomonas fluorescens.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
NCBI_TaxID=294;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SBW25;
RA "Type III secretion in plant growth-promoting Pseudomonas fluorescens
SBW25.";

RL MOL. Microbiol. 0:0-0(2001).
DR EMBL; AF292566; AAK81917.1; -.
SQ SEQUENCE 183 AA; 21443 MW; 47589E431FBE866 CRC64;

Query Match 75.6%; Score 34; DB 2; Length 183;
Best Local Similarity 71.4%; Pred. No. 39;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRFVHRR 7
Db 31 RRFVHRR 37

RESULT 10

095TP9 PRELIMINARY; PRT; 217 AA.
AC 095TP9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE ID31286P.
GN RPS6.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Y, CN BW SP;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Fartan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nuncio J., Paclob J., Paragas V., Park S., Phuanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celisier S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY058620; AAL13849.1; -.
SQ SEQUENCE 217 AA; 24696 MW; C2081AE009A2DD8E CRC64;

Query Match 75.6%; Score 34; DB 5; Length 217;
Best Local Similarity 87.5%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RRFVHRR 8
Db 123 RRFVHRR 130

RESULT 11

09VRG7 PRELIMINARY; PRT; 243 AA.
AC 09VRG7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE CG1696 PROTEIN.
GN CG1696.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celisier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,

RA Abn K.H., Doyle C., Baxter E.G., Holt G., Nelson C.R., Miklos G.L.G.,
RA Mavr J.F., Agbayanl A., An H.-J., Andrews-Pearnkoob C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.I., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borckova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Butris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cusley S., Dahlke C., Davenport L.B., Davies P.,
RA de Palacios B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.,
RA Dodson K., Doup L.E., Downes M., Durzan-Rocha S., Dunkov B.C., Dunn P.,
RA Dublin K.J., Evangelista C.C., Feiraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.D., Harvey D., Heyman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwa C.,
RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mekulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacel J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puti V., Reese M.G.,
RA Reinelt K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Svirker E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svalistas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodgate T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C. ;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
DR EMBL: AEO03568; AAF50833.1; -
DR FLYBase: FBgn0031173; CG1966.
DR InterPro: IPR004274; NIF.
DR Pfam: PF03031; NIF.1.
SQ SEQUENCE 243 AA; 28486 MW; 1E278DD1DB8DF60C6 CRC64;

Query Match	75.68;	Score 34;	DB 4;	Length 244;
Best Local Similarity	75.08;	Pred. No. 51;		
Matches	6;	Conservative	1;	Mismatches 1;
				Indels 0;
				Gaps 0;

13

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no sapiens
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31 TaxID=96

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3L; BC00929

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6, C

1 REVHRRP

05 REVVHKRP

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karyota; Me

31_TaxID=62

SEQUENCE FROM

DLINE=99069

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Science 282:2

SEQUENCE FROM
RAIN-BRISTOL

Walker C.;

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SEQUENCE FROM

erston R.;

omitted (NO

DR EMBL: AC024848; AAK68545.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 254 AA; 27600 MW; 32895C8BDF425785 CRC64;

Query Match 75.6%; Score 34; DB 5; Length 254;
 Best Local Similarity 75.0%; Pred. No. 53;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RRFVHRP 8
 ||| ||:|
 DB 73 RRFVHRP 80

RESULT 15

O9F218 PRELIMINARY; PRT; 322 AA.
 ID O9F218
 AC O9F218;
 DT 01-MAR-2001 (TRENBLREL. 16, Created)
 DT 01-MAR-2001 (TRENBLREL. 16, last sequence update)
 DT 01-DEC-2001 (TRENBLREL. 19, last annotation update)
 DE CYANOPHYCINASE.
 GN CPHB.
 OS Synechococcus elongatus (Thermosynechococcus elongatus).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
 OX NCBI_TaxID=32046;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20408669; PubMed-10951215;
 RA Berg H., Ziegler K., Piotukh K., Baier K., Lockau W.,
 RA Volkermer-Engert R.;
 RT "Biosynthesis of the cyanobacterial reserve polymer multi-L-arginyl-
 RT poly-L-aspartic acid (cyanophycin): Mechanism of the cyanophycin
 RT synthetase reaction studied with synthetic primers.";
 RL Eur. J. Biochem. 267:5561-5570(2000).
 DR EMBL: AJ288949; CAC07986.1; -
 SQ SEQUENCE 322 AA; 35502 MW; 8D319403DA5245B7 CRC64;

Query Match 75.6%; Score 34; DB 2; Length 322;
 Best Local Similarity 71.4%; Pred. No. 67;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 RRFVHRP 8
 ||:|| |
 DB 28 RRFVHRP 34

Search completed: August 15, 2002, 11:57:54
 Job time: 529 sec

PI for creating or preventing streptococcus pneumoniae infection in a
PT subject

[illegible]

PS Claim 6; Page 43; 58pp; English.

XX
 CC AAY0351-54 represent immunogenic peptides which are derived from
 CC a pneumococcal surface adhesion A protein (PsaA). The specification
 CC describes monoclonal antibodies which bind epitopes of the PsaA protein
 CC (e.g present sequence). The peptides can be used in vaccines to prevent
 CC Streptococcus pneumoniae infections. The antibodies of the invention
 CC can also be used to detect S. pneumoniae in a sample or individual.

SQ Sequence 15 AA;

QY 1 TVSRVPTAWAFHGY 15
 Db 1 tvsrvpwafhgy 15

Query Match 100.0%; Score 91; DB 20; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.8e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
 ID ABG05173 standard; Protein: 73 AA.
 XX
 AC ABG05173;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #5164.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN W0200175067-A2.
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR N-PSDB; AAS69360.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 PS Claim 20; SEQ ID No 35532; 103pp; English.

XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations

CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG03077 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 73 AA;

QY 2 VSRVPTAWAFHGY 15
 Db 60 vskipwawpfisy 73

Query Match 51.6%; Score 47; DB 22; Length 73;
 Best Local Similarity 50.0%; Pred. No. 6.3;
 Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

RESULT 3
 ID AAU52411 standard; Protein: 113 AA.
 XX
 AC AAU52411;
 XX
 DT 27-FEB-2002 (first entry)
 XX
 DE Propionibacterium acnes immunogenic protein #13307.
 XX
 KW SAPHO syndrome; synovitis; acne; pustulosis; hyperostosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteophthic; neuroprotectant.
 XX
 OS Propionibacterium acnes.
 XX
 PN W0200181581-A2.
 PD 01-NOV-2001.
 XX
 PF 20-APR-2001; 2001WO-US12865.
 XX
 PR 21-APR-2000; 2000US-199047P.
 PR 02-JUN-2000; 2000US-208841P.
 PR 07-JUL-2000; 2000US-216747P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Skeiky YAM, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
 XX
 DR WPI; 2001-616774/71.
 DR N-PSDB; AAS59554.
 XX
 PT Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris -
 XX
 PS Example 1; SEQ ID No 13606; 1069pp; English.

XX
 CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hyperostosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies

CC specific for *P. acnes* proteins. These antibodies can be used to
CC downregulate expression and activity of *P. acnes* polypeptides and
CC therefore treat *P. acnes* infections. The antibodies may also be used as
CC diagnostic agents for determining *P. acnes* presence, for example, by
CC enzyme linked immunosorbent assay (ELISA).
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at [ftp.wipo.int/pub/published_pct_sequences](ftp:wipo.int/pub/published_pct_sequences).
XX
SQ Sequence 113 AA;

Query Match 50.5%; Score 46; DB 22; Length 113;
Best Local Similarity 58.3%; Pred. No. 14;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 TVSRVPTWMAF 12
| | : || | | | :
Db 27 tcsmpwtpmaw 38

RESULT 4
AAG77743
ID AAG77743 standard; Protein; 84 AA.
XX
AC AAG77743;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen protein SEQ ID NO: 8509.
XX
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW colorectal carcinoma.
XX
OS Homo sapiens.
XX
PN WO200122920-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-US26524.
XX
PR 29-SEP-1999; 99US-0157137.
PR 03-NOV-1999; 99US-0163280.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Birse CE, Rosen CA;
DR WPI; 2001-235357/24.
DR N-PSDB; AAH37150.
XX
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
XX useful for preventing, diagnosing and/or treating colorectal cancers -
XX
XX Claim 11; Page 9762-9763; 9803pp; English.

AAH32943 to AAH37195 and AAG77788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where
CC the proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene
CC therapy and vaccine production. N and P may be used in the prevention,
CC diagnosis and treatment of diseases associated with inappropriate P
CC expression. For example, N and P may be used to treat disorders
CC associated with decreased expression by rectifying mutations or deletions
CC in a patient's genome that affect the activity of P by expressing
CC inactive proteins or to supplement the patient's own production of P.
CC Additionally, N may be used to produce the colon cancer-associated Ps,
CC by inserting the nucleic acids into a host cell and culturing the cell
CC to express the proteins. N and P can be used in the prevention, diagnosis
CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
CC and AAG77789 represent sequences used in the exemplification of the
CC present invention.

CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
CC missing at time of publication, meaning no sequences are present for
CC SEQ ID NO:1027 to 1052, 7921 and 7922.
XX
SQ Sequence 84 AA;

Query Match 49.5%; Score 45; DB 22; Length 84;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6 PWTWMAFH 13
| | | | | | |
Db 63 pwtawxxh 70

RESULT 5
AAG14880
ID AAG14880 standard; Protein; 185 AA.
XX
AC AAG14880;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 14909.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
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Query Match 49.5%; Score 45; DB 21; Length 436;
Best Local Similarity 85.7%; Pred. No. 79;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.
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PD 06-SEP-2000.
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Query Match 49.5%; Score 45; DB 21; Length 454;
Best Local Similarity 85.7%; Pred. No. 82;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 PWTAAE 12
Db 32 pwtaway 38

RESULT 9
AAGS2038
ID AAGS2038 standard; Protein; 463 AA.

XX AAGS2038;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 66107.

KW Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;

KW termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

PR 09-MAR-1999; 99US-0123180.

PR 05-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 16-APR-1999; 99US-0128714.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 28-APR-1999; 99US-0130891.

PR 30-APR-1999; 99US-0131449.

PR 04-MAY-1999; 99US-0132407.

PR 05-MAY-1999; 99US-0132484.

PR 06-MAY-1999; 99US-0132485.

PR 06-MAY-1999; 99US-0132486.

PR 07-MAY-1999; 99US-0132487.

PR 11-MAY-1999; 99US-0132863.

PR 14-MAY-1999; 99US-0134218.

PR 14-MAY-1999; 99US-0134219.

PR 14-MAY-1999; 99US-0134221.

PR 18-MAY-1999; 99US-0134370.

PR 19-MAY-1999; 99US-0134768.

PR 20-MAY-1999; 99US-0134941.

PR 20-MAY-1999; 99US-0135124.

PR 21-MAY-1999; 99US-0135353.

PR 24-MAY-1999; 99US-0135629.

PR 25-MAY-1999; 99US-0136021.

PR 27-MAY-1999; 99US-0136392.

PR 28-MAY-1999; 99US-0136782.

PR 01-JUN-1999; 99US-0137222.

PR 03-JUN-1999; 99US-0137528.

PR 04-JUN-1999; 99US-0137502.

PR 07-JUN-1999; 99US-0137724.

PR 08-JUN-1999; 99US-0138094.

PR 10-JUN-1999; 99US-0138540.

PR 10-JUN-1999; 99US-0138847.

PR 14-JUN-1999; 99US-0139119.

PR 16-JUN-1999; 99US-0139452.

PR 16-JUN-1999; 99US-0139453.

PR 17-JUN-1999; 99US-0139492.

PR 18-JUN-1999; 99US-0139454.

PR 18-JUN-1999; 99US-0139455.

PR 18-JUN-1999; 99US-0139456.

PR 18-JUN-1999; 99US-0139457.

PR 18-JUN-1999; 99US-0139458.

PR 18-JUN-1999; 99US-0139459.

PR 18-JUN-1999; 99US-0139460.

PR 18-JUN-1999; 99US-0139461.

PR 18-JUN-1999; 99US-0139462.

PR 18-JUN-1999; 99US-0139463.

PR 18-JUN-1999; 99US-0139750.

PR 18-JUN-1999; 99US-0139763.

PR 21-JUN-1999; 99US-0139817.

PR 22-JUN-1999; 99US-0139899.

PR 23-JUN-1999; 99US-0140353.

PR 23-JUN-1999; 99US-0140354.

PR 24-JUN-1999; 99US-0140695.

PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140961.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145591.
PR 27-JUL-1999; 99US-0145591.
PR 27-JUL-1999; 99US-0145591.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149902.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151066.
PR 30-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.

PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 49.5%; Score 45; DB 21; Length 463;
Best Local Similarity 85.7%; Pred. No. 84;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PWTAMAF 12
|||||:
Db 32 pwtaway 38

RESULT 10
ABG28607
ID ABG28607 standard; Protein; 21 AA.
XX
AC ABG28607;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #28598.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX Homo sapiens.
OS
XX
PN W0200175067-A2.
XX
PD 11-OCT-2001.
XX

PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI: 2001-639362/73.
 DR N-PSDB: AAS92794.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity
 XX
 PS Claim 20; SEQ ID No 58966; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 SQ Sequence 21 AA;

Query Match 48.4%; Score 44; DB 22; Length 21;
 Best Local Similarity 35.7%; Pred. No. 4.8;
 Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 2 VSRVPTANAFHG 15
 : : : : :
 Db 8 lylklpwavvsfsqy 21

RESULT 11
 ABG04577
 ID ABG04577 standard; Protein; 395 AA.
 XX
 AC ABG04577;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #4568.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.

XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI: 2001-639362/73.
 DR N-PSDB: AAS68764.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity
 XX
 PS Claim 20; SEQ ID No 34936; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 SQ Sequence 395 AA;

Query Match 48.4%; Score 44; DB 22; Length 395;
 Best Local Similarity 66.7%; Pred. No. 1e+02;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 6 PWTAMAFHG 14
 : : : : :
 Db 386 pwtlwaifqg 394

RESULT 12
 AAR37442
 ID AAR37442 standard; Protein; 602 AA.
 XX
 AC AAR37442;
 XX
 DT 06-OCT-1993 (first entry)
 XX
 DE Full-length human pseudocholesterase.
 XX
 KW butylcholinesterase; acylcholine acylhydrolase; EC3.1.1.8; psi-CHE;
 KW pseudo-CHE; neurotransmitter; organophosphorus insecticide; OP-poison;
 KW antidote.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FH Peptide
 FT Modified-site
 FT Location/Qualifiers
 FT 1..24
 FT /note= "putative leader peptide"
 FT 45..47
 FT /note= "potential N-glycosylation site"

FT Modified-site 134..136
 FT /note= "potential N-glycosylation site"
 FT Modified-site 269..271
 FT /note= "potential N-glycosylation site"
 FT Modified-site 284..286
 FT /note= "potential N-glycosylation site"
 FT Modified-site 369..371
 FT /note= "potential N-glycosylation site"
 FT Modified-site 509..511
 FT /note= "potential N-glycosylation site"
 FT Modified-site 514..516
 FT /note= "potential N-glycosylation site"
 FT Active-site 226
 FT /note= "active site Serine"
 XX US5215909-A.
 XX
 XX PD 01-JUN-1993.
 XX
 XX PE 18-JUN-1986; 86US-0875737.
 XX
 XX PR 18-JUN-1986; 86US-0875737.
 XX PR 21-AUG-1987; 87US-0087724.
 XX PR 15-AUG-1990; 90US-0572911.
 XX
 XX PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 XX PI Scoreq H;
 XX
 XX DR WPI: 1993-188509/23.
 XX DR N-PSDB; AAQ42496.
 XX
 XX PT Recombinant human gene encoding human pseudo-cholinesterase -
 XX PT used to treat organo-phosphorus poisoning
 XX
 XX PS Disclosure; Columns 35-40; 34pp; English.
 XX
 XX CC A cDNA library prepared from foetal brain mRNA was screened with
 XX CC degenerate probe pools based on the organophosphorus binding site of
 XX CC cholinesterases. A 764 nucleotide insert (designated FBChE12) was
 XX CC isolated from one positive clone and sequenced. This insert (AAQ42495),
 XX CC containing an ORF large enough to code for about half the subunit
 XX CC size of human cholinesterase, was used as a probe to obtain the full-
 XX CC length pseudocholinesterase sequence (AAQ42496).
 XX
 XX SQ Sequence 602 AA;
 XX
 XX
 XX Query Match 48.4%; Score 44; DB 14; Length 602;
 XX Best Local Similarity 46.7%; Pred. No. 1.5e+02;
 XX Matches 7; Conservative 2; Mismatches 4; Indels 2; Gaps 1;
 XX
 XX QY 3 SRVPWTAN-AFHGX 15
 XX 1::11 1 111
 XX Db 454 sklpewmgywhgy 468
 XX
 XX RESULT 13
 XX ID AAY44573 standard; Protein; 602 AA.
 XX
 XX AC AAY44573;
 XX
 XX DT 04-APR-2000 (first entry)
 XX
 XX DE Human wild type Butyrylcholinesterase (BChE) protein.
 XX
 XX KW Butyrylcholinesterase; BChE allele; neurological disease; treatment;
 XX KW therapy; allelic variant; BChE-K; apoE4 allele; neurofibromatosis;
 XX KW non-AD neurological disease; Alzheimer's disease; Huntington's disease;
 XX KW depression; amyotrophic lateral sclerosis; multiple sclerosis; stroke;
 XX KW Parkinson's disease; multi-infarct dementia; human.
 XX

OS Homo sapiens.
 XX
 XX PN WO9966072-A2.
 XX
 XX PD 23-DEC-1999.
 XX
 XX PF 16-JUN-1999; 99WO-IB01298.
 XX
 XX PR 16-JUN-1998; 98US-0089406.
 XX
 XX PA (NOVA-) NOVA MOLECULAR INC.
 XX
 XX PI Seviigny P, Wiedusch H, Schappert K;
 XX
 XX DR WPI: 2000-126550/11.
 XX DR N-PSDB; AAZ49470.
 XX
 XX PT Prediction of drug efficacy for treating neurological diseases like
 XX PT Alzheimer's disease, neurofibromatosis, Huntington's disease -
 XX
 XX PS Example 1; Fig 3; 37pp; English.
 XX
 XX CC The present sequence is the wild type human butyrylcholinesterase (BChE)
 XX CC protein. Determining BChE allele status of a patient helps predicting
 XX CC risk for neurological diseases' efficacy of therapy and determining
 XX CC treatment protocol. Presence of BChE allelic variant, BChE-K and
 XX CC apoE4 allele indicate patient's risk for having a neurological
 XX CC disease. This method enables treating Alzheimer's disease, depression,
 XX CC neurofibromatosis, Huntington's disease, amyotrophic lateral sclerosis,
 XX CC multiple sclerosis, stroke, Parkinson's disease, multi-infarct dementia
 XX CC and other non-AD neurological diseases.
 XX
 XX SQ Sequence 602 AA;
 XX
 XX
 XX Query Match 48.4%; Score 44; DB 21; Length 602;
 XX Best Local Similarity 46.7%; Pred. No. 1.5e+02;
 XX Matches 7; Conservative 2; Mismatches 4; Indels 2; Gaps 1;
 XX
 XX QY 3 SRVPWTAN-AFHGX 15
 XX 1::11 1 111
 XX Db 454 sklpewmgywhgy 468
 XX
 XX RESULT 14
 XX ID AAY44574 standard; Protein; 602 AA.
 XX
 XX AC AAY44574;
 XX
 XX DT 04-APR-2000 (first entry)
 XX
 XX DE Human Butyrylcholinesterase-K (BChE-K) protein.
 XX
 XX KW Butyrylcholinesterase-K; BChE-K; BChE allele; neurological disease;
 XX KW therapy; treatment; allelic variant; apoE4 allele; neurofibromatosis;
 XX KW non-AD neurological disease; Alzheimer's disease; Huntington's disease;
 XX KW depression; amyotrophic lateral sclerosis; multiple sclerosis; stroke;
 XX KW Parkinson's disease; multi-infarct dementia; human.
 XX
 XX OS Homo sapiens.
 XX
 XX FH Key Location/Qualifiers
 XX FT Misc-difference 567 /note= "Wild type Ala replaced with Thr"
 XX
 XX PN WO9966072-A2.
 XX
 XX PD 23-DEC-1999.
 XX
 XX PF 16-JUN-1999; 99WO-IB01298.
 XX
 XX PR 16-JUN-1998; 98US-0089406.
 XX

XX (NOVA-) NOVA MOLECULAR INC.
XX
XX
PI Sevigny P, Wiebusch H, Schappert K;
XX
XX WPI: 2000-126550/11.
DR N-PSDB; AA249471.
XX
XX
PT Prediction of drug efficacy for treating neurological diseases like
PT Alzheimer's disease, neurofibromatosis, Huntington's disease -
XX
XX
XX Disclosure: Fig 4; 37pp; English.
XX
XX The present sequence is the human polymorphic variant
CC butyrylcholinesterase-K (BChE-K) protein. BChE-K is an allelic variant
CC of BChE. Determining BChE allele status (homozygous or heterozygous) of a
CC patient helps predicting risk of neurological diseases, efficacy of
CC therapy and determining treatment protocol. BChE-K and apoE4 allele
CC status also indicate patient's risk for having a neurological disease.
CC This method enables treating Alzheimer's disease, Huntington's disease,
CC depression, neurofibromatosis, amyotrophic lateral sclerosis, stroke,
CC multiple sclerosis, Parkinson's disease, multi-infarct dementia and
CC other non-AD neurological diseases.
XX
XX
SQ Sequence 602 AA;

Query Match 48.4%; Score 44; DB 21; Length 602;
Best Local Similarity 46.7%; Pred. No. 1.5e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 2; Gaps 1;
QY 3 SRVPTAW--AFHG 15
1::||| 1 |||
DB 454 sklpwemgmymhy 468

RESULT 15
AAV49471
ID AAV49471 standard; protein; 602 AA.
XX
XX AAV49471;
AC
XX
XX 27-MAR-2000 (first entry)
DT
XX
XX Human wild-type butyryl cholinesterase (BChE).
DE
XX
XX Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;
KW butyrylcholinesterase; BChE; carboxylesterase; CAE; sheep dip; human;
KW nerve agent; organophosphorus acid anhydride; OPAA.
XX
XX Homo sapiens.
OS
XX
XX US6001625-A.
PN
XX
XX 14-DEC-1999.
PD
XX
XX 19-MAY-1995; 95US-0446100.
PE
XX
XX 19-MAY-1995; 95US-0446100.
PR
XX
XX (USSA) US SEC OF ARMY.
PA
XX
XX Broomfield CA, Lockridge O, Millard CB;
PI
XX
XX WPI: 2000-096137/08.
DR
XX
XX
PT Enhancing the organophosphate detoxifying capabilities of esterases for
PT the treatment of organophosphate poisoning -
XX
XX
PS Disclosure; Columns 3-4; 64pp; English.
XX
XX The invention provides a method of enhancing organophosphate detoxifying
CC capabilities of esterases (either human acetylcholinesterases (AChE),

CC human butyrylcholinesterases (BChE) and/or carboxylesterases (CAE),
CC that comprises substituting a histidine residue for 1 or more amino
CC acid(s) within 6 Angstrom of an active site serine. The method may be
CC used for enhancing organophosphate detoxifying capabilities of esterases
CC (either human AChE, human BChE and/or human CAE). The modified esterases
CC may then be used to treat agricultural workers poisoned with
CC organophosphates through contact with chemical such as sheep dips. They
CC may also be used to treat military personnel contaminated by chemical
CC weaponry such as nerve agents. Additionally, the esterases may also be
CC used to decontaminate ground and buildings and equipment used to store,
CC or contaminated by organophosphates. The method produces esterases with
CC improved detoxification properties over naturally occurring
CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
CC less likely to be inactivated by the OPAA.
XX
XX
SQ Sequence 602 AA;

Query Match 48.4%; Score 44; DB 21; Length 602;
Best Local Similarity 46.7%; Pred. No. 1.5e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 2; Gaps 1;
QY 3 SRVPTAW--AFHG 15
1::||| 1 |||
DB 454 sklpwemgmymhy 468

Search completed: August 15, 2002, 11:38:24
Job time: 265 sec

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OM protein - protein search, using sw model

Run on: August 15, 2002, 11:34:34 ; Search time 26.88 Seconds
(without alignments)
13.630 Million cell updates/sec

Title: US-09-613-092A-5
Perfect score: 91
Sequence: 1 TVSRPWTAWAFHG 15

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	48.4	572	6 5200183-5	Patent No. 5200183
2	44	48.4	573	6 5215909-12	Patent No. 5215909
3	44	48.4	602	3 US-08-446-100-1	Sequence 1, Appl
4	44	48.4	602	3 US-08-446-100-2	Sequence 2, Appl
5	44	48.4	602	3 US-08-446-100-3	Sequence 3, Appl
6	44	48.4	602	3 US-08-446-100-4	Sequence 4, Appl
7	44	48.4	602	3 US-08-446-100-5	Sequence 5, Appl
8	44	48.4	602	3 US-08-446-100-6	Sequence 6, Appl
9	44	48.4	602	3 US-08-446-100-7	Sequence 7, Appl
10	44	48.4	602	3 US-08-446-100-8	Sequence 8, Appl
11	44	48.4	602	3 US-08-446-100-9	Sequence 9, Appl
12	44	48.4	602	3 US-08-446-100-10	Sequence 10, Appl
13	44	48.4	602	3 US-08-446-100-11	Sequence 11, Appl
14	44	48.4	602	3 US-08-446-100-12	Sequence 12, Appl
15	44	48.4	602	3 US-08-446-100-13	Sequence 13, Appl
16	44	48.4	602	3 US-08-446-100-14	Sequence 14, Appl
17	44	48.4	602	3 US-08-446-100-15	Sequence 15, Appl
18	44	48.4	602	3 US-08-446-100-16	Sequence 16, Appl
19	44	48.4	602	3 US-08-446-100-17	Sequence 17, Appl
20	44	48.4	602	3 US-08-446-100-18	Sequence 18, Appl
21	44	48.4	602	3 US-08-446-100-19	Sequence 19, Appl
22	44	48.4	602	4 US-09-334-489-3	Sequence 24, Appl
23	44	48.4	602	4 US-09-334-489-4	Sequence 3, Appl
24	44	48.4	602	4 US-09-334-489-5	Sequence 4, Appl
25	44	48.4	635	6 5215909-10	Patent No. 5215909
26	42	46.2	171	4 US-08-611-587-5	Sequence 5, Appl
27	42	46.2	761	1 US-07-906-395-2	Sequence 2, Appl

28	42	46.2	761	1 US-08-192-632-2	Sequence 2, Appl
29	42	46.2	761	1 US-08-710-676-2	Sequence 2, Appl
30	42	46.2	761	3 US-09-099-902B-2	Sequence 2, Appl
31	42	46.2	761	5 PCT-US93-06080-2	Sequence 2, Appl
32	40	44.0	1038	4 US-08-334-179A-10	Sequence 10, Appl
33	40	44.0	1038	4 US-08-334-179A-8	Sequence 8, Appl
34	39	42.9	53	2 US-08-799-173A-13	Sequence 13, Appl
35	39	42.9	55	1 US-07-862-021B-20	Sequence 20, Appl
36	39	42.9	55	5 PCT-US93-03164-20	Sequence 20, Appl
37	39	42.9	807	1 US-07-862-021B-10	Sequence 10, Appl
38	39	42.9	807	1 US-08-313-288B-10	Sequence 10, Appl
39	39	42.9	807	5 PCT-US93-03164-10	Sequence 10, Appl
40	39	42.9	984	4 US-09-287-354-2	Sequence 2, Appl
41	39	42.9	1189	4 US-09-287-354-3	Sequence 3, Appl
42	39	42.9	1189	4 US-09-287-354-4	Sequence 4, Appl
43	38	41.8	22	1 US-08-178-708-2	Sequence 2, Appl
44	38	41.8	22	1 US-08-457-552-2	Sequence 2, Appl
45	38	41.8	22	1 US-08-456-430-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
5200183-5
; Patent No. 5200183
; APPLICANT: TANG, JORDAN J.N.; RANG, CHI-SUN
; TITLE OF INVENTION: RECOMBINANT BLUE SALT ACTIVATED LIPASES
; NUMBER OF SEQUENCES: 22
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/537,426
; FILING DATE: 12-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 504,635
; FILING DATE: 04-APR-1990
; APPLICATION NUMBER: 122,410
; FILING DATE: 19-NOV-1987
; SEQ ID NO:5
; LENGTH: 572
5200183-5

Query Match 48.4%; Score 44; DB 6; Length 572;
Best Local Similarity 46.7%; Pred. No. 53;
Matches 7; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY 3 SRVPWTAW-AFHGY 15
Db 424 SKLPWPMGVMHG 438

RESULT 2
5215909-12
; Patent No. 5215909
; APPLICANT: SOREO, HERMONA
; TITLE OF INVENTION: HUMAN CHOLINESTERASE GENES
; NUMBER OF SEQUENCES: 13
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/572,911
; FILING DATE: 15-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 87,724
; FILING DATE: 21-AUG-1987
; APPLICATION NUMBER: 875,737
; FILING DATE: 18-JUN-1986
; SEQ ID NO:12
; LENGTH: 573
5215909-12

Query Match 48.4%; Score 44; DB 6; Length 573;
Best Local Similarity 46.7%; Pred. No. 53;
Matches 7; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY 3 SRVPMWTAW--AFHGY 15
|:|:| |
Db 427 SKLPWPMWGMVGHGY 441

RESULT 3
US-08-446-100-1
; Sequence 1, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
; US-08-446-100-1

Query Match 48.4%; Score 44; DB 3; Length 602;
Best Local Similarity 46.7%; Pred. No. 56;
Matches 7; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY 3 SRVPMWTAW--AFHGY 15
|:|:| |
Db 454 SKLPWPMWGMVGHGY 468

RESULT 4
US-08-446-100-2
; Sequence 2, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
; US-08-446-100-2

Query Match 48.4%; Score 44; DB 3; Length 602;
Best Local Similarity 46.7%; Pred. No. 56;
Matches 7; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY 3 SRVPMWTAW--AFHGY 15
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Db 454 SKLPWPMWGMVGHGY 468

RESULT 5
US-08-446-100-3
; Sequence 3, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435


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; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
; US-08-446-100-3

Query Match 48.4%; Score 44; DB 3; Length 602;
Best Local Similarity 46.7%; Pred. No. 56;
Matches 7; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY 3 SRVPTAW--AFHGY 15
Db 454 SKLPPEMGMVGHGY 468

RESULT 6
US-08-446-100-4
; Sequence 4, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
; US-08-446-100-5
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; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
; US-08-446-100-4

Query Match 48.4%; Score 44; DB 3; Length 602;
Best Local Similarity 46.7%; Pred. No. 56;
Matches 7; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY 3 SRVPTAW--AFHGY 15
Db 454 SKLPPEMGMVGHGY 468

RESULT 7
US-08-446-100-5
; Sequence 5, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
; US-08-446-100-5

Query Match 48.4%; Score 44; DB 3; Length 602;
Best Local Similarity 46.7%; Pred. No. 56;
Matches 7; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY 3 SRVPTAW--AFHGY 15
Db 454 SKLPPEMGMVGHGY 468

RESULT 8
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US-08-446-100-6
; Sequence 6, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: Broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
;
US-08-446-100-6

Query Match      48.4%; Score 44; DB 3; Length 602;
Best Local Similarity 46.7%; Pred. No. 56;
Matches 7; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY      3 SRPWTAW-AFHGY 15
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Db      454 SKLPWPMWGMVHGXY 468

RESULT      9
US-08-446-100-7
; Sequence 7, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
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COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: Broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
;
US-08-446-100-7

Query Match      48.4%; Score 44; DB 3; Length 602;
Best Local Similarity 46.7%; Pred. No. 56;
Matches 7; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY      3 SRPWTAW-AFHGY 15
       |::||| | |||
Db      454 SKLPWPMWGMVHGXY 468

RESULT      10
US-08-446-100-8
; Sequence 8, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: Broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
```


;; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
;; NUMBER OF SEQUENCES: 31
;; CORRESPONDENCE ADDRESSES:
;; ADDRESSEE: Hendricks and Assoc.
;; STREET: 9669 A Main Street, P.O. Box 2509
;; CITY: Fairfax
;; STATE: VA
;; COUNTRY: US
;; ZIP: 22031
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentln Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/446,100
;; FILING DATE: 19-MAY-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hendricks, Glenna
;; REGISTRATION NUMBER: 32,535
;; REFERENCE/DOCKET NUMBER: broomfield
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 425-4250
;; TELEFAX: (703) 425-2767
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 602 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: YES
;; ANTI-SENSE: YES
;; FRAGMENT TYPE: N-terminal
;; ORIGINAL SOURCE:
;; ORGANISM: human esterases
;; US-08-446-100-11

Query Match 48.4%; Score 44; DB 3; Length 602;
Best Local Similarity 46.7%; Pred. No. 56;
Matches 7; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY 3 SRVPTAW-AFHGY 15
|::||| | |||
Db 454 SKLPPEWVGVMHGY 468

RESULT 14
US-08-446-100-12
; Sequence 12, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100

;; FILING DATE: 19-MAY-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hendricks, Glenna
;; REGISTRATION NUMBER: 32,535
;; REFERENCE/DOCKET NUMBER: broomfield
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 425-4250
;; TELEFAX: (703) 425-2767
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 602 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: YES
;; ANTI-SENSE: YES
;; FRAGMENT TYPE: N-terminal
;; ORIGINAL SOURCE:
;; ORGANISM: human esterases
;; US-08-446-100-12

Query Match 48.4%; Score 44; DB 3; Length 602;
Best Local Similarity 46.7%; Pred. No. 56;
Matches 7; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY 3 SRVPTAW-AFHGY 15
|::||| | |||
Db 454 SKLPPEWVGVMHGY 468

RESULT 15
US-08-446-100-13
; Sequence 13, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein

```
;
;   HYPOTHETICAL: YES
;   ANTI-SENSE: YES
;   FRAGMENT TYPE: N-terminal
;   ORIGINAL SOURCE:
;   ORGANISM: human esterases
US-08-446-100-13
```

```
Query Match      48.4%; Score 44; DB 3; Length 602;
Best Local Similarity 46.7%; Pred. No. 56;
Matches 7; Conservative 2; Mismatches 4; Indels 2; Gaps 1;
```

```
Qy      3 SRVPTAW--AFHGY 15
      1::| | | | |
Db      454 SKLPPEPMGVHGY 468
```

```
Search completed: August 15, 2002, 11:38:58
Job time: 264 sec
```

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 11:36:19 ; Search time 35.58 Seconds
(without alignments)
40.510 Million cell updates/sec

Title: US-09-613-092a-5
Perfect score: 91
Sequence: 1 TVSRVPMWTAMAFHG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR-71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	49.5	278	2	hypothetical prote
2	45	49.5	454	2	P9L1.4 protein - A
3	45	49.5	537	2	hypothetical prote
4	44	48.4	350	2	probable membrane
5	44	48.4	581	2	cholinesterase (EC
6	44	48.4	602	1	cholinesterase (EC
7	44	48.4	603	2	cholinesterase (EC
8	43.5	47.8	310	2	hypothetical prote
9	43.5	47.8	457	2	probable NAM-1-like
10	43	47.3	302	2	hypothetical prote
11	43	47.3	351	2	hypothetical prote
12	43	47.3	441	2	hypothetical prote
13	43	47.3	505	2	hypothetical prote
14	43	47.3	505	2	probable two compo
15	43	47.3	658	2	sensor histidine k
16	43	47.3	722	2	endoglucanase 3 (E
17	43	47.3	1120	2	hypothetical prote
18	42	46.2	142	2	DNM-directed RNA p
19	42	46.2	247	2	tapetum-specific p
20	42	46.2	297	2	conserved hypothet
21	42	46.2	299	2	hypothetical prote
22	42	46.2	317	2	hypothetical prote
23	42	46.2	650	2	hypothetical prote
24	42	46.2	651	2	probable amine oxi
25	42	46.2	656	2	conserved hypothet
26	42	46.2	656	2	hypothetical prote
27	42	46.2	666	1	hypothetical prote
28	42	46.2	750	2	MG032 homolog B01_
29	42	46.2	750	2	cation-transportin
30	42	46.2	750	2	cation-transportin

30	42	46.2	752	2	G70751	probable ctbp prot
31	42	46.2	761	2	D70750	probable ctbp prot
32	42	46.2	766	2	F87157	probable cation-tr
33	42	46.2	780	2	S77652	cation-transportin
34	41	45.1	232	2	T08513	trbp protein - Ent
35	41	45.1	461	2	T25671	hypothetical prote
36	41	45.1	543	2	T27000	hypothetical prote
37	41	45.1	602	2	T37254	acetylcholinestera
38	41	45.1	1263	2	AH2011	heterocyst glycoli
39	40	44.0	155	2	AB1226	hypothetical prote
40	40	44.0	155	2	AD1579	hypothetical prote
41	40	44.0	200	2	F70900	hypothetical prote
42	40	44.0	242	2	A43904	homeotic protein G
43	40	44.0	277	2	B88690	protein F41H0.5 [
44	40	44.0	353	2	S37873	hypothetical prote
45	40	44.0	379	2	S27502	hypothetical prote

ALIGNMENTS

RESULT 1
S46681
hypothetical protein YHR192w - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein H9998.8
C:Species: Saccharomyces cerevisiae
C>Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 23-Mar-2001
C:Accession: S46681
R:Macri, C.
Submitted to the EMBL Data Library, February 1994
A:Description: The sequence of S. cerevisiae cosmid 9998.
A:Reference number: S46674
A:Accession: S46681
A:Molecule type: DNA
A:Residues: 1-278 <MAC>
A:Cross-references: EMBL:U00030; NID:g458927; PIDN:AAB68359.1; PID:g458933; MIPS:YHR1
C:Genetics:
A:Map position: 8R
C:Keywords: transmembrane protein

Query Match 49.5% Score 45; DB 2; Length 278;
Best Local Similarity 46.7% Pred. No. 20;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 TVSRVPMWTAMAFHG 15
|| : : || : |||
Db 62 TVLALSYTYMEYHG 76

RESULT 2
G86284
P9L1.4 protein - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 27-Nov-2001
C:Accession: G86284
R:Thelouis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Hultzar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malt, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.M.
A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: G86284
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-454 <STO>
A:Cross-references: GB:AE005172; NID:g5103809; PIDN:AAD39639.1; GSPDB:GN00141
C:Genetics:

A;Map position: 1

Query Match 49.5%; Score 45; DB 2; Length 454;
Best Local Similarity 85.7%; Pred. No. 32;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 PWTAMAF 12
| | | | |
Db 32 PWTAMAY 38

RESULT 3

hypothetical protein F13112.30 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C;Accession: T45634
R;Choisne, N.; Robert, C.; Brotlier, P.; Wincker, P.; Catolico, L.; Artiguenave, F.; Sa
submitted to the Protein Sequence Database, November 1999
A;Reference number: Z23010
A;Accession: T45634
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1537 <CHO>
A;Cross-references: EMBL:AL133292
A;Experimental source: cultivar Columbia; BAC clone F13112
C;Genetics:
A;Map position: 3
A;Introns: 35/2; 153/3; 229/2; 350/3; 399/3; 445/3; 457/1
A;Note: F13112.30

Query Match 49.5%; Score 45; DB 2; Length 537;
Best Local Similarity 61.5%; Pred. No. 37;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 SRPWTAMAFHG 15
| | | | |
Db 363 SAVPMSMAFRTG 375

RESULT 4

probable membrane protein YNL264c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein N0815
C;Species: Saccharomyces cerevisiae
C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 20-Jun-2000
C;Accession: S60917; S63237; S65119
R;Sen-Gupta, M.; Lyck, R.; Fleig, U.; Niedenthal, R.N.; Hegemann, J.M.
submitted to the EMBL Data Library, October 1995
A;Description: The sequence of a 24152 bp segment from the left arm of chromosome XIV fr
A;Reference number: S60909
A;Accession: S60917
A;Molecule type: DNA
A;Residues: 1-350 <SPN>
A;Cross-references: EMBL:X02494; NID:g1045236; PIDN:CAA63233.1; PID:g1045245
R;Sen-Gupta, M.; Lyck, R.; Niedenthal, R.K.; Fleig, U.N.; Hegemann, J.H.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S63235
A;Accession: S63237
A;Molecule type: DNA
A;Residues: 1-350 <SEM>
A;Cross-references: EMBL:Z71540; NID:g1302320; PIDN:CAA96171.1; PID:g1302321; MIPS:YNL26
A;Experimental source: strain S288C
R;Sen-Gupta, M.; Lyck, R.; Fleig, U.; Niedenthal, R.K.; Hegemann, J.H.
Yeast 12, 505-514, 1996
A;Title: The sequence of a 24 152 bp segment from the left arm of chromosome XIV from Sa
A;Reference number: S65119; MUID:96310631
A;Accession: S65119
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-350 <SEF>

A;Cross-references: EMBL:X02494; NID:g1045236; PIDN:CAA63233.1; PID:g1045245
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995
C;Genetics:
A;Map position: 14L
A;Note: YNL264
C;Superfamily: probable membrane protein YNL264c; cellular retinaldehyde-binding prot
F;6-231/Domain: cellular retinaldehyde-binding protein homology <CRB>
F;239-255/Domain: transmembrane #status predicted <TM>

Query Match 48.4%; Score 44; DB 2; Length 350;
Best Local Similarity 75.0%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 VPWTAMAF 12
| | | | |
Db 247 IPWTAMAF 254

RESULT 5

cholinesterase (EC 3.1.1.8) - rabbit
N;Alternate names: butyrylcholinesterase
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 14-Feb-1992 #sequence_revision 01-Mar-1996 #text_change 20-Jun-2000
C;Accession: S10255; C39768
R;Jbilo, O.; Chatonnet, A.
Nucleic Acids Res. 18, 3990, 1990
A;Title: Complete sequence of rabbit butyrylcholinesterase.
A;Reference number: S10255; MUID:90326526
A;Accession: S10255
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-581 <JBI>
A;Cross-references: EMBL:X52090; NID:g1476; PIDN:CAA36308.1; PID:g1370277
R;Appagaus, M.; Chatonnet, A.; Masson, P.; Newton, M.; Vaughan, T.A.; Bartels, C.F.;
J. Biol. Chem. 266, 6966-6974, 1991
A;Title: Use of the polymerase chain reaction for homology probing of butyrylcholines
A;Reference number: A39768; MUID:91201348
A;Accession: C39768
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 75-215 <ARP>
A;Cross-references: GB:M62779; NID:g164788; PIDN:AAA31169.1; PID:g164789
C;Genetics:
A;Introns: 485/2; 541/1
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; glycoprotein
F;35-535/Domain: cholinesterase homology <CHE>

Query Match 48.4%; Score 44; DB 2; Length 581;
Best Local Similarity 46.7%; Pred. No. 56;
Matches 7; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY 3 SRPWTAM--AFHG 15
| | | | |
Db 433 SKLPPEWGMVHG 447

RESULT 6

ACHU
cholinesterase (EC 3.1.1.8) precursor [validated] - human
N;Alternate names: acylcholine acylhydrolase; butyrylcholinesterase; choline esterase
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 23-Feb-1996 #text_change 08-Dec-2000
C;Accession: A33769; A26613; A33887; A34668; A00772
R;Appagaus, M.; Kott, M.; Vatsis, K.P.; Bartels, C.F.; La Du, B.N.; Lockridge, O.
Biochemistry 29, 124-131, 1990
A;Title: Structure of the gene for human butyrylcholinesterase. Evidence for a single
A;Reference number: A33769; MUID:90212557
A;Accession: A33769


```

A.Molecule type: DNA
A.Residues: 'MSVQSNINQAGAAASCSIPKYYMFTPCKLYHLCRESEIN',1-602 <ARP>
A.Cross-references: GB:W32391; GB:J02879
A.Note: Two ATG codons found upstream of Met-1 do not lie in a favorable context for translation.
R.Prody, C.A.; Zevin-Sonkin, D.; Gnatt, A.; Goldberg, O.; Soreq, H.
Proc. Natl. Acad. Sci. U.S.A. 84, 3555-3559, 1987
A.Title: Isolation and characterization of full-length cDNA clones coding for cholinesterase
A.Reference number: A26613; MUID:87231856
A.Accession: A26613
A.Molecule type: mRNA
A.Residues: 1-133; 'D',135-602 <PRO>
R.McLerran, C.; Adkins, S.; Chatonnet, A.; Vaughan, T.A.; Bartels, C.F.; Kott, M.; Ross
Proc. Natl. Acad. Sci. U.S.A. 84, 6682-6686, 1987
A.Title: Brain cDNA clone for human cholinesterase.
A.Reference number: A33887; MUID:86016155
A.Accession: A33887
A.Molecule type: mRNA
A.Residues: 'MSVQSNINQAGAAASCSIPKYYMFTPCKLYHLCRESEIN',1-602 <MCT>
A.Note: Two ATG codons found upstream of Met-1 do not lie in a favorable context for translation.
R.Nogueira, C.P.; McGulire, M.C.; Graesser, C.; Bartels, C.F.; Arpagaus, M.; Van der Spek,
Am. J. Hum. Genet. 46, 934-942, 1990
A.Title: Identification of a frameshift mutation responsible for the silent phenotype of
A.Reference number: A34668; MUID:90252779
A.Accession: A34668
A.Molecule type: DNA
A.Residues: 143-145; 'VSNMNIPTCL',<NOS>
A.Note: frameshift mutant in codon for residue 145 (Gly)
R.Lockridge, O.; Bartels, C.F.; Vaughan, T.A.; Mong, C.K.; Norton, S.E.; Johnson, L.L.
J. Biol. Chem. 262, 549-557, 1987
A.Title: Complete amino acid sequence of human serum cholinesterase.
A.Reference number: A00772; MUID:87109144
A.Accession: A00772
A.Molecule type: protein
A.Residues: 29-602 <LOC>
A.Experimental source: Plasma
A.Comment: Cholinesterase is present in most cells (except erythrocytes).
C.Genetics:
A.Gene: GDB:BCHE; CHE1
A.Cross-references: GDB:120558; OMIM:177400
A.Map position: 3q26.1-3q26.2
A.Introns: 506/2; 562/1
C.Function:
A.Description: hydrolyzes acylcholines to choline and a carboxylic acid
A.Note: This cholinesterase is highly reactive with organophosphate esters
A.Superfamily: cholinesterase; cholinesterase homology
C.Keywords: carboxylic ester hydrolase; glycoprotein; homotetramer
F.1-28/Domain: signal sequence #status predicted <STG>
F.29-602/Product: cholinesterase #status experimental <MAT>
F.56-556/Domain: cholinesterase homology <CHS>
F.45,85,134,269,284,369,483,505,514/Binding site: carbohydrate (Asn) (covalent) #status
F.226/Active site: Ser #status experimental

```

A:Molecule type: nucleic acid
A:Residues: 1-603 <TAY>
A:Cross-references: EMBL:M994992; NID:G191579; PIDN:AAA37328.1; PID:G191580
R:Rachlinsky, T.L.; Camp, S.; Li, Y.; Ekstroem, T.J.; Newton, M.; Taylor, P.
Neuron 5, 317-327, 1990
A:Title: Molecular cloning of mouse acetylcholinesterase: tissue distribution of altele
A:Reference number: JH0314; MUID:90380429
A:Accession: S15680
A:Status: nucleic acid sequence not shown
A:Molecule type: nucleic acid
A:Residues: 30-128, 'P', 130-603 <RAC>
A:Cross-references: EMBL:M99492
R:Ripagans, M.; Chatonnet, A.; Masson, P.; Newton, M.; Vaughan, T.A.; Bartels, C.F.;
J. Biol. Chem. 266, 6966-6974, 1991
A:Title: Use of the polymerase chain reaction for homology probing of butyrylcholines
A:Reference number: A39768; MUID:91201348
A:Accession: A39768
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 97-128, 'P', 130-237 <ARP>
A:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; glycoprotein
P:57-557/Domain: cholinesterase homology <CHD>

Query Match	48.4%	Score 44	DB 2	Length 603
Best Local Similarity	46.7%	Pred. No. 58		
Matches 7	Conservative	2	Mismatches 4	Indels 2
				Gaps 1
QY	3	SNRPWTAW--AFHCY	15	
DB	455	SKLPWPEWGVNHGY	469	

RESULT 8
T01939
hypothetical protein F1104.5 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 26-Feb-1999 #sequence_rev199 26-Feb-1999 #text_change 24-Mar-1999
C:Accession: T01939
R:Abu-Mhreideh, J.; Stoneking, T.; Langston, Y.; Treweek, E.
submitted to the EMBL Data Library, October 1998
A:Description: The sequence of A. thaliana F1104.
A:Reference number: Z14466
A:Accession: T01939
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-310 <ABU>
A:Cross-references: EMBL:AF096370; NID:g3695372; PID:g3695378
A:Experimental source: cultivar Columbia
C:Genetics:
A:Map position: 4
A:Introns: 28/1; 118/3; 165/3
A>Note: F1104.5

Query Match	47.8%	Score 43.5	DB 2	length 310
Best Local Similarity	53.3%	Prod No. 37		
Matches	8	Conservative	0	Mismatches 4; Indels 3; Gaps 1;
OY	4	RVP---WTAMAFHGY	15	
Db	95	RVPKGVTPVMHGY	109	

RESULT 9
 B85020
 Probable NAM-like protein [imported] - Arabidopsis thaliana
 C.Species: Arabidopsis thaliana (mouse-ear cress)
 C.Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_Change 16-Feb-2001
 C.Accession: B85020
 R.anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, 1999
 Nature 402, 769-777, 1999

A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
 A:Reference number: AB5001; MUID:20083488
 A:Accession: B85020
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-457 <STO>
 A:Cross-references: GB:NC_001268; NID:g7268198; PIDN:CAB77725.1; GSPDB:GND0140
 C:Genetics:
 A:Gene: AT4G01550
 A:Map position: 4

Query Match 47.8%; Score 43.5; DB 2; Length 457;
 Best Local Similarity 53.3%; Pred. No. 53;
 Matches 8; Conservative 0; Mismatches 4; Indels 3; Gaps 1;

QY 4 RVP--WTAMAFHG 15
 ||| ||| |||
 DB 119 RVPKGVTPWVMEHY 133

RESULT 10
 S50579
 hypothetical protein YER076C - yeast (Saccharomyces cerevisiae)
 C:Species: Saccharomyces cerevisiae
 C:Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 23-Mar-2001
 C:Accession: S50579
 R:Dieterich, F.S.
 Submitted to the EMBL Data Library, December 1994
 A:Description: The sequence of S. cerevisiae cosmids 9747, 8198, 9781, and lambda clones
 A:Reference number: S50436
 A:Accession: S50579
 A:Molecule type: DNA
 A:Residues: 1-302 <DIE>
 A:Cross-references: EMBL:U18839; NID:g603313; PID:g603314; GSPDB:GND00005; MIPS:YER076C
 C:Genetics:
 A:Gene: MIPS:YER076C
 A:Map position: 5R

Query Match 47.3%; Score 43; DB 2; Length 302;
 Best Local Similarity 75.0%; Pred. No. 42;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 WTAMAFHG 14
 ||| ||| ||
 DB 180 WVAWAVHG 187

RESULT 11
 S63197
 hypothetical protein YNL231c - yeast (Saccharomyces cerevisiae)
 N:Alternate names: hypothetical protein N1158
 C:Species: Saccharomyces cerevisiae
 C:Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 20-Jun-2000
 C:Accession: S63197; S67367; S72085
 R:Pandolfo, D.; De Antoni, A.; Lanfranchi, G.; Valle, G.
 Submitted to the Protein Sequence Database, April 1996
 A:Reference number: S63188
 A:Accession: S63197
 A:Molecule type: DNA
 A:Residues: 1-351 <PAN>
 A:Cross-references: EMBL:Z71507; NID:g1302256; PIDN:CAA96136.1; PID:g1302257; MIPS:YNL231
 A:Experimental source: strain S288C
 R:Pandolfo, D.; de Antoni, A.; Lanfranchi, G.; Valle, G.
 submitted to the EMBL Data Library, February 1996
 A:Description: DNA sequence of cosmid 14-5 from chromosome XIV.
 A:Reference number: S67355
 A:Accession: S67367
 A:Molecule type: DNA
 A:Residues: 1-351 <PAW>
 A:Cross-references: EMBL:Z69381; NID:g1183970; PIDN:CAA93367.1; PID:g1183983
 R:Pandolfo, D.; de Antoni, A.; Lanfranchi, G.; Valle, G.

Yeast 12, 1071-1076, 1996
 A:Title: The DNA sequence of cosmid 14-5 from chromosome XIV reveals 21 open reading
 A:Reference number: S72073; MUID:97051596
 A:Accession: S72085
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-351 <PAF>
 A:Cross-references: EMBL:Z69381; NID:g1183970; PIDN:CAA93367.1; PID:g1183983
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
 C:Genetics:
 A:Map position: 14L
 A:Note: YNL231c
 C:Superfamily: probable membrane protein YNL264c; cellular retinaldehyde-binding prot
 F:g1-289/Domain: cellular retinaldehyde-binding protein homology <CRB>

Query Match 47.3%; Score 43; DB 2; Length 351;
 Best Local Similarity 45.5%; Pred. No. 49;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 VSRVPWTAMAF 12
 :: ||| |||
 DB 242 LTNPMLATWF 252

RESULT 12
 G83212
 hypothetical protein PA3464 [imported] - Pseudomonas aeruginosa (strain PA01)
 C:Species: Pseudomonas aeruginosa
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C:Accession: G83212
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
 .; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
 A:Reference number: AB2950; MUID:20437337
 A:Accession: G83212
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-441 <STO>
 A:Cross-references: GB:AE004767; GB:AE004091; NID:g9949604; PIDN:AAG06852.1; GSPDB:GN
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA3464

Query Match 47.3%; Score 43; DB 2; Length 441;
 Best Local Similarity 85.7%; Pred. No. 60;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 PWTAMAF 12
 ||||| |
 DB 144 PWTAMRF 150

RESULT 13
 AB1806
 probable two component sensor kinase NMA1803 [imported] - Neisseria meningitidis (str
 C:Species: Neisseria meningitidis
 C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
 C:Accession: AB1806
 R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo
 ; Holroyd, S.; Jørgensen, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre
 Nature 404, 502-506, 2000
 A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491
 A:Reference number: AB1775; MUID:20222556
 A:Accession: AB1806
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-505 <PAR>
 A:Cross-references: GB:AL162757; GB:AL157959; NID:g7380371; PIDN:CAB85029.1; PID:g738
 A:Experimental source: serogroup A, strain Z2491

C:Genetics:
A:Gene: NMA1803

Query Match 47.3%; Score 43; DB 2; Length 505;
Best Local Similarity 85.7%; Pred. No. 69;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 WTMAAFH 13
|||||
DB 51 WTMAAFY 57

RESULT 14
H81064

sensor histidine kinase NMB1606 [imported] - Neisseria meningitidis (strain MC58 serogroup C)
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: H81064
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; et al., H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignan, V.; Pizza, M. Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Vignani, A.; et al.
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755
A:Accession: H81064
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-505 <TEXT>
A:Cross-references: GB:AE002511; GB:AE002098; NID:g7226857; PIDN:AAF41958.1; PID:g722685.
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB1606

Query Match 47.3%; Score 43; DB 2; Length 505;
Best Local Similarity 85.7%; Pred. No. 69;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 WTMAAFH 13
|||||
DB 51 WTMAAFY 57

RESULT 15
A33598

endoglucanase 3 (EC 3.2.1.-) - Fibrobacter succinogenes (strain S85)
C:Species: Fibrobacter succinogenes
C:Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 08-Oct-1999
C:Accession: A33598
R:McGavin, M.J.; Forsberg, C.W.; Crosby, B.; Bell, A.W.; Dignard, D.; Thomas, D.Y. J. Bacteriol. 171, 5587-5595, 1989
A:Title: Structure of the cel-3 gene from Fibrobacter succinogenes S85 and characterization of the gene product.
A:Reference number: A33598; MUID:9008798
A:Accession: A33598
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-658 <MCG>
A:Cross-references: GB:M29047; NID:g148570; PIDN:AAA24893.1; PID:g148571; GB:M29681
C:Keywords: glycosidase; hydrolase

Query Match 47.3%; Score 43; DB 2; Length 658;
Best Local Similarity 45.5%; Pred. No. 88;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 4 RVPWTAMAFHG 14
:|||||:|
DB 625 QIPWTHMGYTG 635

Search completed: August 15, 2002, 11:39:40
Job time: 201 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 11:39:04 ; Search time 18.67 seconds

(without alignments)
31.108 Million cell updates/sec

Title: US-09-613-092a-5
Sequence: 1 TVSRVPWTAMAFHGY 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Swissprot_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	49.5	278	YH22_YEAST	P38878 saccharomyc
2	48.4	350	YN04_YEAST	P53844 saccharomyc
3	48.4	581	CHLE_RABIT	P21927 oryctolagus
4	48.4	602	CHLE_HUMAN	P06276 homo sapien
5	48.4	603	CHLE_MOUSE	O03311 mus musculi
6	47.3	176	VPI_BPP2	P26701 bacteriophia
7	47.3	302	YEO6_YEAST	P40049 saccharomyc
8	47.3	351	YNX1_YEAST	P53860 saccharomyc
9	47.3	658	GUN3_FIBSU	P14250 fibrobacter
10	47.3	1120	RPOK_SCHPO	O13993 schizosacch
11	46.2	299	YOG8_YEAST	P40363 saccharomyc
12	46.2	666	YV35_MYCPN	P75079 mycoplasma
13	46.2	750	CTPB_MYCLE	P46840 mycobacteri
14	46.2	752	CTPB_MYCTU	O10877 mycobacteri
15	46.2	761	CTPA_MYCTU	O10876 mycobacteri
16	46.2	780	CTPA_MYCLE	P46839 mycobacteri
17	44.0	200	YEO1_MYCTU	P71669 mycobacteri
18	44.0	353	YKPL_YEAST	P35735 saccharomyc
19	44.0	379	YISP_BACCS	P29156 bacillus cl
20	44.0	541	YISP_YEAST	P29156 bacillus cl
21	44.0	616	BBR1_SCHCO	P78741 schizophyll
22	44.0	660	CCMF_PSEFL	P48382 homo sapien
23	44.0	1038	CCMF_PSEFL	P52225 pseudomonas
24	44.0	3386	BMR2_MOUSE	O35607 mus musculi
25	44.0	3388	POLG_DEN2	P09866 d genome po
26	44.0	3390	POLG_DEN3	P12823 d genome po
27	44.0	3391	POLG_DEN26	P27915 d genome po
28	44.0	3391	POLG_DEN27	P29990 d genome po
29	44.0	3391	POLG_DEN28	P29991 d genome po
30	44.0	3391	POLG_DEN29	P07564 d genome po
31	44.0	3396	POLG_DEN29	P14340 d genome po
32	42.9	395	SYT8_MOUSE	P33478 d genome po
33	42.9	402	ROO_DESGI	O9f0f6 desulfovibr

ALIGNMENTS

RESULT	ID	YH22_YEAST	STANDARD:	PRT:	278 AA.
AC	P38878:	01-FEB-1995 (Rel. 31, Created)			
DT	01-FEB-1995 (Rel. 31, Last sequence update)				
DT	01-OCT-1996 (Rel. 34, Last annotation update)				
DE	Hypothetical 32.1 kDa protein in CTF8-EGD2 intergenic region.				
GN	YHR192W.				
OS	Saccharomyces cerevisiae (Baker's yeast).				
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;				
OC	Saccharomycetales; Saccharomycetaceae; Saccharomycetes.				
OX	NCBI_TaxID=4932;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=S288C / AB972;				
RX	MEDLINE=94378003; PubMed=8091229;				
RA	Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,				
RA	Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J.,				
RA	Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,				
RA	Latreille P., Louis E.J., Macri C., Mardis E., Meneses S., Mouser L.,				
RA	Nhan M., Rifkin L., Riles L., St Peter H., Trevasakis E., Vaughan K.,				
RA	Vignati D., Wilcox L., Woldman P., Woldman R., Wilson R.,				
RA	Vaudin M.;				
RT	"Complete nucleotide sequence of Saccharomyces cerevisiae chromosome				
RT	VIII.";				
RL	Science 265:2077-2082(1994).				
CC	-----				
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CC	-----				
DR	EMBL: 000030; AAB68359.1; -.				
DR	PIR: S46681; S46681.				
DR	SGD: S0001235; YHR192W.				
KW	Hypothetical protein; Transmembrane.				
FT	TRANSMEM 46 66				
FT	POTENTIAL. 78 98				
FT	SEQUENCE 278 AA; 32062 MW; D896557EEB805C89 CRC64;				
QY	Query Match	49.5%	Score 45;	DB 1;	Length 278;
DB	Best Local Similarity	46.7%	Pred. No. 7.9;		
	Matches 7; Conservative	3;	Mismatches 5;	Indels 0;	Gaps 0;
	1 TVSRVPWTAMAFHGY 15				
	11 : : 1111				
	62 TVLALSTYTWYEHGY 76				
RESULT	2				
	YN04_YEAST				

ID YN04_YEAST STANDARD: PRT: 350 AA.
 AC P53844;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical 40.7 kDa protein in P1K1-POL2 intergenic region.
 GN YNL264C OR N0815.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / FY1679;
 RX MEDLINE=96310631; PubMed=8740425;
 RA Sen-Gupta M., Lyck R., Fleig U., Niedenthal R.K., Hegemann J.H.;
 RT "The sequence of a 24,152 bp segment from the left arm of chromosome
 XIV from *Saccharomyces cerevisiae* between the BNI1 and the POL2
 genes";
 RL Yeast 12:505-514(1996).
 CC -1- SIMILARITY: BELONGS TO THE SEC14 CYTOSOLIC FACTOR FAMILY.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 DR EMBL: X92494; CAA63233.1; -;
 DR EMBL: Z71540; CAA96171.1; -;
 DR SCD: S0005208; YNL264C.
 DR InterPro: IPR001251; CRAL_TRIO.
 DR Pfam: PF00650; CRAL_TRIO.1.
 DR SMART: SM00516; SEC14.1.
 KM Hypothetical protein.
 SQ SEQUENCE 350 AA; 40678 MW; C18F0D225A69DB86 CRC64;

 Query Match 48.4%; Score 44; DB 1; Length 350;
 Best Local Similarity 75.0%; Pred. No. 14;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

 QY 5 VPTWMAF 12
 Db 247 IPWFMAF 254

 RESULT 3
 CHLE_RABIT STANDARD: PRT: 581 AA.
 ID CHLE_RABIT
 AC P21927;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cholinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)
 DE (Choline esterase II) (Butyrylcholine esterase)
 DE (Pseudocholinesterase).
 GN BCHE.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=New Zealand;
 RX MEDLINE=90326526; PubMed=2374720;
 RA Ujilo O., Roudani S., Chaconet A.;
 RT "Complete sequence of rabbit butyrylcholinesterase";
 RL Nucleic Acids Res. 18:3990-3990(1990).
 RN [2]
 RP SEQUENCE OF 75-215 FROM N.A.

RC TISSUE=Liver;
 RA MEDLINE=91201348; PubMed=2016308;
 RA Arpagaus M., Chaconet A., Masson P., Newton M., Vaughan T.A.,
 RA Bartels C.F., Noqueira C.P., La Du B.N., Lockridge O.;
 RT "Use of the polymerase chain reaction for homology probing of
 RT butyrylcholinesterase from several vertebrates";
 RL J. Biol. Chem. 266:6966-6974(1991).
 CC -1- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
 CC carboxylic acid anion.
 CC SUBUNIT: HOMOTETRAMER. THE TETRAMER IS COMPOSED
 CC OF TWO DIMERS. THE TWO SUBUNITS IN A DIMER ARE LINKED BY A
 CC DISULFIDE BOND.
 CC -1- TISSUE SPECIFICITY: PRESENT IN MOST CELLS EXCEPT ERYTHROCYTES.
 CC -1- MISCELLANEOUS: CHOLINESTERASE IS HIGHLY REACTIVE WITH
 CC ORGANOPHOSPHATE ESTERS.
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
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 CC -----
 DR EMBL: X52090; CAA36308.1; -;
 DR EMBL: X52091; CAA36308.1; JOINED.
 DR EMBL: X52092; CAA36308.1; JOINED.
 DR EMBL: M62779; AAA31169.1; -;
 DR PIR: S10255; S10255.
 DR PIR: C39768; C39768.
 DR HSSP: P21836; IMAH.
 DR InterPro: IPR002018; Carboxylesterase.B.
 DR InterPro: IPR000997; Cholinesterase.
 DR InterPro: IPR000379; Est_1ip_thioest_actsite.
 DR Pfam: PF00135; Coesterase.1.
 DR PRINTS: PR00878; CHOLINESTERASE.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
 DR KW Hydrolyase; Serine esterase; Glycoprotein; Signal.
 FT SIGNAL 1 8
 FT CHAIN 9 581
 FT ACT_SITE 205 205
 FT ACT_SITE 332 332
 FT ACT_SITE 445 445
 FT ACT_SITE 72 99
 FT DISULFID 259 270
 FT DISULFID 407 526
 FT DISULFID 578 578
 FT CARBOHYD 64 64
 FT CARBOHYD 113 113
 FT CARBOHYD 248 248
 FT CARBOHYD 263 263
 FT CARBOHYD 348 348
 FT CARBOHYD 462 462
 FT CARBOHYD 488 488
 FT CARBOHYD 492 492
 FT CARBOHYD 493 493
 SQ SEQUENCE 581 AA; 66156 MW; FE8B199E7B3EB0A CRC64;

 Query Match 48.4%; Score 44; DB 1; Length 581;
 Best Local Similarity 46.7%; Pred. No. 21;
 Matches 7; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

 QY 3 SRVPTWAF-AFHGY 15
 Db 433 SKLPFPMGVMGHGY 447

 RESULT 4
 CHLE_HUMAN STANDARD: PRT: 602 AA.
 ID CHLE_HUMAN

AC P06276: 01-JAN-1988 (Rel. 06, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cholinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)
DE (Choline esterase II) (Butyrylcholine esterase)
DE (Pseudocholinesterase).
GN BCHE OR CHE1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-90212557; PubMed-2322535;
RA Arpagaus M., Kott M., Vatsis K.P., Bartels C.F., la Du B.N.,
RA Lockridge O.;
RT "Structure of the gene for human butyrylcholinesterase. Evidence for
RT a single copy."
RL Biochemistry 29:124-131(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Fetal;
RX MEDLINE-87231856; PubMed-3035536;
RA Prody C.A., Zevin-Sonkin D., Gnatt A., Goldberg O., Soreq H.;
RT "Isolation and characterization of full-length cDNA clones coding for
RT cholinesterase from fetal human tissues."
RL Proc. Natl. Acad. Sci. U.S.A. 84:3555-3559(1987).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-Brain;
RX MEDLINE-88016155; PubMed-3477799;
RA McIernan C., Adkins S., Chaconet A., Vaughan T.A., Bartels C.F.,
RA Kott M., Rosenberry T.L., la Du B.N., Lockridge O.;
RT "Brain cDNA clone for human cholinesterase."
RL Proc. Natl. Acad. Sci. U.S.A. 84:6682-6686(1987).
RN [4]
RP SEQUENCE OF 29-602.
RC TISSUE-Plasma;
RX MEDLINE-87109144; PubMed-3542989;
RA Lockridge O., Bartels C.F., Vaughan T.A., Wong C.K., Norton S.E.,
RA Johnson L.L.;
RT "Complete amino acid sequence of human serum cholinesterase."
RL J. Biol. Chem. 262:549-557(1987).
RN [5]
RP DISULFIDE BONDS.
RX MEDLINE-88007487; PubMed-3115973;
RA Lockridge O., Adkins S., la Du B.N.;
RT "Location of disulfide bonds within the sequence of human serum
RT cholinesterase."
RL J. Biol. Chem. 262:12945-12952(1987).
RN [6]
RP REVIEW.
RX MEDLINE-89149758; PubMed-5067729;
RA Lockridge O.;
RT "Structure of human serum cholinesterase."
RL Bioessays 9:125-128(1988).
RN [7]
RP VARIANT ATYPICAL GLY-98.
RX MEDLINE-89128896; PubMed-2915989;
RA McGuire M.C., Nogueira C.P., Bartels C.F., Lightstone H., Hajta A.,
RA van der Spek A.F.L., Lockridge O., la Du B.N.;
RT "Identification of the structural mutation responsible for the
RT diacetylcholine-resistant (atypical) variant form of human serum
RT cholinesterase."
RL Proc. Natl. Acad. Sci. U.S.A. 86:953-957(1989).
RN [8]
RP VARIANT ILE-358.
RX MEDLINE-96287386; PubMed-8680411;
RA Tida S., Kinoshita M., Fujii H., Moriyama Y., Nakamura Y., Yura N.,
RA Moriwaki K.;
RT "Mutations of human butyrylcholinesterase gene in a family with
RT hypocholinesterasemia.";

RE	Hum. Mutat. 6:349-351(1995).	
CC	-I- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a	
CC	carboxylic acid anion.	
CC	-I- SUBUNIT: HOMOTETRAMER. THE TETRAMER IS COMPOSED	
CC	OF TWO DIMERS. THE TWO SUBUNITS IN A DIMER ARE LINKED BY A	
CC	DISULFIDE BOND.	
CC	-I- TISSUE SPECIFICITY: PRESENT IN MOST CELLS EXCEPT ERYTHROCYTES.	
CC	-I- DISEASE: MUTANT ALLELES OF CHB1 ARE RESPONSIBLE FOR	
CC	HYPCHOLINESTEREMIA RESULTING IN SUKAMETHONIUM SENSITIVITY.	
CC	HOMOZOOGUS PERSONS SUSTAIN PROLONGED APEPA AFTER ADMINISTRATION	
CC	OF THE MUSCLE RELAXANT SUKAMETHONIUM IN CONNECTION WITH SURGICAL	
CC	ANESTHESIA.	
CC	-I- MISCELLANEOUS: CHOLINESTERASE IS HIGHLY REACTIVE WITH	
CC	ORGANOPHOSPHATE ESTERS.	
CC	-I- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.	
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CC	-----	
DR	EMBL; M32391; AAA99296.1; -.	
DR	EMBL; M32389; AAA99296.1; JOINED.	
DR	EMBL; M32390; AAA99296.1; JOINED.	
DR	EMBL; M16541; AAA98113.1; -.	
DR	EMBL; M16474; AAA52015.1; -.	
DR	PIR; A00772; ACBU.	
DR	PIR; A26613; A26613.	
DR	PIR; A33769; A33769.	
DR	PIR; A33887; A33887.	
DR	HSSP: P21836; IMMA.	
DR	MM; 177400; -.	
DR	InterPro; IPR002018; Carboxylesterase_B.	
DR	InterPro; IPR000997; Cholinesterase.	
DR	InterPro; IPR003379; Est_hlp_chioest_actsite.	
DR	Pfam; PF00135; Coesterase; 1.	
DR	PRINTS: PR00878; CHOLINESTERASE.	
DR	PROSITE: PS00142; CARBOXYLESTERASE_B_1; 1.	
DR	PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.	
KM	Hydrolase; Serine esterase; Glycoprotein; Signal; Disease mutation;	
KM	Polymorphism.	
FT	SIGNAL	1 28
FT	CHAIN	29 602
FT	ACT_SITE	226 226
FT	ACT_SITE	353 353
FT	ACT_SITE	466 466
FT	ACT_SITE	120 120
FT	DISULFID	280 291
FT	DISULFID	428 547
FT	DISULFID	599 599
FT	CARBOHD	45 45
FT	CARBOHD	85 85
FT	CARBOHD	134 134
FT	CARBOHD	269 269
FT	CARBOHD	284 284
FT	CARBOHD	369 369
FT	CARBOHD	483 483
FT	CARBOHD	509 509
FT	CARBOHD	514 514
FT	CARBOHD	98 98
FT	VARIANT	
FT		
FT	VARIANT	271 271
FT		
FT	VARIANT	358 358
FT		
FT	VARIANT	418 418
FT		
FT	VARIANT	567 567
FT		

FT SEQUENCE 602 AA; 68418 MW; C9836409D9057E27 CRC64;
SQ

Query Match 48.4%; Score 44; DB 1; Length 602;
Best Local Similarity 46.7%; Pred. No. 22;
Matches 7; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY 3 SRVPTAM--AFHGY 15
|:|:|
Db 454 SKLPWPMGVMHGY 468

RESULT 5
CHIE_MOUSE STANDARD; PRT; 603 AA.
ID CHIE_MOUSE
AC 003311;
DT 01-OCT-1993 (Rel. 27, Created)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Cholinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)
DE (Choline esterase II) (Butyrylcholine esterase)
DE (Pseudocholinesterase).
GN BChE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RX MEDLINE=90380429; PubMed=2400605;
RT "Molecular cloning of mouse acetylcholinesterase: tissue distribution of alternatively spliced mRNA species.";
RN Neuron 5:317-327(1990).
[2]
RP SEQUENCE OF 97-237 FROM N.A.
RC TISSUE=Liver;
RA MEDLINE=91201348; PubMed=2016308;
RA Appagou M., Chatonnet A., Masson P., Newton M., Vaughan T.A.,
RA Bartels C.F., Nogueira C.P., La Du B.N., Lockridge O.;
RT "Use of the polymerase chain reaction for homology probing of butyrylcholinesterase from several vertebrates.";
RL J. Biol. Chem. 266:6966-6974(1991).
CC -1- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
CC carboxylic acid anion.
CC -1- SUBUNIT: HOMOTETRAMER. THE TETRAMER IS COMPOSED
CC OF TWO DIMERS. THE TWO SUBUNITS IN A DIMER ARE LINKED BY A
CC DISULFIDE BOND.
CC -1- TISSUE SPECIFICITY: PRESENT IN MOST CELLS (EXCEPT ERYTHROCYTES).
CC -1- MISCELLANEOUS: CHOLINESTERASE IS HIGHLY REACTIVE WITH
CC ORGANOPHOSPHATE ESTERS.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
CC -----
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CC -----
DR EMBL, M99492; AAA37328.1; -.
DR PIR, A39768; A39768.
DR HSSP, P21836; 1MAH.
DR MGD, MGI:894278; Bche.
DR InterPro: IPR002018; Carboxylesterase_B.
DR InterPro: IPR000997; Cholinesterase.
DR InterPro: IPR000373; Est_11p_choest_actsite.
DR Pfam, PF00133; Coesterase_1.
DR PRINTS, PR00878; CHOLINESTRASE.
DR PROSITE, PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE, PS00941; CARBOXYLESTERASE_B_2; 1.

KW Hydrolyase; Serine esterase; Glycoprotein; Signal.
FT SIGNAL 1 29
FT CHAIN 30 603
FT ACT_SITE 227 227 CHOLINESTERASE.
FT ACT_SITE 354 354 BY SIMILARITY.
FT ACT_SITE 467 467 BY SIMILARITY.
FT ACT_SITE 467 467 BY SIMILARITY.
FT DISULFID 94 121 BY SIMILARITY.
FT DISULFID 281 292 BY SIMILARITY.
FT DISULFID 429 548 BY SIMILARITY.
FT DISULFID 600 600 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 270 270 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 370 370 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 484 484 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 510 510 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 515 515 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 129 129 R -> P (IN REF. 2).
SQ SEQUENCE 603 AA; 68521 MW; 719B1B20D1E5367 CRC64;

Query Match 48.4%; Score 44; DB 1; Length 603;
Best Local Similarity 46.7%; Pred. No. 22;
Matches 7; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY 3 SRVPTAM--AFHGY 15
|:|:|
Db 455 SKLPWPMGVMHGY 469

RESULT 6
VPL_BPP2 STANDARD; PRT; 176 AA.
ID VPL_BPP2
AC P26701;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Tail protein I (GPI).
GN I.
OS Bacteriophage P2.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC P2-like viruses.
OC P2-like viruses.
OX NCBI_TaxID=10679;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92165720; PubMed=1531648;
RA Haggard-Ljungquist E., Halling C., Calendar R.;
RT "DNA sequences of the tail fiber genes of bacteriophage P2: evidence
RT for horizontal transfer of tail fiber genes among unrelated
RT bacteriophages.";
RL J. Bacteriol. 174:1462-1477(1992).
[2]
RN SEQUENCE FROM N.A.
RX MEDLINE=96036485; PubMed=7483254;
RA Haggard-Ljungquist E., Jacobsen E., Rishoyd S., Slix E.W., Nilsen O.,
RA Sunshine M.G., Lindqvist B.H., Kim K.-J., Barreiro V., Koonin E.V.,
RA Calendar R.;
RT "Bacteriophage P2: genes involved in baseplate assembly.";
RL Virology 213:109-121(1995).
CC -----
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CC -----
DR EMBL, AF063097; AAD03285.1; -.
DR Structural Protein.
KW SEQUENCE 176 AA; 19584 MW; EADA23BCAFCECF1E CRC64;

Query Match 47.3%; Score 43; DB 1; Length 176;
Best Local Similarity 75.0%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 VMTAMAF 12
: || || || ||
DB 46 LPLMAAF 53

RESULT 7

YEO6_YEAST STANDARD; PRT; 302 AA.
AC P40049;

DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 33.5 kDa protein in PRP3-SER3 intergenic region
DE precursor.
GN YER076C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
[1]

RP SEQUENCE FROM N.A.
RC STRAIN-S288C / AB972;
RA Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R.,
RA Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M.,
RA Chung E., Duncan M., Guzman E., Hartzell D., Hunnicke-Smith S.,
RA Hyman R., Kayser A., Komp C., Laskari D., Lew H., Lin D.,
RA Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C.,
RA Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V.,
RA Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
CC -1 SIMILARITY: TO YEAST KILLER TOXIN KHR.

CC -----
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DR EMBL: U18839; AAB64631.1; -
DR SGD: S0000878; YER076C.
KM Hypothetical protein; Glycoprotein; Signal.
FT SIGNAL 1 23
FT CHAIN 24 302
FT CARBOHD 65 65
FT CARBOHD 86 86
FT CARBOHD 93 93
FT CARBOHD 220 220
FT CARBOHD 231 231
SQ SEQUENCE 302 AA; 33466 MW; 43E3AC5FA2BF378F CRC64;

Query Match 47.3%; Score 43; DB 1; Length 302;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 7 WTAMAFHG 14
: || || || ||
DB 180 WVMAMVHG 187

RESULT 8

YXN1_YEAST STANDARD; PRT; 351 AA.
AC P53860;

DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical 40.7 kDa protein in CSL4-URE2 intergenic region.
GN YNL231C OR N1158.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
[1]

RP SEQUENCE FROM N.A.
RX MEDLINE=97051596; PubMed=8896273;
RA Pandolfo D., de Antoni A., Lanfranchi G., Valle G.;
RT "The DNA sequence of cosmid 14-5 from chromosome XIV reveals 21 open
RT reading frames including a novel gene encoding a globin-like
RT domain.";
RL Yeast 12:1071-1076(1996).

CC -1 SIMILARITY: BELONGS TO THE SEC14 CYTOSOLIC FACTOR FAMILY.
CC -----
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DR EMBL: 269381; CAA93367.1; -
DR EMBL: 271507; CAA96136.1; -
DR SGD: S0005175; YNL231C
DR InterPro: IPR001251; CRAL_TRIO.
DR Pfam: PF00650; CRAL_TRIO; 1.
DR SMART: SM00516; SEC14; 1.
KW Hypothetical protein.
SQ SEQUENCE 351 AA; 40714 MW; 24C5B3262016F037 CRC64;

Query Match 47.3%; Score 43; DB 1; Length 351;
Best Local Similarity 45.5%; Pred. No. 19;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 VSRVPTAMAF 12
: || || || ||
DB 242 LTNIPWLAFTF 252

RESULT 9

GUN3_FIBSU STANDARD; PRT; 658 AA.
AC P14250;

DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Endoglucanase 3 precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase)
DE (Cellulase) (EG3).
GN CEL-3.

OS Fibrobacter succinogenes (Bacteroides succinogenes).
OC Bacteria; Fibrobacter/Acidobacteria group; Fibrobacter group;
OC Fibrobacter.

OX NCBI_TaxID=833;
[1]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 266-287.
RC STRAIN=585;

RX MEDLINE=90008798; PubMed=2676979;
RA McGavin M.J., Forsberg C.W., Crosby B., Bell A.W., Dignard D.,
RA Thomas D.Y.;

RT "Structure of the cel-3 gene from Fibrobacter succinogenes S85 and
RT characteristics of the encoded gene product, endoglucanase 3.";
RL J. Bacteriol. 171:5587-5595(1989).

CC -1 FUNCTION: EXHIBITS BOTH ENDOGLUCANASE AND CELLOBIOSIDASE
CC ACTIVITIES.

CC -1 CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
CC linkages in cellulose.

CC -1 SUBUNIT: MONOMER.

CC -1 PTM: MAY BE A LIPOPROTEIN AND MAY BE GLYCOSYLATED.
CC -1 SIMILARITY: BELONGS TO CELLULOSE FAMILY A (FAMILY 5 OF GLYCOSYL

CC HYDROLASES).
CC -----
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CC -----
CC EMBL; M29047; AAA24893.1; -
CC PIR; A33598; A33598.
CC HSP; P07985; 1CEN.
CC InterPro; IPR001547; Glyco_hydro.F5.
CC Pfam; PF00150; cellulase; 1.
CC PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
CC PROSITE; PS00659; GLYCOSYL_HYDROL_F5; 1.
CC Cellulose degradation; Hydrolase; Glycosidase; Zymogen; Lipoprotein;
KM Signal.
FT SIGNAL 1 23 POTENTIAL.
FT PROPEP 24 265
FT CHAIN 266 658 ENDOGLUCANASE 3.
FT LIPID 24 24 N-ACYL DIGLYCERIDE (POTENTIAL).
FT ACT_SITE 448 448 PROTON DONOR (BY SIMILARITY).
FT ACT_SITE 597 597 NUCLEOPHILE (BY SIMILARITY).
SQ SEQUENCE 658 AA; 73424 MW; 1C96E64C3F7109A6 CRC64;

Query Match 47.3%; Score 43; DB 1; Length 658;
Best Local Similarity 45.5%; Pred. No. 33;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 RVPWTAMAFHG 14
:|||||:
Db 625 QIPWTHMGYTG 635

RESULT 10
RPOW_SCHPO STANDARD; PRT; 1120 AA.
ID RPOW_SCHPO
AC 013993;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-1999 (Rel. 38, Last annotation update)
DE DNA-directed RNA polymerase, mitochondrial precursor (EC 2.7.7.6).
GN SPAC6H5.12.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=972;
RL Oliver K., Harris D., Barrell B.G., Rajandream M.A., Wood V.;
Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC - FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC - CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC (RNA)(N).
CC - SUBCELLULAR LOCATION: Mitochondrial.
CC - SIMILARITY: BELONGS TO THE PHAGE AND MITOCHONDRIAL RNA POLYMERASES
CC FAMILY.
CC -----
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CC -----

DR EMBL; Z99126; CAB16197.1; -.
DR HSP; P00573; IARO.
DR InterPro; IPR002092; RNA_pol_phage.
DR Pfam; PF00940; RNA_pol; 1.
DR PROSITE; PS00900; RNA_POL_PHAGE_1; 1.
DR PROSITE; PS00489; RNA_POL_PHAGE_2; 1.
KW Translase; DNA-directed RNA polymerase; Transcription;
KW Mitochondrion; Transl peptide.
FT TRANSIT 1 2 MITOCHONDRION.
FT CHAIN 2 1120 DNA-DIRECTED RNA POLYMERASE.
FT ACT_SITE 787 787 BY SIMILARITY.
FT ACT_SITE 856 856 BY SIMILARITY.
FT ACT_SITE 1027 1027 BY SIMILARITY.
SQ SEQUENCE 1120 AA; 127268 MW; 22D206A1F2831A23 CRC64;

Query Match 47.3%; Score 43; DB 1; Length 1120;
Best Local Similarity 50.0%; Pred. No. 53;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 VSRVPTAMAFHG 15
:|||||:
Db 519 VTRPWTSMIDGY 532

RESULT 11
YUG8_YEAST STANDARD; PRT; 299 AA.
ID YUG8_YEAST
AC P40363;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 33.9 kDa esterase in SMC3-MRPL8 intergenic region
DE (EC 3.1.1.-).
GN YU068C OR J1102 OR HRE299.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=95282514; PubMed=7762302;
RA Vandenbol M., Durand P., Dion C., Portetelle D., Hilger F.;
RT "Sequence of a 17.1 kb DNA fragment from chromosome X of
RT Saccharomyces cerevisiae includes the mitochondrial ribosomal protein
RT L8.";
RL Yeast 11:57-60(1995).
RN [2]
RP SEQUENCE OF 15-299 FROM N.A.
RC STRAIN=S288C;
RA Sor F.J.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
CC - SIMILARITY: STRONG. TO HUMAN ESTERASE D.
CC -----
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CC -----
CC EMBL; Z34288; CAA84054.1; -
DR EMBL; Z49343; CAA89359.1; -
DR EMBL; X88851; CAA61307.1; -
DR PIR; S47122; S47122.
DR SGD; S0003604; YU068C.
DR InterPro; IPR000379; Est_lip_thioest_actsite.
DR InterPro; IPR000801; Esterase_put.
DR Pfam; PF00756; Esterase; 1.
KW Hypothetical protein; Hydrolase.
FT ACT_SITE 161 161 BY SIMILARITY.

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SQ SEQUENCE 299 AA; 33934 MW; BFA5DC02729E9AEF CRC64;

Query Match 46.2%; Score 42; DB 1; Length 299;
Best Local Similarity 61.5%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 SRVPTAMAFHG 15
   | | | | | | |
DB 193 SNVPMGQKAFKGY 205

RESULT 12
YA35_MYCPN ID YA35_MYCPN STANDARD; PRT; 666 AA.
AC P75079;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MPN035 (B01_orf666).
GN MPN035 OR MP119.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 29342 / M129;
RA MEDLINE=97105885; PubMed=8948633;
RA Himmelfeich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
RA Hermann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT pneumoniae.";
RL Nucleic Acids Res. 24:4420-4449(1996).
CC -1- SIMILARITY: BELONGS TO THE MG032 / MG096 / MG288 FAMILY.
CC -----
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CC -----
DR EMBL: AE000014; AAB95767.1; -
DR InterPro: IPR004306; DUF237.
DR InterPro: IPR004319; DUF240.
DR Pfam: PF03072; DUF237; 1.
DR Pfam: PF03086; DUF240; 1.
DR KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 666 AA; 76898 MW; DF096AA4B475402D CRC64;

Query Match 46.2%; Score 42; DB 1; Length 666;
Best Local Similarity 70.0%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5 VPTAMAFHG 14
   | | | | | | |
DB 557 VAWMAAFKG 566

RESULT 13
CTPB_MYCLE ID CTPB_MYCLE STANDARD; PRT; 750 AA.
AC P46840;
DT 01-NOV-1995 (Rel. 32, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Cation-transporting P-type ATPase B (EC 3.6.3.-).
GN CTPB OR ME2000.
OS Mycobacterium leprae.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

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OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=96059637; PubMed=7476188;
RA Fshl H., Cole S.T.;
RT "The Mycobacterium leprae genome: systematic sequence analysis
RT identifies key catabolic enzymes, ATP-dependent transport systems and
RT a novel pola locus associated with genomic variability.";
RL Mol. Microbiol. 16:909-919(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-TN;
RX MEDLINE=21128732; PubMed=11234002;
RA Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Feltham T., Fraser A., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
RA Ruter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrell B.G.;
RT "Massive gene decay in the leprosy bacillus.";
RL Nature 409:1007-1011(2001).
CC -1- CATABOLIC ACTIVITY: ATP + H(2)O = ADP + PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
CC (E1-E2 ATPASES). SUBFAMILY 1B.
CC -1- SIMILARITY: CONTAINS 1 HMA DOMAIN.
CC -----
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CC -----
DR EMBL: Z46257; CAAB6363.1; -
DR EMBL: AL583924; CAC30955.1; -
DR HSPB; P04129; IAEY.
DR Leproma; ML2000; -
DR InterPro: IPR001756; Cu_ATPase.
DR InterPro: IPR001757; E1-E2_ATPase.
DR InterPro: IPR001934; HMA.
DR InterPro: IPR001454; Hydrolyase.
DR Pfam: PF00122; E1-E2_ATPase; 1.
DR Pfam: PF00403; HMA; 1.
DR Pfam: PF00702; Hydrolyase; 1.
DR PRINTS: PR00119; CATAPPASE.
DR PRINTS: PR00943; CUATPAASE.
DR PROSITE: PS00154; ATPASE_E1-E2; 1.
DR PROSITE: PS01047; HMA_1; 1.
DR PROSITE: PS50846; HMA_2; 1.
DR KW Hydrolyase; Transmembrane; Phosphorylation; Magnesium; ATP-binding;
KW Metal-binding; Complete proteome.
FT TRANSMEM 104 124 POTENTIAL.
FT TRANSMEM 129 149 POTENTIAL.
FT TRANSMEM 167 187 POTENTIAL.
FT TRANSMEM 200 220 POTENTIAL.
FT TRANSMEM 360 380 POTENTIAL.
FT TRANSMEM 389 409 POTENTIAL.
FT TRANSMEM 471 491 POTENTIAL.
FT TRANSMEM 500 520 POTENTIAL.
FT TRANSMEM 547 567 POTENTIAL.
FT TRANSMEM 663 683 POTENTIAL.
FT TRANSMEM 693 713 POTENTIAL.
FT TRANSMEM 715 735 POTENTIAL.
FT DOMAIN 18 81 HMA.
FT MOD_RES 445 445 PHOSPHORYLATION (PROBABLE).
FT METAL 28 28 POTENTIAL.
FT METAL 31 31 POTENTIAL.

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FT CONFLICT 544 548 EGRSR -> RRRIT (IN REF. 1).
SQ SEQUENCE 750 AA: 78100 MW: 1D58477D4A69B00D CRC64;

Query Match
Best Local Similarity 66.7%; Score 42; DB 1; Length 750;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5 VPMWMAFH 13
   1 1 1 1 1
Db 144 VPMWMAFH 152

RESULT 14
CTPA_MYCTU STANDARD; PRT; 752 AA.
ID CTPA_MYCTU 010877; P77905;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 41, Last annotation update)
DE Cation-transporting P-type ATPase B (EC 3.6.3.-).
GN CTPB OR RV0103C OR MT0112 OR MTCY251.22C.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
   Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NC NCBL_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RA Aranooff D.D., Krishna S.K., Griffin G.E., Mangan J.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RA MEDLINE=98295987; PubMed=9634230;
   Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
   Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
   Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
   Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S.,
   Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
   Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
   Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
   Sultson J.E., Taylor K., Whitehead S., Barrell B.G.;
RA "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544(1998).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
   Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
   Kolony J.F., Nelson W.C., Umayan L.A., Esmolaeva M.D., Salzberg S.L.,
   Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
   Bishai W.;
RA "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + ORTHOPHOSPHATE.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
   (E1-E2 ATPASES). SUBFAMILY 1B.
CC -1- SIMILARITY: CONTAINS 1 HMA DOMAIN.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
DR EMBL: Y07638; CAA68915.1; -.
DR EMBL: Z74410; CAA98939.1; -.

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DR EMBL: AE006923; AAK44334.1; -.
DR TIGR: MT0112; -.
DR TubercuList; RV0103c; -.
DR InterPro; IPR000579; Cat_P_ATPaseA.
DR InterPro; IPR001757; E1-E2_ATPase.
DR InterPro; IPR001934; HMA.
DR InterPro; IPR001454; Hydrolase.
DR Pfam; PF00122; E1-E2_ATPase; 1.
DR Pfam; PF00403; HMA; 1.
DR Pfam; PF00702; Hydrolase; 1.
DR PRINTS; PR00940; CATPATPASEA.
DR PROSITE; PS00154; ATPASE_E1_E2; 1.
DR PROSITE; PS01047; HMA_1; 1.
DR PROSITE; PS50846; HMA_2; 1.
DR Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP-binding;
KM Complete proteome.
FT TRANSMEM 105 125 POTENTIAL.
FT TRANSMEM 132 152 POTENTIAL.
FT TRANSMEM 167 187 POTENTIAL.
FT TRANSMEM 201 221 POTENTIAL.
FT TRANSMEM 361 381 POTENTIAL.
FT TRANSMEM 390 410 POTENTIAL.
FT TRANSMEM 491 511 POTENTIAL.
FT TRANSMEM 714 734 POTENTIAL.
FT DOMAIN 16 79 HMA.
FT MOD_RES 446 446 PHOSPHORYLATION (BY SIMILARITY).
FT METAL 26 26 BY SIMILARITY.
FT METAL 29 29 BY SIMILARITY.
FT CONFLICT 22 22 L -> S (IN REF. 3).
SQ SEQUENCE 752 AA: 77509 MW: 21563FEA84407505 CRC64;

Query Match
Best Local Similarity 66.7%; Score 42; DB 1; Length 752;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5 VPMWMAFH 13
   1 1 1 1 1
Db 145 VPMWMAFH 153

RESULT 15
CTPA_MYCTU STANDARD; PRT; 761 AA.
ID CTPA_MYCTU 010876;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Cation-transporting P-type ATPase A (EC 3.6.3.-).
GN CTPA OR RV0052 OR MT0101 OR MTCY251.11.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
   Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NC NCBL_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RA MEDLINE=98295987; PubMed=9634230;
   Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
   Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
   Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
   Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S.,
   Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
   Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
   Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
   Sultson J.E., Taylor K., Whitehead S., Barrell B.G.;
RA "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544(1998).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

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RA Peterson J., Deboy R., Dodson R., Gwin M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
laboratory strains";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -I- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + PHOSPHATE.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
(EI-E2 ATPASES) SUBFAMILY 1B.

CC -I- SIMILARITY: CONTAINS 1 HMA DOMAIN.

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CC or send an email to license@isb-sib.ch).

CC EMBL: Z74410; CAA98928.1; -
CC EMBL: AE006921; AAK4324.1; -
CC TIGR: MT0101; -
DR Tuberculist; RV0092; -
DR InterPro: IPR000579; Cat_P_ATPase.
DR InterPro: IPR001757; EI-E2_ATPase.
DR InterPro: IPR001934; HMA.
DR InterPro: IPR001454; Hydrolyase.
DR Pfam; PF00122; EI-E2_ATPase; 1.
DR Pfam; PF00403; HMA; 1.
DR Pfam; PF00702; Hydrolyase; 1.
DR PRINTS: PR00940; CATPATPASEA.
DR PROSITE: PS00154; ATPASE_EI_E2; 1.
DR PROSITE: PS01047; HMA_1; 1.
DR PROSITE: PS0846; HMA_2; 1.
DR Hydrolyase; Transmembrane; Phosphorylation; Magnesium; ATP-binding;
KW Complete proteome.
FT TRANSMEM 102 122 POTENTIAL.
FT TRANSMEM 129 149 POTENTIAL.
FT TRANSMEM 164 184 POTENTIAL.
FT TRANSMEM 199 219 POTENTIAL.
FT TRANSMEM 361 381 POTENTIAL.
FT TRANSMEM 387 407 POTENTIAL.
FT TRANSMEM 548 568 POTENTIAL.
FT TRANSMEM 650 670 POTENTIAL.
FT TRANSMEM 703 723 POTENTIAL.
FT DOMAIN 13 79 HMA.
FT MOD_RES 443 443 PHOSPHORYLATION (BY SIMILARITY).
FT METAL 25 25 BY SIMILARITY.
FT METAL 28 28 BY SIMILARITY.
SQ SEQUENCE 761 AA: 78850 MW: D397901EC5C513BE CRC64:

Query Match 46.2%; Score 42; DB 1; Length 761;
Best Local Similarity 66.7%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 5 VPMWAFH 13
| | | | |
DB 142 YTWAMPFH 150

Search completed: August 15, 2002, 11:47:41
Job time: 517 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 11:38:29 ; Search time 58.4 Seconds
(without alignments)
44.434 Million cell updates/sec

Title: US-09-613-092A-5

Perfect score: 91

Sequence: 1 TVSRVPMWTAMAFHGY 15

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	49.5	297	10	Q9FTE7
2	45	49.5	413	2	Q9K3G1
3	45	49.5	454	10	Q9X1S9
4	45	49.5	537	10	Q9S0D5
5	45	49.5	890	3	Q9HGE4
6	44	48.4	349	6	Q9GKJ6
7	44	48.4	597	11	Q9JUC1
8	44	48.4	603	13	Q90ZK8
9	43.5	47.8	310	10	Q82590
10	43.5	47.8	457	10	Q9M126
11	43	47.3	176	9	Q37841
12	43	47.3	344	10	Q9LSP1
13	43	47.3	392	16	Q92MA2
14	43	47.3	433	16	Q9A0U1
15	43	47.3	441	16	Q9HYE2
16	43	47.3	505	16	Q9JYF5

17	43	47.3	505	16	Q9JTE0	Q9JTE0 neisseria m
18	43	47.3	572	2	P72076	P72076 neisseria g
19	43	47.3	602	6	O62760	O62760 felis silve
20	43	47.3	602	6	O62761	O62761 panthera ti
21	43	47.3	657	2	O59446	O59446 fibrobacter
22	43	47.3	668	2	O9ALX8	O9ALX8 burkholderi
23	43	47.3	669	2	O59445	O59445 fibrobacter
24	43	47.3	722	10	O04514	O04514 arabisdops
25	43	47.3	938	10	O9AV04	O9AV04 oryza sativ
26	42	46.2	81	5	Q9VBC3	Q9VBC3 dirosophila
27	42	46.2	141	11	Q9CZ41	Q9CZ41 mus musculu
28	42	46.2	142	10	Q9SUN7	Q9SUN7 arabisdops
29	42	46.2	247	17	O27503	O27503 methanot
30	42	46.2	297	16	Q9KDS0	Q9KDS0 bacillus ha
31	42	46.2	317	16	O9KES0	O9KES0 bacillus ha
32	42	46.2	548	4	O14818	O14818 homo sapien
33	42	46.2	602	5	O76999	O76999 brachiost
34	42	46.2	623	4	O14819	O14819 homo sapien
35	42	46.2	650	10	O23349	O23349 arabisdops
36	42	46.2	668	10	O48552	O48552 arabisdops
37	42	46.2	884	12	O98XW8	O98XW8 elmeria bru
38	41	45.1	130	2	O9X4J8	O9X4J8 salmone
39	41	45.1	141	2	O9WTB5	O9WTB5 escherichia
40	41	45.1	164	10	O9F5I8	O9F5I8 hordeum vul
41	41	45.1	174	2	O9K414	O9K414 streptomyce
42	41	45.1	232	2	O9AHG5	O9AHG5 comanens t
43	41	45.1	232	2	P71191	P71191 enterobacte
44	41	45.1	305	2	O9F132	O9F132 pseudomonas
45	41	45.1	385	16	O98HG1	O98HG1 rhizobium 1

ALIGNMENTS

RESULT 1
ID Q9FTE7 PRELIMINARY; PRT; 297 AA.
AC Q9FTE7:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE P0698A04.4 PROTEIN (P0494A10.20 PROTEIN).
OS P0698A04.4 OR P0494A10.20.
GN Oryza sativa (Rice).
OC Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(Ga3) genomic DNA, chromosome 1, PAC
clone:P0698A04.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(Ga3) genomic DNA, chromosome 1, PAC
clone:P0494A10.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP002868: BAB17143.1; -;
DR EMBL: AP002541: BAB55480.1; -;
DR InterPro: IPR004277; PSS.
DR Pfam: PF03034; PSS; 1.
SQ SEQUENCE 297 AA; 34429 MW; E1730EFC71208E09 CRC64;

Query Match 49.5%; Score 45; DB 10; Length 297;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 PWTAMAF 12
 ID 111111:
 Db 32 PWTAMAF 38

RESULT 2

Q9K3G1 PRELIMINARY; PRT; 413 AA.
 AC Q9K3G1;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE CONSERVED HYPOTHETICAL PROTEIN.
 GN 25CG18.27C.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
 NCBI_TaxID=1902;

RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Brown S.P., Harris D.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN [12]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Cerdano A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN [13]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA MEDLINE-97000351; PubMed-8843436;
 RA Redenbach M., Kleser H.M., Denapate D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 the 8 mb streptomyces coelicolor A3(2) chromosome."
 RL Mol. Microbiol. 21:77-96(1998).
 DR EMBL: ALJ90188; CAB99160.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 413 AA; 44536 MW; 2C841BDA72FCB3D CRC64;

Query Match 49.5%; Score 45; DB 2; Length 413;
 Best Local Similarity 50.0%; Pred. No. 37;
 Matches 7; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TVSRVPTWAMAFHG 14
 ID 111111:
 Db 113 TDDRPPMDVWLVRG 126

RESULT 3
 Q9X159 PRELIMINARY; PRT; 454 AA.
 AC Q9X159;
 DT 01-NOV-1999 (TReMBLrel. 12, Created)
 DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE F9L1.4 PROTEIN.
 GN F9L1.4.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RA Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
 RA Lee J., Liu A., Li J., Kremenetskaia I., Luros J., Gonzalez A.,
 RA Alatafi H., Araujo R., Brooks S., Buehler E., Chao Q., Conn L.,
 RA Conway A.B., Dunn P., Hansen N., Huizar L., Khan S., Kim C., Palm C.,
 RA Rowley D., Shinn P., Walker M., Davis R.W., Becker J.R.,

RA Federspiel N.A., Theologis A.;
 RT "Arabidopsis thaliana chromosome 1 BAC F9L1 sequence."
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC007591; AAD39639.1; -.
 DR InterPro: IPR004277; PSS.
 DR Pfam: PF03034; PSS; 1.
 SQ SEQUENCE 454 AA; 52610 MW; 1EDC8AA5A4188A44 CRC64;

Query Match 49.5%; Score 45; DB 10; Length 454;
 Best Local Similarity 61.5%; Pred. No. 48;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 PWTAMAF 12
 ID 111111:
 Db 32 PWTAMAF 38

RESULT 4

Q9SD75 PRELIMINARY; PRT; 537 AA.
 AC Q9SD75;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE HYPOTHETICAL 58.5 KDA PROTEIN.
 GN F13112.30.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 NCBI_TaxID=3702;

RP SEQUENCE FROM N.A.
 RA Choiane N., Robert C., Brothier P., Mincker P., Catolico L.,
 RA Attiguenave F., Saurin W., Weissenbach J., Mewes H.W., Lemcke K.,
 RA Mayer K.F.X., Queller F., Salanoubat M.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 RN [12]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 CC - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC - SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
 DR EMBL: AL133292; CAB61944.1; -.
 DR InterPro: IPR003662; sub.transporter.
 DR Pfam: PF00083; sugar tr; 1.
 KW Hypothetical protein; Transmembrane.
 SQ SEQUENCE 537 AA; 58503 MW; E4D85E54B9429A67 CRC64;

Query Match 49.5%; Score 45; DB 10; Length 537;
 Best Local Similarity 61.5%; Pred. No. 48;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 SRVPTWAMAFHG 15
 ID 111111:
 Db 363 SAVPWSMAAFG 375

RESULT 5
 Q9HGE4 PRELIMINARY; PRT; 890 AA.
 AC Q9HGE4;
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE CHITIN SYNTHASE 1.
 OS Arabidopsis thaliana.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Onygenales; Arthrodermataceae; Arthroderma.
 NCBI_TaxID=63400;
 RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN-VUT-77011;
RA Kano R.;
RT "Arthropoda benhamiae gene for chitin synthase 1, complete."
RL Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AB050933; BAB17766.1; -;
DR InterPro: IPR002923; Chitin_synth.
DR InterPro: IPR001173; Glycos_transf_2.
DR Pfam: PF01644; Chitin_synth.1.
DR Prodom: PD002998; Chitin_synth.1.
SQ SEQUENCE 890 AA: 101598 MW: 547C38823E64B565 CRC64;

Query Match 49.5%; Score 45; DB 3; Length 890;
Best Local Similarity 46.7%; Pred. No. 78;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 TVSRPWTAW-AFHGY 15
DB 154 SISRIPLTRMTQDGY 168

RESULT 6
O9GKJ6 PRELIMINARY; PRT; 349 AA.

DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE BUTYRYLCHOLINESTERASE (FRAGMENT).
GN BHE.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Van Poucke M., Yerle M., Tuglie C., Chardon P., Van Zeveren A.,
RA Peelam L.J.;
RT "Integration of porcine chromosome 13 maps."
RL Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: AF222914; AAG41127.1; -;
DR HSSP: P21836; IMAA.
DR InterPro: IPR002018; Carboxylesterase_B.
DR InterPro: IPR000997; Cholinesterase.
DR InterPro: IPR000379; Est_lip_thioest_acsite.
DR Pfam: PF00135; Coesterase; 1.
DR PRINTS: PR00878; CHOLINESTRASE.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
KW Hydrolyase.
FT NON_TER 349 1
FT NON_TER 349 1
SQ SEQUENCE 349 AA: 39061 MW: D66354B14725BE58 CRC64;

Query Match 48.4%; Score 44; DB 6; Length 349;
Best Local Similarity 46.7%; Pred. No. 45;
Matches 7; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

OY 3 SRVPWTAW-AFHGY 15
DB 314 SKLPPEWGMGVHGY 328

RESULT 7
O9JKC1 PRELIMINARY; PRT; 597 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE BUTYRYLCHOLINESTERASE.

OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART;
RA Li B., Stribley J., Tieu A., Xie W., Schopfer L.M., Hammond P.,
RA Brimloun S., Hinrichs S.H., Lockridge O.;
RT "Abundant Tissue Butyrylcholinesterase and its Possible Function in
the Acetylcholinesterase Knockout Mouse."
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: AF244349; AAF44713.1; -;
DR HSSP: P21836; IMAA.
DR InterPro: IPR002018; Carboxylesterase_B.
DR InterPro: IPR000997; Cholinesterase.
DR InterPro: IPR000379; Est_lip_thioest_acsite.
DR Pfam: PF00135; Coesterase; 1.
DR PRINTS: PR00878; CHOLINESTRASE.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolyase.
SQ SEQUENCE 597 AA: 67776 MW: 771204D166CTEAC CRC64;

Query Match 48.4%; Score 44; DB 11; Length 597;
Best Local Similarity 46.7%; Pred. No. 76;
Matches 7; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

OY 3 SRVPWTAW-AFHGY 15
DB 449 SKLPPEWGMGVHGY 463

RESULT 8
O90ZK8 PRELIMINARY; PRT; 603 AA.

DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE BUTYRYLCHOLINESTERASE PRECURSOR (EC 3.1.1.8).
GN BHE.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Geisler K., Chatonnet A., Layer P.G.;
RT "Chicken Butyrylcholinesterase."
RL Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ306928; CAC37792.1; -;
KW Signal; Hydrolase.
FT CHAIN 1 29 POTENTIAL.
FT CHAIN 30 603 BUTYRYLCHOLINESTERASE.
SQ SEQUENCE 603 AA: 68480 MW: A350FDF68574ADF CRC64;

Query Match 48.4%; Score 44; DB 13; Length 603;
Best Local Similarity 46.7%; Pred. No. 76;
Matches 7; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

OY 3 SRVPWTAW-AFHGY 15
DB 454 SKLPPEWGMGVHGY 468

RESULT 9
O82590 PRELIMINARY; PRT; 310 AA.

AC 082590;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE F1104.5 PROTEIN.
GN F1104.5.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA WashU;
RT "The A. thaliana Genome Sequencing Project.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Abu-Threideh J., Stoneking T., Langston Y., Trevasakis E.;
RT "The sequence of A. thaliana F1104.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Waterston R.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF096370; AAC62781.1; -;
DR InterPro: IPR003441; NAM.
DR Pfam: PF02365; NAM.1
SQ SEQUENCE 310 AA; 35370 MW; 4CE95002CD638F32 CRC64;

Query Match 47.8%; Score 43.5; DB 10; Length 310;
Best Local Similarity 53.3%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 4; Indels 3; Gaps 1;

QY 4 RVP---WTANAFHCY 15
||| ||| |
Db 95 RVPKGVWTPWVMHEY 109

RESULT 10
Q9M126 PRELIMINARY; PRT; 457 AA.
AC Q9M126;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE PUTATIVE NAM-LIKE PROTEIN.
GN AT4G01550.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Lamar B., Stoneking T., Stumpf J., Mewes H.W., Lemcke K.,
Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL161492; CAB77725.1; -;
DR InterPro: IPR003441; NAM.
DR Pfam: PF02365; NAM.1.
SQ SEQUENCE 457 AA; 51816 MW; 9CBBCE615F0538B3 CRC64;

Query Match 47.8%; Score 43.5; DB 10; Length 457;

Best Local Similarity 53.3%; Pred. No. 69;
Matches 8; Conservative 0; Mismatches 4; Indels 3; Gaps 1;

QY 4 RVP---WTANAFHCY 15
||| ||| |
Db 119 RVPKGVWTPWVMHEY 133

RESULT 11
Q37841 PRELIMINARY; PRT; 176 AA.
AC Q37841;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE ORF38.
OS Bacteriophage 186.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC P2-like viruses.
OX NCBI_TaxID=29252;
RN [1]
RP SEQUENCE OF 174-176 FROM N.A.
RX MEDLINE=95407087; PubMed=7676622;
RA Xue Q., Egan J.B.;
RT "DNA sequence of tail fiber genes of coliphage 186 and evidence for a
common ancestor shared by dsDNA phage fiber genes.";
RL Virology 212:128-133(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Xue Q.;
RT "Studies on the tail region of the temperate coliphage 186 genome.";
RL Thesis (1993), University of Adelaide.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=98371265; PubMed=9705261;
RA Portelli R., Dodd I.B., Xue Q., Egan J.B.;
RT "The late-expressed region of the temperate coliphage 186 genome.";
RL Virology 248:117-130(1998).
RN [4]
RP SEQUENCE FROM N.A.
RA Dodd I.B., Egan J.B.;
RT "Bacteriophage 186 complete genome.";
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Xue Q., Egan J.B.;
RL EMBL: U32222; AAC34163.1; -;
SQ SEQUENCE 176 AA; 19643 MW; E53F5764AB650182 CRC64;

Query Match 47.3%; Score 43; DB 9; Length 176;
Best Local Similarity 75.0%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 VPTANAF 12
: || |||||
Db 46 LPWLAWAF 53

RESULT 12
Q9LSPI PRELIMINARY; PRT; 344 AA.
AC Q9LSPI;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE PECTINESTERASE-LIKE PROTEIN.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;

[1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
RL Submitted (Apr-1999) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=20277480; PubMed=10819329;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT clones."
RL DNA Res. 7:131-135(2000).
DR EMBL: AB026536; BAA94984.1; -;
DR InterPro: IPR000070; Pectinesterase.
DR Pfam: PF01095; Pectinesterase_1.
DR PROSITE: PS00503; PECTINESTERASE_2; 1.
SQ SEQUENCE 344 AA; 38812 MW; 8C01BD9C8836EC9 CRC64;

Query Match 47.3%; Score 43; DB 10; Length 344;
Best Local Similarity 62.5%; Pred. No. 63;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 7 WTMAAFHG 14
DB 280 WTNMSYHG 287
|||::|||

RESULT 13
O92MA2 PRELIMINARY; PRT; 392 AA.
AC O92MA2;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PUTATIVE PHOSPHOSERINE AMINOTRANSFERASE PROTEIN (EC
DE 2.6.1.52).
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21368234; PubMed=11474104;
RA Galibert F., Finan T.M., Long S.R., Puehler A., Abola P., Ampe F.,
RA Barloy-Hubler F., Barnett M.J., Becker A., Bolstad P., Bothe G.,
RA Boutry M., Bowser L., Buhrmester J., Cadieu E., Capela D., Chain P.,
RA Cowie A., Davis R.W., Dreano S., Federspiel N.A., Fisher R.F.,
RA Gloux S., Godrie T., Goffeau A., Golding B., Gouzy J., Gurjal M.,
RA Hernandez-Lucas I., Hong A., Huizar L., Hyman R.W., Jones T., Kahn D.,
RA Kahn M.L., Kaiman S., Keating D.H., Kiss E., Komp C., Lelaure V.,
RA Masny D., Palm C., Peck M.C., Pohl T.M., Portetelle D., Purnelle B.,
RA Rasperger U., Surzycki R., Thebault P., Vandebol M.,
RA Vorholter F.J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J.;
RT "The composite genome of the legume symbiont Sinorhizobium meliloti."
RL Science 293:668-672(2001).
DR EMBL: AL591791; CAC47310.1; -;
KW Transferrase; Amino transferase; Complete proteome.
SQ SEQUENCE 392 AA; 42336 MW; 1BFD16E10E39F78A CRC64;

Query Match 47.3%; Score 43; DB 16; Length 392;
Best Local Similarity 75.0%; Pred. No. 71;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 VPWTAMAF 12
DB 373 MPWTAMAF 380
|||||

RESULT 14
O9A0U1 PRELIMINARY; PRT; 433 AA.
ID O9A0U1
AC O9A0U1;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOTHETICAL PROTEIN SPY0621.
GN SPY0621.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / SERO TYPE M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najaf F.Z., Ren O., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes."
RT Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
RL EMBL: AE006517; AAK33592.1; -;
DR InterPro: IPR002819; HD.
DR InterPro: IPR003607; HDC.
DR Pfam: PF01966; HD; 1.
DR SMART: SM00471; HDC; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 433 AA; 50500 MW; 0A1FC654A87E758 CRC64;

Query Match 47.3%; Score 43; DB 16; Length 433;
Best Local Similarity 53.8%; Pred. No. 78;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 VSRPWTAMAFHG 14
DB 36 IKVPTTATFTFHG 48
: |||::|||

RESULT 15
O9HYE2 PRELIMINARY; PRT; 441 AA.
ID O9HYE2
AC O9HYE2;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE HYPOTHETICAL PROTEIN PA3464.
GN PA3464.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q., Erwin A.L., Mizoguchi S.D., Watterer P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garner R.L., Goltzy R., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kras A., Lardig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olsson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen."
RL Nature 406:959-964(2000).
DR EMBL: AE004767; AAG06852.1; -;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 441 AA; 49000 MW; 4923F37C2A044DA2 CRC64;

Query Match 47.3%; Score 43; DB 16; Length 441;

Best Local Similarity 85.7%; Pred. No. 80;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 6 PWTAWAF 12
 |||||
 Db 144 PWTAWRF 150

Search completed: August 15, 2002, 11:47:16
 Job time: 527 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 11:38:24 ; Search time 73.69 seconds
(without alignments)
22.610 Million cell updates/sec

Title: US-09-613-092a-6
Perfect score: 87
Sequence: 1 RSYQHDLRAVGFWRLL 15

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.Geneseq_032802:*

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- 11: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1990.DAT:*
- 12: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1991.DAT:*
- 13: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1992.DAT:*
- 14: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1993.DAT:*
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- 19: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT:*
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- 21: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT:*
- 22: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	100.0	15	20	AAV30352
2	47	54.0	554	22	ABG19731
3	47	54.0	554	22	ABG19785
4	47	54.0	1007	22	ABG03083
5	44	50.6	267	22	ABG26189
6	44	50.6	1114	21	AA808517
7	44	50.6	1262	22	AAW79463
8	44	50.6	1289	22	AAW79447
9	44	50.6	1891	22	ABG04331
10	43	49.4	459	21	AAV75223
11	43	49.4	459	21	AAV75225

12	42	48.3	652	22	ABB67974	Drosophila melanog
13	42	48.3	951	20	AAV34536	Porphyrionas ging
14	42	48.3	953	20	AAV34403	Porphyrionas ging
15	41	47.1	111	22	ABG10728	Novel human diagno
16	41	47.1	111	22	ABG25967	Novel human diagno
17	41	47.1	588	22	AAU27909	Human contig polyp
18	41	47.1	651	22	ABG08359	Novel human diagno
19	40	46.0	87	22	ABG08529	Novel human diagno
20	40	46.0	249	21	AAG06462	Arabidopsis thalia
21	40	46.0	266	21	AAG06461	Arabidopsis thalia
22	40	46.0	311	21	AAG06460	Arabidopsis thalia
23	40	46.0	340	22	AAV32076	Bacillus cereus in
24	40	46.0	634	22	ABG10625	Novel human diagno
25	40	46.0	920	22	AAE09955	Methylomonas 16a n
26	39	44.8	198	22	AAU69448	Human purified sec
27	39	44.8	229	17	AAW05051	Human thrombopoiet
28	39	44.8	263	22	ABG04508	Novel human diagno
29	39	44.8	263	22	ABG17554	Novel human diagno
30	39	44.8	263	22	AAU32821	Novel human secret
31	39	44.8	282	17	AAW05045	Human thrombopoiet
32	39	44.8	282	17	AAE97701	Human Mpl receptor
33	39	44.8	286	16	AAE80827	Human MCPD-3. Hom
34	39	44.8	286	17	AAW05044	Human thrombopoiet
35	39	44.8	286	17	AAE91948	Human platelet pro
36	39	44.8	286	17	AAE91964	Megakaryocyte diff
37	39	44.8	286	17	AAE88430	Human MCPD-3. Hom
38	39	44.8	286	21	AAV51117	Human platelet-pro
39	39	44.8	286	21	AAV51118	Human platelet-pro
40	39	44.8	352	22	AAU47738	Propionibacterium
41	39	44.8	356	20	AAV34471	Porphyrionas ging
42	39	44.8	433	22	AAE98942	E. coli growth and
43	39	44.8	491	20	AAV34347	Porphyrionas ging
44	39	44.8	671	22	ABG17780	Novel human diagno
45	39	44.8	696	22	ABE60920	Drosophila melanog

ALIGNMENTS

RESULT 1	AAV30352	standard: Peptide: 15 AA.
XX	AAV30352:	
AC	09-NOV-1999 (first entry)	
XX		
DT	Epitope derived from pneumococcal surface adhesion A protein.	
XX		
DE	Pneumococcal surface adhesion A protein: PsaA; monoclonal antibody:	
XX		
KW	vaccine; Streptococcus pneumoniae infection.	
KW		
XX		
OS	Streptococcus pneumoniae.	
XX		
PN	WO9945121-A1.	
XX		
PD	10-SEP-1999.	
XX		
PF	26-FEB-1999: 99WO-US04326.	
XX		
PR	02-MAR-1998: 98US-0076565.	
XX		
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.	
PI	Ades EW, Carlone GM, Sampson JS, Tharpe JA, Westerink MAJ;	
PI	Zeller JL;	
XX		
DR	WPI: 1999-540849/45.	
XX		
PT	New peptides corresponding to Streptococcus pneumoniae PsaA, used	
PT	for treating or preventing Streptococcus pneumoniae infection in a	
PT	subject	
XX		

RESULT 8
AAM79447
ID AAM79447 standard; Protein: 1289 AA.
XX
XX AAM79447:
XX
DT 06-NOV-2001 (first entry)
XX
DE Human protein SEQ ID NO 3093.
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
OS Homo sapiens.
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PE 05-FEB-2001; 2001WO-US04098.
XX
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.
XX
XX (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
XX WPI: 2001-476283/51.
DR N-PSDB: AAK52580.
XX
PT Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
XX
PS Claim 20; Page 250-251; 6221pp: English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAM80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
XX
SQ Sequence 1289 AA;

Query Match 50.6%; Score 44; DB 22; Length 1289;
Best Local Similarity 58.3%; Pred. No. 89;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 YOHDLRAGGFW 14
||| | | | | |
Db 205 yqhrtylygwk 216

RESULT 9
ABG04331
ID ABG04331 standard; Protein: 1891 AA.
XX
XX ABG04331;
XX
DT 13-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #4322.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
KW
OS Homo sapiens.
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PE 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
XX WPI: 2001-639362/73.
DR N-PSDB: AAS68518.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID NO 34690; 103pp: English.
XX
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX
SQ Sequence 1891 AA;

Query Match 50.6%; Score 44; DB 22; Length 1891;
Best Local Similarity 53.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RSYOHLRATYGF 13
||:|: ||| | | |
Db 120 rayradrlrlygw 132

RESULT 10
AAV75223
ID AAV75223 standard; Protein: 459 AA.
XX
AC AAV75223;
XX
DT 21-MAR-2000 (first entry)
XX
DE Neisseria gonorrhoeae ORF 607 protein sequence SEQ ID NO:1920.
XX
KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KM antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
KW antibacterial; gene therapy.
XX
OS Neisseria gonorrhoeae.
XX
PN MO9957280-A2.
XX
PD 11-NOV-1999.
XX
PF 30-APR-1999; 99WO-US09346.
XX
PR 01-MAY-1998; 98US-0083758.
PR 31-JUL-1998; 98US-0094869.
PR 02-SEP-1998; 98US-0098994.
PR 02-SEP-1998; 98US-0099062.
PR 09-OCT-1998; 98US-0103749.
PR 09-OCT-1998; 98US-0103794.
PR 09-OCT-1998; 98US-0103796.
PR 25-FEB-1999; 99US-0121528.
XX
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX
PI Fraser C, Galeotti C, Grandi G, Hickey E, Maignani V, Mora M;
PI Petersen J, Pizsa M, Rappunli R, Ratti G, Scalato E, Scarselli M;
PI Tettelin H, Venter JC;
XX
DR WPI: 2000-062150/05.
DR N-PSDB; AA253985.
XX
PT Novel Neisserial polypeptides predicted to be useful antigens for
PT vaccines and diagnostics -
XX
PS Claim 2; Page 967; 1453pp; English.
XX
CC AA253015 to AA254536, AA254577 to AA254615, and AAV74253 to AAV75941
CC represent novel Neisseria meningitis and N. gonorrhoeae polynucleotides
CC and polypeptides. AA254537 to AA254576 and AA254616 to AA25473 represent
CC PCR primers used in the exemplification of the present invention. The
CC polypeptides, the polynucleotides, antibodies and compositions of
CC the invention can be used as vaccines, as diagnostic reagents, and as
CC immunogenic compositions. The polypeptides can be used in the
CC manufacture of medicaments for treating or preventing infection due to
CC Neisserial bacteria (e.g. meningitis and septicemia), to detect the
CC presence of Neisseria bacteria, or to raise antibodies. They may also
CC be used to screen for agonists or antagonists, which may themselves
CC have use as antibacterial agents. The polynucleotides of the invention
CC may also be used in gene therapy protocols.
XX
SQ Sequence 459 AA;

Query Match 49.4%; Score 43; DB 21; Length 459;
Best Local Similarity 50.0%; Pred. No. 45;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 SYQHDLRAYGFW 13
: : : : :
Db 416 ayrfdmgygfw 427

RESULT 11
AAV75225
ID AAV75225 standard; Protein: 459 AA.
XX
AC AAV75225;
XX
DT 21-MAR-2000 (first entry)
XX
DE Neisseria meningitidis ORF 607 protein sequence SEQ ID NO:1924.
XX
KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KM antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
KW antibacterial; gene therapy.
XX
OS Neisseria meningitidis.
XX
PN MO9957280-A2.
XX
PD 11-NOV-1999.
XX
PF 30-APR-1999; 99WO-US09346.
XX
PR 01-MAY-1998; 98US-0083758.
PR 31-JUL-1998; 98US-0094869.
PR 02-SEP-1998; 98US-0098994.
PR 02-SEP-1998; 98US-0099062.
PR 09-OCT-1998; 98US-0103749.
PR 09-OCT-1998; 98US-0103794.
PR 09-OCT-1998; 98US-0103796.
PR 25-FEB-1999; 99US-0121528.
XX
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX
PI Fraser C, Galeotti C, Grandi G, Hickey E, Maignani V, Mora M;
PI Petersen J, Pizsa M, Rappunli R, Ratti G, Scalato E, Scarselli M;
PI Tettelin H, Venter JC;
XX
DR WPI: 2000-062150/05.
DR N-PSDB; AA253987.
XX
PT Novel Neisserial polypeptides predicted to be useful antigens for
PT vaccines and diagnostics -
XX
PS Claim 2; Page 969; 1453pp; English.
XX
CC AA253015 to AA254536, AA254577 to AA254615, and AAV74253 to AAV75941
CC represent novel Neisseria meningitis and N. gonorrhoeae polynucleotides
CC and polypeptides. AA254537 to AA254576 and AA254616 to AA25473 represent
CC PCR primers used in the exemplification of the present invention. The
CC polypeptides, the polynucleotides, antibodies and compositions of
CC the invention can be used as vaccines, as diagnostic reagents, and as
CC immunogenic compositions. The polypeptides can be used in the
CC manufacture of medicaments for treating or preventing infection due to
CC Neisserial bacteria (e.g. meningitis and septicemia), to detect the
CC presence of Neisseria bacteria, or to raise antibodies. They may also
CC be used to screen for agonists or antagonists, which may themselves
CC have use as antibacterial agents. The polynucleotides of the invention
CC may also be used in gene therapy protocols.
XX
SQ Sequence 459 AA;

Query Match 49.4%; Score 43; DB 21; Length 459;
Best Local Similarity 50.0%; Pred. No. 45;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 SYQHDLRAYGFW 13
: : : : :
Db 416 ayrfdmgygfw 427

RESULT 12

ID	ABB67974
AB	BB67974 standard; Protein; 652 AA.
XX	
AC	ABB67974;
XX	
DT	26-MAR-2002 (first entry)
XX	
DE	Drosophila melanogaster polypeptide SEQ ID NO 30714.
XX	
KW	Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
XX	
OS	Drosophila melanogaster.
PX	
PN	WO200171042-A2.
PD	
PT	27-SEP-2001.
PF	
PP	23-MAR-2001; 2001WO-US09231.
PR	
PR	23-MAR-2000; 2000US-191637P.
PA	11-JUL-2000; 2000US-061415O.
PE	(PEKE) PE CORP NY.
PI	
PI	Venter JC, Adams M, Li PWD, Myers EW;
DR	
DR	WPI: 2001-656860/75.
DR	N-PDB; ABLI2077.
PT	
PT	New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
PS	
PS	Disclosure; SEQ ID NO 30714; 21pp + Sequence listing; English.
XX	
CC	The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLI6176-ABLI30511), expressed DNA sequences (ABLI01840-ABLI6175) and the encoded proteins (ABBS7737-ABR2072).
CC	
CC	The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
CC	
SO	Sequence 652 AA;
Query Match	48.3%; Score 42; DB 22; Length 652;
Best Local Similarity	53.8%; Pred. No. 95;
Matches	7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
OY	1 RSYQHDLRATCFW 13 :: Db 557 tsfgyslctdylfw 569
RESULT 13	
AAAY34536	
ID	AAAY34536 standard; Protein; 951 AA.
XX	
AC	AAAY34536;
XX	
DT	25-AUG-1999 (first entry)
XX	
DE	Porphyromonas gingivalis protein PG67.
XX	
KW	Porphyromonas gingivalis; PG; periodontal disease; gingivitis;
KW	vaccine; antigenic.
XX	

OS	Porphorymonas gingivallis.
XX	
PN	W09929870-A1.
XX	
PD	17-JUN-1999.
XX	
PF	10-DEC-1998; 98WO-AU01023.
XX	
PR	04-AUG-1998; 98AU-0005028.
PR	10-DEC-1997; 97AU-0000839.
PR	31-DEC-1997; 97AU-0001182.
PR	30-JAN-1998; 98AU-0001546.
PR	10-MAR-1998; 98AU-0002264.
PR	09-APR-1998; 98AU-0002911.
PR	23-APR-1998; 98AU-0003128.
PR	05-MAY-1998; 98AU-0003338.
PR	22-MAY-1998; 98AU-0003654.
PR	29-JUL-1998; 98AU-0004917.
PA	(CSLC-) CSL LTD.
XX	
PI	Agius CT, Barr IG, Hocking DM, Margetts MB, Patterson MA;
PI	Ross BC, Rothel LJ, Webb EA;
XX	
DR	WPI; 1999-385613/32.
DR	N-PDSB; AAX91754.
XX	
PT	Antigenic Porphyromonas gingivallis peptides for preventing
PT	gingivitis
XX	
PS	Claim 1; Page 526-527; 588pp; English.
XX	
CC	AAX91536 to AAX91801 encode two hundred and sixty six antigenic
CC	Porphyromonas gingivallis (PG) polypeptide sequences given in AAY34318 to
CC	AAY34553. AAX91802 to AAX91989 represent PCR primers used in the
CC	isolation of the PG polypeptides. The PG polypeptides have antibacterial
CC	activity with a vaccine mechanism of action. The PG polypeptides can be
CC	used as vaccines especially against Porphyromonas gingivallis. Probes can
CC	be used to detect Porphyromonas gingivallis in standard hybridisation
CC	assays. Porphyromonas gingivallis is involved in periodontal disease
CC	especially gingivitis.
SQ	Sequence 951 AA;
Query Match	48.3%; Score 42; DB 20; Length 951;
Best Local Similarity	56.2%; Pred. No. 1.4e+02;
Matches 9; Conservative	0; Mismatches 5; Indels 2; Gaps 1.
OY	2 SYQHDL--RAYGEWRL I5
	.
DB	599 sympdftkrrygfweI 614
RESULT 14	
AAY34403	
ID	AAY34403 standard; Protein; 953 AA.
XX	
AC	AAY34403;
XX	
DT	25-AUG-1999 (first entry)
XX	
DE	Porphyromonas gingivallis protein PG67.
XX	
KW	Porphyromonas gingivallis; PG; periodontal disease; gingivitis;
XX	vaccine; antigenic.
OS	Porphyromonas gingivallis.
XX	
PN	W09929870-A1.
XX	
PD	17-JUN-1999.

PF 10-DEC-1998; 98MO-A001023.
 XX 04-AUG-1998; 98AU-0005028.
 PR 10-DEC-1997; 97AU-0000839.
 PR 31-DEC-1997; 97AU-0001182.
 PR 30-JAN-1998; 98AU-0001546.
 PR 10-MAR-1998; 98AU-0002264.
 PR 09-APR-1998; 98AU-0002911.
 PR 23-APR-1998; 98AU-0003128.
 PR 05-MAY-1998; 98AU-0003338.
 PR 22-MAY-1998; 98AU-0003654.
 PR 29-JUL-1998; 98AU-0004917.
 XX
 PA (CSLC-) CSL LTD.
 XX
 PI Ajius CT, Barr IG, Hocking DM, Margetts MB, Patterson MA;
 PI Ross BC, Rothel LJ, Webb EA;
 XX
 DR WPI: 1999-385613/32.
 DR N-PSDB; AAX91621.
 XX
 PT Antigenic Porphyromonas gingivalis peptides for preventing
 PT gingivitis
 XX
 PS Claim 1; Page 373-375; 588pp; English.
 XX
 CC AAX91536 to AAX91801 encode two hundred and sixty six antigenic
 CC Porphyromonas gingivalis (PG) polypeptide sequences given in AAY34318 to
 CC AAY34583. AAX91802 to AAX91989 represent PCR primers used in the
 CC isolation of the PG polypeptides. The PG polypeptides have antibacterial
 CC activity with a vaccine mechanism of action. The PG polypeptides can be
 CC used as vaccines especially against Porphyromonas gingivalis. Probes can
 CC be used to detect Porphyromonas gingivalis in standard hybridisation
 CC assays. Porphyromonas gingivalis is involved in periodontal disease
 CC especially gingivitis.
 CC
 SO Sequence 953 AA;
 XX
 QY 2 SYQHDL--RAYGFWRLL 15
 DB 601 sympdfkrrygfwe1 616
 XX
 DE 13-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #10719.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001MO-US08631.
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.

XX
 PI Drmanac RT, Liu C, Tang YT;
 DR WPI: 2001-639362/73.
 DR N-PSDB; AAS74915.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity
 XX
 PS Claim 20; SEQ ID NO 41087; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 SO Sequence 111 AA;
 XX
 QY 1 RSYQHDLRAYGFWR 13
 DB 51 rgtfndirgfagw 63
 XX
 DE 15-AUG-2002 (first entry)
 XX
 DE Novel human diagnostic protein #10719.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001MO-US08631.
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.

Search completed: August 15, 2002, 11:38:26
 Job time: 267 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 11:38:58 ; Search time 26.88 Seconds
(without alignments)
13.630 Million cell updates/sec

Title: US-09-613-092a-6
Perfect score: 87
Sequence: 1 RSYQHDLRAYGFWRL 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 10%
Listing first 45 summaries

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2: /cgn2-6/ptodata/2/1aa/5B.COMB.pep: *
3: /cgn2-6/ptodata/2/1aa/6A.COMB.pep: *
4: /cgn2-6/ptodata/2/1aa/6B.COMB.pep: *
5: /cgn2-6/ptodata/2/1aa/PCITUS.COMB.pep: *
6: /cgn2-6/ptodata/2/1aa/Backfillres1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	44.8	265	1	US-08-413-803-27
2	39	44.8	265	5	PCT-US95-03776-29
3	39	44.8	286	1	US-08-321-488A-27
4	39	44.8	2104	2	US-08-808-793-4
5	39	44.8	2104	3	US-08-772-512A-4
6	39	44.8	2105	2	US-08-808-793-3
7	39	44.8	2105	3	US-08-772-512A-3
8	38	43.7	66	4	US-08-936-165A-376
9	38	43.7	148	3	US-08-946-329A-65
10	38	43.7	320	1	US-08-362-739-2
11	38	43.7	1111	1	US-08-317-450B-15
12	38	43.7	1111	4	US-08-800-593-15
13	38	43.7	1171	1	US-08-445-135-1
14	38	43.7	1193	4	US-08-317-450B-13
15	38	43.7	1193	4	US-08-800-593-13
16	37	42.5	76	4	US-09-227-357-456
17	37	42.5	187	4	US-09-247-155-102
18	37	42.5	567	2	US-08-504-459-2
19	37	42.5	567	2	US-08-504-459-6
20	37	42.5	616	1	US-08-149-100-2
21	37	42.5	695	6	5460961-5
22	37	42.5	877	1	US-08-430-925A-4
23	37	42.5	940	2	US-08-938-365-4
24	37	42.5	941	1	US-08-343-760A-2
25	36	41.4	74	2	US-08-743-130A-41
26	35.5	40.8	67	2	US-08-248-839C-100
27	35.5	40.8	607	3	US-08-781-891-75

28	35	40.2	53	4	US-09-187-789-65	Sequence 65, Appl
29	35	40.2	140	1	US-07-946-421-24	Sequence 24, Appl
30	35	40.2	140	1	US-07-946-421-28	Sequence 28, Appl
31	35	40.2	201	2	US-08-716-317-1	Sequence 1, Appl
32	35	40.2	214	4	US-08-861-774E-74	Sequence 74, Appl
33	35	40.2	214	4	US-08-861-774E-78	Sequence 78, Appl
34	35	40.2	242	2	US-08-553-497A-26	Sequence 26, Appl
35	35	40.2	242	2	US-08-553-497A-28	Sequence 28, Appl
36	35	40.2	242	4	US-09-019-095A-23	Sequence 23, Appl
37	35	40.2	244	2	US-08-553-497A-20	Sequence 20, Appl
38	35	40.2	244	2	US-08-553-497A-22	Sequence 22, Appl
39	35	40.2	246	2	US-08-553-497A-24	Sequence 24, Appl
40	35	40.2	260	4	US-09-187-789-2	Sequence 2, Appl
41	35	40.2	463	4	US-09-163-444-2	Sequence 2, Appl
42	35	40.2	474	3	US-09-022-669-2	Sequence 2, Appl
43	35	40.2	485	2	US-08-446-803-1	Sequence 1, Appl
44	35	40.2	485	2	US-08-861-837-1	Sequence 1, Appl
45	35	40.2	485	2	US-08-600-908A-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-08-413-803-27
Sequence 27, Application US/08413803
Patent No. 5766581
GENERAL INFORMATION:
APPLICANT: Bartley, Timothy D.
APPLICANT: Bogenberger, Jakob M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Hunt, Pamela
APPLICANT: Kinsler, Olaf B.
APPLICANT: Samal, Babu B.
TITLE OF INVENTION: METHODS FOR TREATING MAMMALS WITH
TITLE OF INVENTION: MONO-PEGYLATED PROTEINS THAT STIMULATE MEGAKARYOCYTE
TITLE OF INVENTION: GROWTH AND DIFFERENTIATION
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSER: AMGEN INC.
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: US
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/413, 803
APPLICATION NUMBER: US/08/413, 803
FILING DATE: 30-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,768
FILING DATE: 31-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/252,628
FILING DATE: 31-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/321,488
FILING DATE: 12-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/347,780
FILING DATE: 30-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Cook Ph.D., Robert R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-290D
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 265 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-413-803-27

Query Match 44.8%; Score 39; DB 1; Length 265;
Best Local Similarity 58.3%; Pred. No. 24;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 SYQHLRAGFW 13
|:|:|:|:|:|:
Db 130 SFQHLRGKDFW 141

RESULT 2
PCT-US95-03776-29
Sequence 29, Application PC/TUS9503776
GENERAL INFORMATION:
APPLICANT: AMGEN INC.
TITLE OF INVENTION: Compositions and Methods for Stimulating
TITLE OF INVENTION: Megakaryocyte Growth and Differentiation
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Denavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03776
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Cook, Robert R.
REFERENCE/DOCKET NUMBER: A-290-C
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 265 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-03776-29

Query Match 44.8%; Score 39; DB 5; Length 265;
Best Local Similarity 58.3%; Pred. No. 24;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 SYQHLRAGFW 13
|:|:|:|:|:|:
Db 130 SFQHLRGKDFW 141

RESULT 3
US-08-321-488A-27
Sequence 27, Application US/08321488A
Patent No. 5795569
GENERAL INFORMATION:
APPLICANT: Bartley, Timothy D.
APPLICANT: Bogenberger, Jakob M.
APPLICANT: Bosselman, Robert A.
APPLICANT: Hunt, Pamela
APPLICANT: Kinstler, Olaf B.
APPLICANT: Samal, Badru B.
TITLE OF INVENTION: MONO-PEGYLATED PROTEINS THAT STIMULATE
TITLE OF INVENTION: MEGAKARYOCYTE GROWTH AND DIFFERENTIATION

NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: 1840 Denavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/321,488A
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/252,628
FILING DATE: 31-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,768
FILING DATE: 31-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Cook, Robert R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-290B
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-321-488A-27

Query Match 44.8%; Score 39; DB 1; Length 286;
Best Local Similarity 58.3%; Pred. No. 26;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 SYQHLRAGFW 13
|:|:|:|:|:|:
Db 151 SFQHLRGKDFW 162

RESULT 4
US-08-808-793-4
Sequence 4, Application US/08808793
Patent No. 5858713
GENERAL INFORMATION:
APPLICANT: Soderlund, David M.
APPLICANT: Ingles, Patricia J.
TITLE OF INVENTION: CALCIUM PERMEABLE INSECT SODIUM CHANNELS
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,793
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/034,361


```

1      FILING DATE: 24-DEC-1996
2      CLASSIFICATION: 435
3      PRIOR APPLICATION DATA:
4      APPLICATION NUMBER: US 60/012,649
5      FILING DATE: 01-MAR-1996
6      CLASSIFICATION: 435
7      ATTORNEY/AGENT INFORMATION:
8      NAME: Braman, Susan J.
9      REGISTRATION NUMBER: 34,103
10     REFERENCE/DOCKET NUMBER: 19603/1062 (D-1906A)
11     TELECOMMUNICATION INFORMATION:
12     TELEPHONE: 716-263-1636
13     TELEFAX: 716-263-1600
14     INFORMATION FOR SEQ ID NO.: 4:
15     SEQUENCE CHARACTERISTICS:
16     LENGTH: 2104 amino acids
17     TYPE: amino acid
18     STRANDEDNESS: not relevant
19     TOPOLOGY: linear
20     MOLECULE TYPE: protein
21     OS-08-808-793-4

```

Query Match	44.8%	Score 39;	DB 2;	Length 2104;
Best Local	53.8%	Pred. NO. 2.2e+02;		
Matches	7; Conservative	2; Mismatches	4; Indels	0; Gaps 0

```

QY      3 YQNDLRAYGEWRL 15
      ||| | : | | | :
Db      383 YQNVLQDAAGRWNN 395

```

```

1      RESULT      5
2      US-08-772-512A-4
3      : Sequence 4, Application US/08772512A
4      : Patent No. 6022705
5      :
6      : GENERAL INFORMATION:
7      : APPLICANT: Soderlund, David M.
8      : APPLICANT: Knipple, Douglas C.
9      : APPLICANT: Ingles, Patricia J.
10     : TITLE OF INVENTION: INSECT SODIUM CHANNELS FROM
11     : TITLE OF INVENTION: INSECTICIDE-SUSCEPTIBLE AND INSECTICIDE-RESISTANT HOUSE
12     : TITLE OF INVENTION: FILES
13     : NUMBER OF SEQUENCES: 19
14     : CORRESPONDENCE ADDRESS:
15     : ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
16     : STREET: P. O. Box 1051, Clinton Square
17     : CITY: Rochester
18     : STATE: New York
19     :
20     : COUNTRY: USA
21     :
22     : ZIP: 14603
23     :
24     : COMPUTER READABLE FORM:
25     : MEDIUM TYPE: Floppy disk
26     :
27     : COMPUTER: IBM PC compatible
28     : OPERATING SYSTEM: PC-DOS/MS-DOS
29     : SOFTWARE: Patentin Release #1.0, Version #1.30
30     : CURRENT APPLICATION DATA:
31     : APPLICATION NUMBER: US/08/772,512A
32     : FILING DATE:
33     :
34     : CLASSIFICATION: 435
35     :
36     : PRIORITY APPLICATION DATA:
37     : APPLICATION NUMBER: US 08/608,618
38     : FILING DATE: 01-MAR-1996
39     : ATTORNEY/AGENT INFORMATION:
40     : NAME: Braham, Susan J.
41     :
42     : REGISTRATION NUMBER: 34,103
43     :
44     : REFERENCE/DOCKET NUMBER: 19603/601(CRPD-16577)
45     :
46     : TELECOMMUNICATION INFORMATION:
47     : TELEPHONE: 716-263-1636
48     : TELEFAX: 716-263-1600
49     :
50     : INFORMATION FOR SEQ. ID NO.: 4:
51     : SEQUENCE CHARACTERISTICS:
52     : LENGTH: 2104 amino acids

```

```

;      TYPE: amino acid
;      STRANDEDNESS: not relevant
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
US-08-772-512A-4

```

Query Match	44.88;	Score 39;	DB 3;	Length 2104;
Best Local Similarity	53.88;	Pred. No. 2.e+02;		
Matches	7;	Conservative	2;	Mismatches 4; Indels 0; Gaps 0

```
QY      3 YQHDLRAYGEWRL 15      ||| | : | | :
Db      383 YQHVLRQDAGRWNM 395
```

```

1      RESULT      6
2      US-08-808-793-3
3      : Sequence 3, Application US/08080793
4      : Patent No. 5858713
5      :
6      : GENERAL INFORMATION:
7      : APPLICANT: Soderlund, David M.
8      : APPLICANT: Ingles, Patricia J.
9      : TITLE OF INVENTION: CALCIUM PERMEABLE INSECT SODIUM CHANNELS
10     : TITLE OF INVENTION: AND USE THEREOF
11     : NUMBER OF SEQUENCES: 32
12     :
13     : CORRESPONDENCE ADDRESS:
14     : ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
15     : STREET: Clinton Square, P.O. Box 1051
16     : CITY: Rochester
17     : STATE: New York
18     : COUNTRY: USA
19     : ZIP: 14603
20     :
21     : COMPUTER READABLE FORM:
22     : MEDIUM TYPE: Floppy disk
23     : COMPUTER: IBM PC compatible
24     : OPERATING SYSTEM: PC-DOS/MS-DOS
25     : SOFTWARE: PatentIn Release #1.0, Version #1.30
26     :
27     : CURRENT APPLICATION DATA:
28     : APPLICATION NUMBER: US/08/808,793
29     : FILING DATE:
30     : CLASSIFICATION: 435
31     : PRIOR APPLICATION DATA:
32     : APPLICATION NUMBER: US 60/034,361
33     : FILING DATE: 24-DEC-1996
34     : CLASSIFICATION: 435
35     : PRIOR APPLICATION DATA:
36     : APPLICATION NUMBER: US 60/012,649
37     : FILING DATE: 01-MAR-1996
38     : CLASSIFICATION: 435
39     : ATTORNEY/AGENT INFORMATION:
40     : NAME: Braman, Susan J.
41     : REGISTRATION NUMBER: 34,103
42     : REFERENCE/DOCKET NUMBER: 19603/1062 (D-1906A)
43     : TELECOMMUNICATION INFORMATION:
44     : TELEPHONE: 716-263-1636
45     : TELEFAX: 716-263-1600
46     : INFORMATION FOR SEQ ID NO: 3:
47     : SEQUENCE CHARACTERISTICS:
48     : LENGTH: 2105 amino acids
49     : TYPE: amino acid
50     : STRANDEDNESS: not relevant
51     : TOPOLOGY: linear
52     : MOLECULE TYPE: protein
53     :
54     : US-08-808-793-3

```

Query Match	44.8%;	Score 39;	DB 2;	Length 2105;
Best Local Similarity	53.8%;	Pred. No. 2.2e+02;		
Matches	7;	Conservative	2;	Mismatches 4;
				Indels 0;
				Gaps 0.
QY	3	YOHDLRAYGFRL	15	

Db 383 YOHVLQAGPWHM 395

RESULT 7

US-08-772-512A-3

; Sequence 3, Application US/08772512A

; Patent No. 6022705

; GENERAL INFORMATION:

; APPLICANT: Soderlund, David M.

; APPLICANT: Knippler, Douglas C.

; APPLICANT: Ingles, Patricia J.

; TITLE OF INVENTION: INSECT SODIUM CHANNELS FROM

; TITLE OF INVENTION: INSECTICIDE-SUSCEPTIBLE AND INSECTICIDE-RESISTANT HOUSE

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP

; STREET: P.O. Box 1051, Clinton Square

; CITY: Rochester

; STATE: New York

; COUNTRY: USA

; ZIP: 14603

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/772,512A

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/608,618

; FILING DATE: 01-MAR-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Braham, Susan J.

; REGISTRATION NUMBER: 34,103

; REFERENCE/DOCKET NUMBER: 19603/601(CRPD-1657)

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 716-263-1636

; TELEFAX: 716-263-1600

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2105 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-772-512A-3

Query Match 44.8%; Score 39; DB 3; Length 2105;

Best Local Similarity 53.8%; Pred. No. 2.2e+02;

Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 YOHDLRAYGFWR 15

Db 383 YOHVLQAGPWHM 395

RESULT 8

US-08-936-165A-376

; Sequence 376, Application US/08936165A

; Patent No. 6348582

; GENERAL INFORMATION:

; APPLICANT: Black, Michael

; APPLICANT: Burnham, Martin

; APPLICANT: Hodgson, John

; APPLICANT: Knowles, David

; APPLICANT: Lonetto, Michael

; APPLICANT: Nicholas, Richard

; APPLICANT: Pratt, Julie

; APPLICANT: Reichard, Richard

; APPLICANT: Rosenberg, Martin

; APPLICANT: Ward, Judith

; TITLE OF INVENTION: No. 6348582el Prokaryotic Polynucleotides,

; TITLE OF INVENTION: Polypeptides and Their Uses

; NUMBER OF SEQUENCES: 534

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SmtlKline Beecham Corporation

; STREET: 709 Swedeland Road

; CITY: King of Prussia

; STATE: PA

; COUNTRY: USA

; ZIP: 19406-0939

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/936,165A

; FILING DATE: 24-SEP-1997

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/027,032

; FILING DATE: 24-SEP-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Gimmil, Edward R

; REGISTRATION NUMBER: 38,891

; REFERENCE/DOCKET NUMBER: P50549

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-270-4478

; TELEFAX: 610-270-5090

; TELEX:

; INFORMATION FOR SEQ ID NO: 376:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 66 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-936-165A-376

Query Match 43.7%; Score 38; DB 4; Length 66;

Best Local Similarity 50.0%; Pred. No. 8.2;

Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 SYOHLRAYGFWR 15

Db 25 SYEPIEACGTWR 38

RESULT 9

US-08-946-329A-65

; Sequence 65, Application US/08946329A

; Patent No. 6057091

; GENERAL INFORMATION:

; APPLICANT: Beachy, Philip A.

; APPLICANT: Porter, Jeffrey A.

; TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES

; NUMBER OF SEQUENCES: 109

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 4225 Executive Square, Suite 1400

; CITY: La Jolla

; STATE: CA

; COUNTRY: USA

; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; OPERATING SYSTEM: Windows 95

; SOFTWARE: FastSeq for Windows Version 2.0b

; CURRENT APPLICATION DATA:

```

: APPLICATION NUMBER: US/08/946,329A
: FILING DATE: 07-OCT-1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/061,323
: FILING DATE: 07-OCT-1996
: APPLICATION NUMBER: 08/729,743
: FILING DATE: 10-JUL-1996
: APPLICATION NUMBER: 08/567,357
: FILING DATE: 04-DEC-1995
: APPLICATION NUMBER: 08/349,498
: FILING DATE: 02-DEC-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Haile, Lisa A.
: REGISTRATION NUMBER: 38,347
: REFERENCE/DOCKET NUMBER: 07265/140001
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 619/678-5070
: TELEFAX: 619/678-5099
: INFORMATION FOR SEQ ID NO: 65:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 148 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-946-329A-65

```

```

Query Match          43.7%; Score 38; DB 3; Length 148;
Best Local Similarity 53.8%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

```

QY      2 SYQHDLRVGFWR 14
      1 111 1 11
DB      105 SQDHDLEGRGKWR 117

```

```

RESULT 10
US-08-362-739-2
: Sequence 2, Application US/08362739
: Patent No. 5658757
: GENERAL INFORMATION:
: APPLICANT: Haake, David A.
: APPLICANT: Bianco, David R.
: APPLICANT: Champion, Cheryl I.
: APPLICANT: Lovett, Michael A.
: APPLICANT: Miller, James N.
: TITLE OF INVENTION: CLONED Leptospira OUTER MEMBRANE PROTEIN
: NUMBER OF SEQUENCES: 7
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Spensley Horn Jubas & Lubitz
: STREET: 1880 Century Park East, Suite 500
: CITY: Los Angeles
: STATE: California
: COUNTRY: USA
: ZIP: 90067
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/362,739
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/040,747
: FILING DATE: 31-MAR-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Wetherell, Jr. Ph.D., John R.,
: REGISTRATION NUMBER: 31,678
: REFERENCE/DOCKET NUMBER: PD-2097
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 455-5100

```

```

: TELEFAX: (619) 455-5110
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 320 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-362-739-2

```

```

Query Match          43.7%; Score 38; DB 1; Length 320;
Best Local Similarity 46.2%; Pred. No. 44;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

```

```

QY      3 YQHDLRVGFWR 15
      1 1 1111
DB      131 YESDFGKFFFWRV 143

```

```

RESULT 11
US-08-317-450B-15
: Sequence 15, Application US/08317450B
: Patent No. 5660982
: GENERAL INFORMATION:
: APPLICANT: Tryggvason, Karl
: APPLICANT: Kallunki, Pekka
: APPLICANT: Pyke, Charles
: TITLE OF INVENTION: Laminin Chains: Diagnostic and
: TITLE OF INVENTION: Therapeutic Use
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BANNER & ALLEGRETTI, LMD.
: STREET: Ten South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: USA
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/317,450B
: FILING DATE: 04-OCT-1994
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Chao, Mark
: REGISTRATION NUMBER: 37,293
: REFERENCE/DOCKET NUMBER: 94,778
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-715-1000
: TELEFAX: 312-715-1234
: INFORMATION FOR SEQ ID NO: 15:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1111 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-317-450B-15

```

```

Query Match          43.7%; Score 38; DB 1; Length 1111;
Best Local Similarity 87.5%; Pred. No. 17e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 RSYQHDR 8
      11111 11
DB      843 RSYQHSIR 850

```

```

RESULT 12
US-08-800-593-15

```

```
; Sequence 15, Application US/08800593
; Patent No. 6143505
; GENERAL INFORMATION:
; APPLICANT: Tryggvason, Karl
; APPLICANT: Kallunki, Pekka
; APPLICANT: Pyke, Charles
; TITLE OF INVENTION: Laminin Chains: Diagnostic and
; TITLE OF INVENTION: Therapeutic Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/800,593
; FILING DATE: 18-FEB-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/317,450
; FILING DATE: 04-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Chao, Mark
; REGISTRATION NUMBER: 37,293
; REFERENCE/DOCKET NUMBER: 94,778-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1111 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-800-593-15

Query Match          43.7%; Score 38; DB 4; Length 1111;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
; Sequence 13
; US-08-445-135-1
; Patent No. 5658789
; GENERAL INFORMATION:
; APPLICANT: Quaranta, Vito
; APPLICANT: Hornia, Marketta
; TITLE OF INVENTION: Promotion of Epithelial Cell Adhesion
; TITLE OF INVENTION: and Hemidesmosome Assembly by a Laminin-Like Molecule
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; Sequence 14
; US-08-317-450B-13
; Patent No. 5660982
; GENERAL INFORMATION:
; APPLICANT: Tryggvason, Karl
; APPLICANT: Kallunki, Pekka
; APPLICANT: Pyke, Charles
; TITLE OF INVENTION: Laminin Chains: Diagnostic and
; TITLE OF INVENTION: Therapeutic Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: BANNER & ALLEGRETTI, LTD.
; STREET: Ten South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/317,450B
; FILING DATE: 04-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Chao, Mark
; REGISTRATION NUMBER: 37,293
; REFERENCE/DOCKET NUMBER: 94,778
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234

Query Match          43.7%; Score 38; DB 1; Length 1171;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1193 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-317-450B-13

Query Match 43.7%; Score 38; DB 1; Length 1193;
 Best Local Similarity 87.5%; Pred. No. 1.8e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSYOHDLR 8
 |||||
 DB 843 RSYOHSLR 850

RESULT 15
 US-08-800-593-13
 ; Sequence 13, Application US/08800593
 ; Patent No. 6143505
 ; GENERAL INFORMATION:
 ; APPLICANT: trygvason, Karl
 ; APPLICANT: Kallunki, Pekka
 ; APPLICANT: Pyke, Charles
 ; TITLE OF INVENTION: Laminin Chains: Diagnostic and
 ; TITLE OF INVENTION: Therapeutic Use
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
 ; STREET: 300 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/800,593
 ; FILING DATE: 18-FEB-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/317,450
 ; FILING DATE: 04-OCT-1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Chao, Mark
 ; REGISTRATION NUMBER: 37,293
 ; REFERENCE/DOCKET NUMBER: 94,778-B
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312-913-0001
 ; TELEFAX: 312-913-0002
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1193 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-800-593-13

Query Match 43.7%; Score 38; DB 4; Length 1193;
 Best Local Similarity 87.5%; Pred. No. 1.8e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSYOHDLR 8
 |||||
 DB 843 RSYOHSLR 850

Search completed: August 15, 2002, 11:38:58
 Job time: 264 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 11:39:40 ; Search time 35.58 Seconds
(without alignments)
40.510 Million cell updates/sec

Title: US-09-613-092a-6

Perfect score: 87

Sequence: 1 RSYQHDLRAGFWRL 15

Scoring table:

BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	49.4	118	2	G81992
2	43	49.4	118	2	G81221
3	43	49.4	188	2	T02822
4	43	49.4	459	2	D81950
5	42	48.3	444	2	T24844
6	42	48.3	887	2	T03939
7	42	48.3	994	1	SYNCLM
8	41	47.1	188	2	D82248
9	41	47.1	817	2	T43659
10	40	46.0	223	2	A84436
11	40	46.0	274	2	F96961
12	40	46.0	330	2	B96027
13	40	46.0	371	2	T21153
14	40	46.0	414	2	T19912
15	40	46.0	447	2	E72320
16	40	46.0	451	2	T15718
17	40	46.0	516	2	D96682
18	40	46.0	912	2	T31223
19	40	46.0	1177	2	AC0284
20	39.5	45.4	309	2	A95988
21	39.5	45.4	471	2	D95940
22	39	44.8	81	2	A75372
23	39	44.8	103	2	A53461
24	39	44.8	206	2	S40829
25	39	44.8	206	2	H91229
26	39	44.8	206	2	G86076
27	39	44.8	286	2	A55530
28	39	44.8	313	2	AF1973
29	39	44.8	330	2	B97368

30	39	44.8	330	2	AB2586	pfkB family carbox
31	39	44.8	335	2	I36790	hypothetical prote
32	39	44.8	340	2	C83827	polysaccharin bios
33	39	44.8	433	1	B65058	ficD protein homol
34	39	44.8	502	2	B75287	sensor histidine k
35	39	44.8	505	2	F71266	probable tpr prote
36	39	44.8	514	2	H87465	sodium-galactoside
37	39	44.8	700	2	S09699	blb protein - fruI
38	39	44.8	736	2	T06757	hypothetical prote
39	39	44.8	978	2	H81311	transcription-repa
40	39	44.8	1055	2	T31111	Atfape 1 (EC 3.6.1
41	39	44.8	1135	1	JQ1928	G2-G1 polypeptid
42	39	44.8	2108	2	S72458	sodium channel pro
43	38.5	44.3	159	2	AH2118	bacterioferritin c
44	38.5	44.3	307	2	F97639	hypothetical prote
45	38.5	44.3	307	2	AG2862	conserved hypotet

ALIGNMENTS

```

RESULT 1
G81992
NDH dehydrogenase (ubiquinone) (EC 1.6.5.3) I chain A NMA0019 [similarity] - Neisser
C:Species: Neisseria meningitidis
C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: G81992
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo
R.; Holtroyd, S.; Jagsels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre
Nature 404, 502-506, 2000
A>Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis z2491
A:Reference number: AB1775; MUID:20222556
A:Accession: G81992
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-118 <PAR>
A:Cross-references: GB:AL162752; GB:AL157959; NID:g7378778; PIDN:CAB83339.1; PID:g737
A:Experimental source: serogroup A, strain z2491
C:Genetics:
A:Gene: nuoA; NMA0019
C:Superfamily: NDH dehydrogenase (ubiquinone) chain 3
C:Keywords: membrane-associated complex; NAD; oxidoreductase

Query Match 49.4%; Score 43; DB 2; Length 118;
Best Local Similarity 70.0%; Pred. No. 4.5;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 6 DLRYGFWRL 15
DB 86 DLGATGFSM 95

RESULT 2
G81221
NDH dehydrogenase (ubiquinone) (EC 1.6.5.3) I chain A NMB0241 [similarity] - Neisser
C:Species: Neisseria meningitidis
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: G81221
R:Teitelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen,
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignan, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.;
A>Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: AB1000; MUID:20175755
A:Accession: G81221
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-118 <TEP>
A:Cross-references: GB:AE002381; GB:AE002098; NID:g7225455; PIDN:AAF40695.1; PID:g722
A:Experimental source: serogroup B, strain MC58
C:Genetics:

```

A:Gene: NM0241
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 3
C:Keywords: membrane-associated complex; NAD; oxidoreductase

Query Match 49.4%; Score 43; DB 2; Length 118;
Best Local Similarity 70.0%; Pred. No. 4.5;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 DLRAVGFWR 15
|||
Db 86 DLGAVGFWSM 95

RESULT 3
702822
probable membrane protein L2759.14 [imported] - Leishmania major (strain Friedlin)
C:Species: Leishmania major
C>Date: 24-Mar-1999 #sequence-revision 24-Mar-1999 #text-change 19-May-2000
C:Accession: B81459; T02822
R:Myler, P.J.; Audleman, L.; DeVos, T.; Hixson, G.; Kiser, P.; Lemley, C.; Magness, C.;
Proc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999
A:Title: Leishmania major Friedlin chromosome 1 has an unusual distribution of protein-c
A:Reference number: A81455; MUID:99178987
A:Accession: B81459
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-188 <PVL>
A:Cross-references: GB:AE001274; NID:93264850; PIDN:AMC24644.1; PID:g1407729; GSPDB:GNOC
A:Experimental source: strain MHOM/IL/81/Friedlin
C:Genetics:
A:Gene: L2759.14
A:Map position: 1
C:Keywords: transmembrane protein

Query Match 49.4%; Score 43; DB 2; Length 188;
Best Local Similarity 77.8%; Pred. No. 7.3;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 HDLRAYGF 13
|||
Db 46 HDLMAIGF 54

RESULT 4
D81950
probable transmembrane efflux protein NMA1022 [imported] - Neisseria meningitidis (strai
C:Species: Neisseria meningitidis
C>Date: 05-May-2000 #sequence-revision 05-May-2000 #text-change 02-Feb-2001
C:Accession: D81950
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jørgensen, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: A81775; MUID:20222556
A:Accession: D81950
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-459 <PAR>
A:Cross-references: GB:AL162754; GB:AL157959; NID:g7379424; PIDN:CA84291.1; PID:g737972
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA1022
C:Superfamily: conserved hypothetical protein H11612

Query Match 49.4%; Score 43; DB 2; Length 459;
Best Local Similarity 50.0%; Pred. No. 19;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 SYOHDLRAYGF 13
|||

Db 416 AYREDMGIVGF 427

RESULT 5
T24844
hypothetical protein T11F9.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence-revision 15-Oct-1999 #text-change 15-Oct-1999
C:Accession: T24844
R:Lennard, N.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z19941
A:Accession: T24844
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-444 <WIL>
A:Cross-references: EMBL:Z74042; PIDN:CAA98536.1; GSPDB:GN00023; CESP:T11F9.1
A:Experimental source: clone T11F9
C:Genetics:
A:Gene: CESP:T11F9.1
A:Map position: 5
A:Introns: 19/1; 61/2; 130/3; 177/3; 347/3; 375/1; 413/3

Query Match 48.3%; Score 42; DB 2; Length 444;
Best Local Similarity 42.9%; Pred. No. 27;
Matches 9; Conservative 3; Mismatches 3; Indels 6; Gaps 1;

QY 1 RSYOHDLR-----YGFWR 15
|||
Db 189 RYQNLNSALRYEIVGW 209

RESULT 6
T03939
potassium channel protein - maize
C:Species: Zea mays (maize)
C>Date: 23-Apr-1999 #sequence-revision 23-Apr-1999 #text-change 21-Jul-2000
C:Accession: T03939
R:Hoeh, S.; Dreyer, I.; Dietrich, P.; Becker, D.; Mueller-Roeber, B.; Hedrich, R.
Proc. Natl. Acad. Sci. U.S.A. 94, 4806-4810, 1997
A:Title: Molecular basis of plant-specific acid activation of K⁺ uptake channels.
A:Reference number: Z14922; MUID:97272307
A:Accession: T03939
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-887 <HOT>
A:Cross-references: EMBL:Y07632; NID:g2104907; PIDN:CAA68912.1; PID:g2104908
A:Experimental source: strain L551311b, sub-species Apache, coleoptile
C:Superfamily: unassigned ankylrin repeat proteins; ankylrin repeat homology; EGF homol
C:Keywords: potassium channel; transmembrane protein; transport protein; voltage-gate
F:561-593/Domain: ankylrin repeat homology <ANI>
F:658-690/Domain: ankylrin repeat homology <AN2>

Query Match 48.3%; Score 42; DB 2; Length 887;
Best Local Similarity 56.2%; Pred. No. 55;
Matches 9; Conservative 1; Mismatches 0; Indels 6; Gaps 1;

QY 6 DLRAVGF-----WRL 15
|||
Db 163 DLKSTGFNMLRWRL 178

RESULT 7
SYNCLM
leucine--tRNA ligase (EC 6.1.1.4) precursor, mitochondrial - Neurospora crassa
N:Alternate names: leucyl-tRNA synthetase
C:Species: Neurospora crassa
C>Date: 30-Sep-1992 #sequence-revision 30-Sep-1992 #text-change 18-Jun-1999
C:Accession: A33474
R:Chow, C.M.; Metzberg, R.L.; Rajbandary, U.L.
Mol. Cell. Biol. 9, 4631-4644, 1989

A:Title: Nuclear gene for mitochondrial leucyl-tRNA synthetase of *Neurospora crassa*: iso
A:Reference number: A33474; MUID:90097874
A:Accession: A33474
A:Molecule type: DNA
A:Residues: 1-994 <CHO>
A:Cross-references: GB:M30472; NID:g168829; PIDN:AAA33599.1; PID:g168830
C:Genetics:
A:Gene: leu-5
C:Superfamily: leucine-tRNA ligase
C:Keywords: aminoacyl-tRNA synthetase; ATP; ligase; mitochondrion; protein biosynthesis;
P:1-52/Domain: transit peptide (mitochondrion) #status predicted <TNP>
F:53-994/Product: leucine-tRNA ligase #status predicted <MAT>
F:100-103/Region: ATP binding #status predicted
F:503-550/Region: zinc finger CCCC motif

Query Match 48.3%; Score 42; DB 1; Length 994;
Best Local Similarity 60.0%; Pred. No. 62;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 5 HDLRAYGFW 14
||||:|:
DB 403 HDLRHAFWK 412

RESULT 8
D82248
RNA polymerase sigma-70 factor, ECF subfamily VC1045 [imported] - *Vibrio cholerae* (strain
C:Species: *Vibrio cholerae*
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: D82248
R:Heideberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
Chardson, D.; Esmolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, H.
L. R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
A:Reference number: A82035; MUID:20406833
A:Accession: D82248
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-188 <HEI>
A:Cross-references: GB:AE004186; GB:AE003852; NID:g9655507; PIDN:AAF94204.1; GSPDB:GN001
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC1045
A:Map position: 1

Query Match 47.1%; Score 41; DB 2; Length 188;
Best Local Similarity 46.2%; Pred. No. 16;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 RSYOHDLRAYGFW 13
|:|:|:|:
DB 32 RAYHDLRYAYW 44

RESULT 9
T43659
trehalose-phosphatase (EC 3.1.3.12) [similarity] - fission yeast (*Schizosaccharomyces po
M:Alternate names: trehalose-6P phosphatase
C:Species: *Schizosaccharomyces pombe*
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C:Accession: T43659; T38002; T43056
R:Canasdo, J.; Vicente, J.; Soto, T.; Franco, A.; Castillo, R.; Gacto, M.
submitted to the EMBL Data Library, June 1999
A:Description: Isolation and characterization of trehalose-6P phosphatase disrupted muta
A:Reference number: 222608
A:Accession: T43659
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-817 <CAN>
A:Cross-references: EMBL:AJ242743; PIDN:CAB45142.1*

A:Experimental source: strain 972h(-)
R:Oliver, K.; Harris, D.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1997
A:Reference number: 221760
A:Accession: T38002
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-817 <OLD>
A:Cross-references: EMBL:297209; PIDN:CAB10126.1; GSPDB:GN00066; SPDB:SPAC19G12.15c
R:Yoshitoka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
DNA Res. 4, 363-369, 1997
A:Title: Identification of open reading frames in *Schizosaccharomyces pombe* cDNAs.
A:Reference number: 217323; MUID:98162722
A:Accession: T43056
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 505-817 <YOS>
A:Cross-references: EMBL:D89225; NID:g1749657; PIDN:BAAL3886.1; PID:g1749658
A:Experimental source: strain PR45
C:Genetics:
A:Gene: tpp1; SPAC19G12.15c
A:Map position: 1
A:Function:
A:Description: catalyzes the hydrolysis of trehalose 6-phosphate to trehalose
A:Pathway: trehalose biosynthesis
C:Keywords: phosphoric monoester hydrolase; trehalose biosynthesis

Query Match 47.1%; Score 41; DB 2; Length 817;
Best Local Similarity 57.1%; Pred. No. 75;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 RSYOHDLRAYGFW 14
||:|:|:|:
DB 362 RSFQRLRYPEWR 375

RESULT 10
A84436
probable glutathione S-transferase [imported] - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C:Accession: A84436
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umeyam, T.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
A:Reference number: A84420; MUID:20083487
A:Accession: A84436
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-223 <STO>
A:Cross-references: GB:AE002093; NID:g3894170; PIDN:AACT8520.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g02380
A:Map position: 2
C:Superfamily: plaiice glutathione transferase

Query Match 46.0%; Score 40; DB 2; Length 223;
Best Local Similarity 50.0%; Pred. No. 28;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 3 YOHDLRAYGFW 14
|:|:|:|:
DB 8 YQAKRLYSYR 19

RESULT 11
F96961
bacitracin resistance protein (baca) [imported] - *Clostridium acetobutylicum*

C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
C:Accession: F96961
R:Rolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: F96961
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-274 <KUR>
A:Cross-references: GB:AE001437; PIDN:AAK78481.1; PID:g15023362; GSPDB:GN00168
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC0501
C:Superfamily: Escherichia coli bacitracin resistance protein bacA

Query Match 46.0%; Score 40; DB 2; Length 274;
Best Local Similarity 41.7%; Pred. No. 35;
Matches 5; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

OY 4 OHDLRAYGFWR 15
|||:|:|:|:|:
Db 250 RHDFKAFGWYRI 261

RESULT 12
B96027
probable aliphatic sulfonates uptake ABC transporter periplasmic solute-binding protein
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C:Accession: B96027
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhmester, J.; Chain, P.; Vorholter, F.J.; Hernat
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:Title: The complete sequence of the 1,683-kb pSymb megaplasmid from the N2-fixing endo
A:Reference number: A95842; MUID:2136508; PMID:11481431
A:Accession: B96027
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-330 <KUR>
A:Cross-references: GB:AL591985; PIDN:CAC49882.1; PID:g15141370; GSPDB:GN00167
A:Experimental source: strain 1021, megaplasmid pSymb
R:Galibert, F.; Finan, T.M.; Long, S.R.; Punter, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
Pelat, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: SMD20570
A:Genome: plasmid

Query Match 46.0%; Score 40; DB 2; Length 330;
Best Local Similarity 50.0%; Pred. No. 43;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 RSYOHDLRAYGFWR 14
|||:|:|:|:|:
Db 179 RSNQVDIAAGVYQW 192

RESULT 13
T21153
hypothetical protein F20E11.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T21153

R:Ainscough, R.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19383
A:Accession: T21153
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-371 <RTL>
A:Cross-references: EMBL:Z81508; PIDN:CAB04139.1; GSPDB:GN00023; CESP:F20E11.6
A:Experimental source: clone F20E11
C:Genetics:
A:Gene: CESP:F20E11.6
A:Map position: 5
A:Introns: 173/2, 211/3, 247/2

Query Match 46.0%; Score 40; DB 2; Length 371;
Best Local Similarity 87.5%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 8 RAYGFWR 15
|||||:
Db 70 RAYGFWR 77

RESULT 14
T19912
hypothetical protein C43F9.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T19912
R:Mortimore, B.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19195
A:Accession: T19912
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-414 <WLL>
A:Cross-references: EMBL:Z82262; PIDN:CAB05151.1; GSPDB:GN00022; CESP:C43F9.4
A:Experimental source: clone C43F9
C:Genetics:
A:Gene: CESP:C43F9.4
A:Map position: 4
A:Introns: 53/3; 81/2; 111/3; 134/3; 164/3; 219/1; 346/1

Query Match 46.0%; Score 40; DB 2; Length 414;
Best Local Similarity 60.0%; Pred. No. 54;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 4 OHDLRAYGFWR 13
|||:|:|:|:|:
Db 21 KHSLMETGFW 30

RESULT 15
E72320
hypothetical protein TM0884 - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: E72320
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hic
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A:Reference number: A72200; MUID:99287316
A:Accession: E72320
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-447 <ARN>
A:Cross-references: GB:AE001754; GB:AE000512; NID:g4981417; PIDN:PAD35965.1; PID:g4998
A:Experimental source: strain MSB8
C:Genetics:

A:Gene: TM0884

Query Match 46.08; Score 40; DB 2; Length 447;
 Best Local Similarity 66.78; Pred. No. 59;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5 HDLRAYGFW 13
 || || || ||
 Db 11 HDEAAYDFW 19

Search completed: August 15, 2002, 11:39:41
 Job time: 202 sec

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QY 1 RSYOHDLRAYGFW 14
 ||:| || || ||
 Db 362 RSYOHDLRAYGFW 375

RESULT 15

09FV66 PRELIMINARY; PRT; 854 AA.
 ID 09FV66
 AC 09FV66;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE TRANSPOSASE.
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
 OC Poaceae; Andropogoneae; Zea.
 ON NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-W22; TRANSPOSON-DOPPIA4;
 RA Bercury S.D., Walker E.L.;
 RT "Molecular analysis of the structure and function of the DopPIA
 RT transposable element of maize."
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF187822; AAG17043.1; -;
 SQ SEQUENCE 854 AA; 99057 MW; C3F745C5EB706EA CRC64;

Query Match

Best Local Similarity 47.1%; Score 41; DB 10; Length 854;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 HDLRAYGFW 13
 || || || ||
 Db 425 HDLRAYGFW 433

Search completed: August 15, 2002, 11:47:17
 Job time: 528 sec

QY 2 SYOHDLRAYGFV 13
:|:| | | |
DB 202 AVEHKERYFGIW 213

RESULT 12
052212 PRELIMINARY: PRT: 404 AA.

AC 052212:
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE TNPA.
GN Serratia marcescens.
OC Plasmid R471a.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Serratia.
OX NCBI_TaxID=615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=75096689; PubMed=1089756;
RA Hedges R.W., Rodriguez-Lemoin V., Datta N.;
RT "R factors from Serratia marcescens.";
RL J. Gen. Microbiol. 86:88-92(1975).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93374835; PubMed=8366028;
RA Ho C., Kulaeva O.I., Levine A.S., Woodgate R.;
RT "A rapid method for cloning mutagenic DNA repair genes: isolation of
RT unu-complementing genes from multidrug resistance plasmids R391,
RT R446b, and R471a.";
RL J. Bacteriol. 175:5411-5419(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=98202731.
RA Kulaeva O.I., Koonin E.V., Wootton J.C., Levine A.S., Woodgate R.;
RT "Unusual insertion element polymorphisms in the promoter and
RT terminator regions of the mucAB-like genes of R471a and R446b.";
RL Mutat. Res. 397:247-262(1998).
DR EMBL: AF027768; AAC82523.1; -;
DR InterPro: IPR002560; Transposase_12.
DR Pfam: PF01610; Transposase_12; 1.
KM Plasmid.
SQ SEQUENCE 404 AA: 47498 MW: 2B130E43026E5404 CRC64;

Query Match 47.1%; Score 41; DB 2; Length 404;
Best Local Similarity 50.0%; Pred. No. 90;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 SYOHDLRAYGFV 13
:|:| | | |
DB 268 AVEHKERYFGIW 279

RESULT 13
09X7J2 PRELIMINARY: PRT: 425 AA.

AC 09X7J2:
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PUTATIVE TRANSPOSASE.
OS Pseudomonas stutzeri (Pseudomonas perfectomarina).
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=316;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ML;
RX MEDLINE=99240403; PubMed=10223973;
RA Bolognese F., Di Lecce C., Galli E., Barbieri P.;

RT "Activation and inactivation of Pseudomonas stutzeri methylbenzene
RT catabolism pathways mediated by a transposable element.";
RL Appl. Environ. Microbiol. 65:1876-1882(1999).
DR EMBL: AJ012352; CAB42636.1; -;
DR InterPro: IPR002560; Transposase_12.
DR Pfam: PF01610; Transposase_12; 1.
SQ SEQUENCE 425 AA: 49494 MW: 4EE338A7465586BF CRC64;

Query Match 47.1%; Score 41; DB 2; Length 425;
Best Local Similarity 50.0%; Pred. No. 95;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 SYOHDLRAYGFV 13
:|:| | | |
DB 289 AVEHKERYFGIW 300

RESULT 14
P78875 PRELIMINARY: PRT: 817 AA.

AC P78875:
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE TREHALOSE-6-PHOSPHATASE (EC 3.1.3.12) (TREHALOSE 6-PHOSPHATE
DE PHOSPHATASE) (TTP).
GN TTP1 OR SPAC19G12.15C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Canasado J., Vicente J., Soto T., Franco A., Castillo R., Gacto M.;
RT "Isolation and characterization of trehalose-6p phosphatase disrupted
RT mutants from Schizosaccharomyces pombe.";
RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Oliver K., Harris D., Wood V., Barrell B.G., Rajandream M.A.;
RL Submitted (JUN-1997) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE OF 505-817 FROM N.A.
RC STRAIN=PR745;
RX MEDLINE=98162722; PubMed=9501991;
RA Yoshiohara S., Kato K., Nakai K., Okayama H., Nojima H.;
RT "Identification of open reading frames in Schizosaccharomyces pombe
RT cDNAs.";
RL DNA Res. 4:363-369(1997).
CC -1- CATALYTIC ACTIVITY: TREHALOSE 6-PHOSPHATE + H(2)O = TREHALOSE +
CC ORTHOPHOSPHATE.
CC -1- SIMILARITY: CONTAINS A DOMAIN FOUND IN ALL THE PROTEINS OF THE
CC TPS COMPLEX.
CC EMBL: AJ242743; CAB45142.1; -;
DR EMBL: 297209; CAB10126.1; -;
DR EMBL: D89225; BAB13886.1; -;
DR InterPro: IPR001830; Glyco_transf_20.
DR InterPro: IPR003337; Trehalose_Phase.
DR Pfam: PF00982; Glyco_transf_20; 1.
DR Pfam: PF02358; Trehalose_Phase; 1.
KM Hydrolase.
FT DOMAIN 1 547 TPS COMPLEX DOMAIN.
SQ SEQUENCE 817 AA: 93877 MW: 23CFD2533505CBA CRC64;

Query Match 47.1%; Score 41; DB 3; Length 817;
Best Local Similarity 57.1%; Pred. No. 19e+02;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OS Leishmania major.
 OC Eukaryota; Eukaryozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FRIEDLIN;
 RA Borzym K., Klages S., Reinhardt R., Beck A., Ivens A.C., Quail M.,
 Rajandream M.A., Barrell B.G.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FRIEDLIN;
 MEDLINE=98146435; PubMed=9477341;
 RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
 Smith D.F.;
 RT "A physical map of the Leishmania major Friedlin genome.";
 RL Genome Res. 8:135-145(1998).
 DR EMBL; ALJ38618; CAB71284.2; -.
 KW Hypothetical protein.
 SQ SEQUENCE 306 AA; 34129 MW; D03DA12477200AE7 CRC64;

Query Match 47.7%; Score 41.5; DB 5; Length 306;
 Best Local Similarity 66.7%; Pred. No. 55;
 Matches 8; Conservative 1; Mismatches 0; Indels 3; Gaps 1;

QY 4 OHDLRAYGFWR. 15
 ||: |||||
 Db 213 QHN---YGFWR. 221

RESULT 9
 Q9H356 PRELIMINARY; PRT; 61 AA.
 AC Q9H356;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE PRO1804.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER.
 RA Zhang C., Yu Y., Zhang S., Zhou G., Wei H., Bi J., Dong C., Zai Y.,
 Xu W., Gao F., Liu M., He F.;
 RT "Functional prediction of the coding sequences of 11 new genes deduced
 by analysis of cDNA clones from human fetal liver.";
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF132201; AAC35547.1; -.
 SQ SEQUENCE 61 AA; 6678 MW; F238B0E082E080C9 CRC64;

Query Match 47.1%; Score 41; DB 4; Length 61;
 Best Local Similarity 58.3%; Pred. No. 11;
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 SYOHLRAYGFW. 13
 ||: |||||
 Db 6 SYOHLRAYGFW. 17

RESULT 10
 Q9KT60 PRELIMINARY; PRT; 188 AA.
 AC Q9KT60;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE PUTATIVE RNA POLYMERASE SIGMA FACTOR.
 GN VCI045.

OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 OX NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EL TOR N16961 / SEROTYPE O1;
 MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
 Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
 McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
 Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 cholerae.";
 RL Nature 406:477-483(2000).
 CC -!- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES
 ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND
 THEN IS RELEASED (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE SIGMA-70 FACTOR FAMILY. ECF SUBFAMILY.
 DR EMBL; AE004186; AAF94204.1; -.
 DR TIGR; VCI045; -.
 DR InterPro; IPR000838; Sigma70_ECF.
 DR Pfam; PF00776; Sigma70_ECF.1.
 DR PROSITE; PS01063; SIGMA70_ECF; UNKNOWN.1.
 KW Complete proteome; DNA-binding; DNA-directed RNA polymerase;
 KW Sigma factor; Transcription regulation.
 SQ SEQUENCE 188 AA; 22547 MW; 313FA8201085A2 CRC64;

Query Match 47.1%; Score 41; DB 16; Length 188;
 Best Local Similarity 46.2%; Pred. No. 39;
 Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 RSYOHLRAYGFW. 13
 ||: |||||
 Db 32 RAYRDLRYAYW. 44

RESULT 11
 Q9Z5V9 PRELIMINARY; PRT; 338 AA.
 AC Q9Z5V9;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE PUTATIVE TRANSPOSASE A.
 GN TNP.A.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=142;
 RA MEDLINE=99240444; PubMed=10224014;
 RA Tsol T.V., Plotnikova E.G., Cole J.R., Guerin W.F., Bagdasarian M.,
 Tiedje J.M.;
 RT "Cloning, expression, and nucleotide sequence of the Pseudomonas
 aeruginosa 142 ohb genes coding for oxygenolytic ortho dehalogenation
 of halobenzoates.";
 RL Appl. Environ. Microbiol. 65:2151-2162(1999).
 DR EMBL; AF121970; AAD20008.1; -.
 DR InterPro; IPR002560; Transposase_12.
 DR Pfam; PF01610; Transposase_12; 1.
 SQ SEQUENCE 338 AA; 39711 MW; E0C3DF2EAB3B329 CRC64;

Query Match 47.1%; Score 41; DB 2; Length 338;
 Best Local Similarity 50.0%; Pred. No. 74;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Matches 9; Conservative 3; Mismatches 3; Indels 6; Gaps 1;
Qy 1 RSYOHDLRA-----YGFNRL 15
Db 189 RSYOHDLRAEYIGYRW 209

RESULT 6
Q9VJH0 PRELIMINARY; PRT; 652 AA.
AC Q9VJH0:
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE CG13283 PROTEIN.
GN CG13283.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxId=7227;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY:
RX MEDLINE-20196006; PubMed-10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abiri J.F., Adayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bertman B.P., Bhandari D., Bolshakov S.,
RA Borova D., Botchan M.R., Bouck J., Brockstein P., Brottier P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durlin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Gang N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jaimel B.E., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel M.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mlshina N.V., Mobarry C., Morris J., Mostrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reibert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang Q., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL: AE003652; AAF53579.1; -
DR Flybase: FBgn0032613; CG13283.
SQ SEQUENCE 652 AA; 77836 MW; 8D4D549AB2D955A2 CRC64;

Query Match 48.3%; Score 42; DB 5; Length 652;
Best Local Similarity 53.8%; Pred. No. 1e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Qy 1 RSYOHDLRAEYIGYRW 13

Db 557 RSFOYSLTDYHFW 569

RESULT 7
ID 004242 PRELIMINARY; PRT; 887 AA.
AC 004242:
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE POTASSIUM CHANNEL.
GN ZMK1.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
NCBI_TaxId=4577;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN-L551311B, AND CV. APACHE; TISSUE-COLEOPTILE;
RX MEDLINE-97272307; PubMed-9114073;
RA Hoth S., Dreyer I., Dietrich P., Becker D., Mueller-Roeber B.,
RA Hedrich R.,
RT "Molecular basis of plant-specific acid activation of K⁺ uptake channels."
Proc. Natl. Acad. Sci. U.S.A. 94:4806-4810(1997).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN-L551311B, AND CV. APACHE; TISSUE-COLEOPTILE;
RX MEDLINE-20604478; PubMed-10518597;
RA Philippat K., Fuchs I., Luthen H., Hoth S., Bauer C.S., Haga K.,
RA Thiel G., Ljung K., Sandberg G., Botiger M., Becker D., Hedrich R.;
RT "Auxin-induced K⁺ channel expression represents an essential step in coleoptile growth and gravitropism."
Proc. Natl. Acad. Sci. U.S.A. 96:12186-12191(1999).
RL EMBL: Y07632; CAA68912.1; -
DR HSSP: Q00420; IAMC.
DR InterPro: IPR002110; ANK.
DR InterPro: IPR000635; Catlon_chan_non_lig.
DR InterPro: IPR001622; Channel_pore_K.
DR InterPro: IPR000595; CNMP_binding.
DR Pfam: PF00023; ank_5.
DR Pfam: PF00027; CNMP_binding; 1.
DR Pfam: PF00520; ion_trans; 1.
DR PRINTS: PR01415; ANKYRIN.
DR SMART: SM00248; ANK; 2.
DR SMART: SM00100; CNMP; 1.
DR PROSITE: PS50088; ANK_REPEAT; 2.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE: PS50042; CNMP_BINDING_3; 1.
KW ANK repeat; Repeat.
SQ SEQUENCE 887 AA; 99265 MW; D85605200A6B419D CRC64;

Query Match 48.3%; Score 42; DB 10; Length 887;
Best Local Similarity 56.2%; Pred. No. 1.5e+02;
Matches 9; Conservative 1; Mismatches 0; Indels 6; Gaps 1;
Qy 6 DLRAEYGF-----WRL 15
Db 163 DLRSYGFNRLRLWRL 178
RESULT 8
Q9NEG4 PRELIMINARY; PRT; 306 AA.
AC Q9NEG4:
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE HYPOTHETICAL 34.1 KDA PROTEIN.
L2954.12.

DT 01-DEC-2001 (TReMBLrel. 19, last annotation update)
 DE NADH DEHYDROGENASE I, A SUBUNIT.
 GN NMB0241.
 OS Neisseria meningitidis (serogroup B).
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=491;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MC58 / SEROGROUP B;
 RX MEDLINE=20175755; PubMed=10710307;
 RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
 Eisen J.A., Ketchum K.A., Hood D.W., Feden J.F., Dodson R.J.,
 Nelson W.C., Gwinn M.L., Deboy R., Peterson J.D., Hickey E.K.,
 Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
 Mason T., Ciecko A., Parksey D.S., Blair E., Ciftone H., Clark E.B.,
 Cotton M.D., Ulfersack T.R., Khouri H., Qin H., Vamathevan J.,
 Gill J., Scarlato V., Maignani V., Pizarra M., Grandi G., Sun L.,
 Smith H.O., Fraser C.M., Moxon E.R., Kappuoli R., Venter J.C.,
 RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
 MC58.";
 RL Science 287:1809-1815(2000).
 DR EMBL: AE002381; AAF40695.1; -.
 DR TIGR: NMB0241; -.
 DR InterPro: IPR000440; Oxidored_q4.
 DR Pfam: PF00507; Oxidored_q4; 1.
 KW Complete proteome.
 SQ SEQUENCE 118 AA; 13598 MW; 21F58B3BAC579F84 CRC64;

Query Match 49.4%; Score 43; DB 16; Length 118;
 Best Local Similarity 70.0%; Pred. No. 11;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 6 DLDRYGFWR 15
 || ||||| :
 Db 86 DLGAYGFWSM 95

RESULT 3
 Q9JX78 PRELIMINARY; PRT; 118 AA.
 AC Q9JX78;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, last annotation update)
 DE NADH DEHYDROGENASE I CHAIN A (EC 1.6.5.3).
 GN NDOA OR NMA0019.
 OS Neisseria meningitidis (serogroup A).
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=65699;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=22491 / SEROGROUP A / SEROTYPE 4A;
 RX MEDLINE=20222556; PubMed=10761919;
 RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
 Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
 Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
 Jorgels K., Leather S., Moule S., Mungall K., Quail M.A.,
 Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
 Whitehead S., Spratt B.G., Barrall B.G.,
 RT "Complete DNA sequence of a serogroup A strain of Neisseria
 meningitidis 22491.";
 RL Nature 404:502-506(2000).
 DR EMBL: AL162752; CAB83339.1; -.
 DR InterPro: IPR000440; Oxidored_q4.
 DR Pfam: PF00507; Oxidored_q4; 1.
 KW Oxidoreductase; Complete proteome.
 SQ SEQUENCE 118 AA; 13584 MW; 38C401130EDDAE17 CRC64;

Query Match 49.4%; Score 43; DB 16; Length 118;
 Best Local Similarity 70.0%; Pred. No. 11;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 6 DLDRYGFWR 15
 || ||||| :
 Db 86 DLGAYGFWSM 95

RESULT 4
 Q25352 PRELIMINARY; PRT; 188 AA.
 AC Q25352;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, last annotation update)
 DE L2759.14.
 DE L2759.14.
 OS Leishmania major.
 OC Eukaryota; Euzoocoea; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FRIDLIN;
 RX MEDLINE=99178987; PubMed=10077609;
 RA Myler P.J., Audleman L., deVos T., Hixson G., Kiser P., Lemley C.,
 Magness C., Rickel E., Sisk E., Sunkin S., Swartzell S., Westlake T.,
 Bastien P., Fu G., Ivens A., Stuart K.;
 RT "Leishmania major Friedlin chromosome 1 has an unusual distribution of
 protein-coding genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:2902-2906(1999).
 DR EMBL: AE001274; AAC24644.1; -.
 SQ SEQUENCE 188 AA; 20964 MW; EE4A9F2B76E093B CRC64;

Query Match 49.4%; Score 43; DB 5; Length 188;
 Best Local Similarity 77.8%; Pred. No. 18;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 HDLRAYGF 13
 || | | | | :
 Db 46 HDLMAIGFW 54

RESULT 5
 Q22405 PRELIMINARY; PRT; 444 AA.
 AC Q22405;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, last annotation update)
 DE T11F9.1 PROTEIN.
 GN T11F9.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloiderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C. elegans: A platform for
 investigating biology.";
 RL Science 282:2012-2018(1998).
 DR EMBL: Z74042; CA98536.1; -.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
 SQ SEQUENCE 444 AA; 51686 MW; 3C07F095C5484892 CRC64;

Query Match 48.3%; Score 42; DB 5; Length 444;
 Best Local Similarity 42.9%; Pred. No. 68;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 11:47:16 ; Search time 58.4 Seconds

(without alignments)
44,434 Million cell updates/sec

Title: US-09-613-092a-6

Perfect score: 87

Sequence: 1 RSYQHDLRAYGFWRL 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP virus:*
16: SP bacteriophage:*
17: SP archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	50.6	1114	4	075984 homo sapien
2	43	49.4	118	16	09XIC3
3	43	49.4	118	16	09JX78
4	43	49.4	188	5	025352
5	42	48.3	444	5	022405
6	42	48.3	652	5	09VJH0
7	42	48.3	887	10	004242
8	41.5	47.7	306	5	09NEG4
9	41	47.1	61	4	09H356
10	41	47.1	188	16	09KT60
11	41	47.1	338	2	09Z5V9
12	41	47.1	404	2	052212
13	41	47.1	425	2	09X7J2
14	41	47.1	817	3	P78875
15	41	47.1	854	10	09FVG6
16	40	46.0	251	2	09LINO

17	40	46.0	274	16	0971Q3	Q971q3 clostridium
18	40	46.0	323	13	090XK7	Q90Xk7 lepisosteus
19	40	46.0	330	5	0926E3	Q926e3 rhizobium m
20	40	46.0	371	5	09XV86	Q9XV86 caenorhabdi
21	40	46.0	414	5	09XUG7	Q9XUG7 caenorhabdi
22	40	46.0	438	10	09XE47	Q9XE47 pinus radia
23	40	46.0	447	16	09WZV6	Q9WZV6 thermotoga
24	40	46.0	497	10	094JZ7	Q94Jz7 arabidopsis
25	40	46.0	516	10	09SHX4	Q9SHx4 arabidopsis
26	40	46.0	518	2	09P915	Q9P915 treponema p
27	40	46.0	619	10	09C7B1	Q9C7b1 arabidopsis
28	40	46.0	637	10	09LHB0	Q9Lhb0 arabidopsis
29	40	46.0	912	2	085931	Q85931 sphingomona
30	39.5	45.4	309	16	092UC0	Q92uc0 rhizobium m
31	39.5	45.4	471	16	092VC0	Q92vc0 rhizobium m
32	39.5	45.4	472	16	098C18	Q98c18 rhizobium l
33	39	44.8	40	4	P78340	P78340 homo sapien
34	39	44.8	58	4	094784	Q94784 homo sapien
35	39	44.8	61	16	098P94	Q98P94 rhizobium l
36	39	44.8	81	16	09RTW0	Q9RTw0 deinococcus
37	39	44.8	209	16	0983X9	Q983x9 rhizobium l
38	39	44.8	242	5	09U0R8	Q9U0r8 plasmodium
39	39	44.8	339	2	059644	Q59644 propionibac
40	39	44.8	340	16	09KDU0	Q9Kdu0 bacillus ha
41	39	44.8	441	16	092QA4	Q92qa4 rhizobium m
42	39	44.8	475	2	0933G0	Q933g0 treponema p
43	39	44.8	476	2	093P67	Q93p67 treponema p
44	39	44.8	499	2	09EUA1	Q9Eua1 treponema p
45	39	44.8	502	16	09RS01	Q9RS01 deinococcus

ALIGNMENTS

RESULT 1	PRELIMINARY;	PRT;	1114 AA.
ID 075984	AC 075984;		
AC 075984	01-NOV-1998 (TREMBlrel. 08, Created)		
DT 01-NOV-1998	(TREMBlrel. 08, last sequence update)		
DT 01-DEC-2001	(TREMBlrel. 19, last annotation update)		
DE D11189B24.4	(NOVEL PUTATIVE PROTEIN SIMILAR TO HYPOTHETICAL PROTEINS		
DE S. POMBE C22F3.14C AND C. ELEGANS C16A3.8) (FRAGMENT).			
GN D11189B24.4.			
GN Homo sapiens (Human).			
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX NCBI_TaxID=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RA Bird C.;			
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.			
DR EMBL; AL030996; CAA19741.1; --			
KW Hypothetical protein.			
FT NON_TER			
FT SEQUENCE	1114 AA; 127642 MW; 2193C2B30E956DDC CRC64;		
Query Match	50.6%;	Score 44;	DB 4; Length 1114;
Best Local Similarity	58.3%;	Pred. No. 87;	
Matches 7;	Conservative	1;	Mismatches 4; Indels 0; Gaps 0;
QY 3 YOHDLRAYGFWRL 14			
DB 32 YOHRRRLYGQWK 43			
RESULT 2	PRELIMINARY;	PRT;	118 AA.
ID 09KIC3	AC 09KIC3;		
AC 09KIC3	01-OCT-2000 (TREMBlrel. 15, Created)		
DT 01-OCT-2000	(TREMBlrel. 15, Last sequence update)		

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 CC EMBL; U91738; AAB58393.1; -
 DR InterPro: IPR001370; BIR.
 DR Pfam: PF00653; BIR: 1.
 DR SMART: SM00238; BIR: 1.
 DR PROSITE: PS01282; BIR_REPEAT_1; 1.
 DR PROSITE: PS50143; BIR_REPEAT_2; 1.
 FT REPEAT 43 106 BIR.
 SQ SEQUENCE 238 AA; 28530 MW; 7024C187D2C55E40 CRC64;

Query Match 43.7%; Score 38; DB 1; Length 238;
 Best Local Similarity 50.0%; Pred. No. 19;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 QHDLRAYGFV 13
 : 1 1 : 111
 Db 90 KHPLOYHGFV 99

Search completed: August 15, 2002, 11:47:41
 Job time: 517 sec

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OY      4 QHDLRAYGFW 13
      :| | :| | |
      76 KHPLOYHGFW 85

RESULT 13
ID      IAPL_ASFC3      STANDARD;      PRT;      224 AA.
AC      011451;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DE      16-OCT-2001 (Rel. 40, Last annotation update)
GN      IAP-1-like protein p27.
OS      African swine fever virus (isolate crocodile/96/3 / C-3) (ASFV).
OC      Viruses: dsDNA viruses, no RNA stage; Asfarviridae;
OX      African swine fever-like viruses.
      NCB1_TaxId=82811;
      [1]
RN      SEQUENCE FROM N.A.
RX      MEDLINE=97288303; PubMed=9143281;
RA      Neilan J.G., Lu Z., Kutish G.F., Zsak L., Burrage T.G.,
RA      Borea M.V., Carrillo C., Rock D.L.;
RT      "A BIR motif containing gene of African swine fever virus, 4CL, is
RT      nonessential for growth in vitro and viral virulence.";
RL      Virology 230:252-264(1997).
CC      -1- FUNCTION: NOT ESSENTIAL FOR GROWTH OR VIRULENCE. DOES NOT HAVE
CC      ANTIAPOPTOTIC FUNCTION.
CC      -1- SIMILARITY: CONTAINS 1 BIR REPEAT.
-----
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-----
DR      EMBL: U91732; AAB58387.1; -.
DR      InterPro: IPR001370; BIR.
DR      Pfam: PF00653; BIR.1.
DR      SMART: SM00238; BIR.1.
DR      PROSITE: PS01282; BIR_REPEAT_1; 1.
DR      PROSITE: PS50143; BIR_REPEAT_2; 1.
FT      REPEAT 29 92 BIR.
SQ      SEQUENCE 224 AA; 26559 MW; 80B376948514946F CRC64;

Query Match      43.7%; Score 38; DB 1; Length 224;
Best Local Similarity 50.0%; Pred. No. 18;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY      4 QHDLRAYGFW 13
      :| | :| | |
      76 KHPLOYHGFW 85

RESULT 14
ID      IAPL_ASFC3      STANDARD;      PRT;      224 AA.
AC      012407;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DE      16-OCT-2001 (Rel. 40, Last annotation update)
GN      IAP-1-like protein p27.
OS      African swine fever virus (isolate Chiredzi/83/1 / Ch1) (ASFV),
OS      African swine fever virus (isolate crocodile/96/1 / Crl) (ASFV), and
OS      African swine fever virus (isolate Pretoriuskop/96/5 / Pr5) (ASFV).
OC      Viruses: dsDNA viruses, no RNA stage; Asfarviridae;
OC      African swine fever-like viruses.
OX      NCB1_TaxId=82812, 82810, 82817;

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```

RN      [1]
RX      SEQUENCE FROM N.A.
RX      MEDLINE=97288303; PubMed=9143281;
RA      Neilan J.G., Lu Z., Kutish G.F., Zsak L., Burrage T.G., Borea M.V.,
RA      Carrillo C., Rock D.L.;
RT      "A BIR motif containing gene of African swine fever virus, 4CL, is
RT      nonessential for growth in vitro and viral virulence.";
RL      Virology 230:252-264(1997).
CC      -1- FUNCTION: NOT ESSENTIAL FOR GROWTH OR VIRULENCE. DOES NOT HAVE
CC      ANTIAPOPTOTIC FUNCTION.
CC      -1- SIMILARITY: CONTAINS 1 BIR REPEAT.
-----
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-----
DR      EMBL: U91730; AAB58385.1; -.
DR      EMBL: U91731; AAB58386.1; -.
DR      EMBL: U91740; AAB58395.1; -.
DR      InterPro: IPR001370; BIR.
DR      Pfam: PF00653; BIR.1.
DR      SMART: SM00238; BIR.1.
DR      PROSITE: PS01282; BIR_REPEAT_1; 1.
DR      PROSITE: PS50143; BIR_REPEAT_2; 1.
FT      REPEAT 29 92 BIR.
SQ      SEQUENCE 224 AA; 26558 MW; 8E579C948E132F05 CRC64;

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OY      4 QHDLRAYGFW 13
      :| | :| | |
      76 KHPLOYHGFW 85

RESULT 15
ID      IAPL_ASFM2      STANDARD;      PRT;      238 AA.
AC      011453;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DE      16-OCT-2001 (Rel. 40, Last annotation update)
GN      IAP-1-like protein p27.
OS      African swine fever virus (isolate Malawi L11 20/1) (ASFV).
OC      Viruses: dsDNA viruses, no RNA stage; Asfarviridae;
OC      African swine fever-like viruses.
OX      NCB1_TaxId=10500;
      [1]
RN      SEQUENCE FROM N.A.
RX      STRAIN-MALAWI;
RX      MEDLINE=97288303; PubMed=9143281;
RA      Neilan J.G., Lu Z., Kutish G.F., Zsak L., Burrage T.G.,
RA      Borea M.V., Carrillo C., Rock D.L.;
RT      "A BIR motif containing gene of African swine fever virus, 4CL, is
RT      nonessential for growth in vitro and viral virulence.";
RL      Virology 230:252-264(1997).
CC      -1- FUNCTION: NOT ESSENTIAL FOR GROWTH OR VIRULENCE. DOES NOT HAVE
CC      ANTIAPOPTOTIC FUNCTION.
CC      -1- SIMILARITY: CONTAINS 1 BIR REPEAT.
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RA Kuhara S., Shiba T., Hattori M., Shingawa H.;
 RT "Complete genome sequence of enterohemorrhagic *Escherichia coli*
 RT O157:H7 and genomic comparison with a laboratory strain K-12.";
 RL DNA Res. 8:11-22(2001).
 RN [6]
 RN SEQUENCE OF 1-137 FROM N.A.
 RC STRAIN-K12 / WJ110;
 RC Lomovskaya O.L., Kidwell J., Malin A.;
 RN Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
 RP [7]
 RP SEQUENCE OF 24-28.
 RC STRAIN-K12 / WJ110;
 RC MEDLINE=98291876; PubMed=9629924;
 RA Molloy M.P., Herbert B.R., Walsh B.J., Tyler M.I., Traini M.,
 RA Sanchez J.-C., Hochstrasser D.F., Williams K.L., Gooley A.A.;
 RT "Extraction of membrane proteins by differential solubilization for
 RT separation using two-dimensional gel electrophoresis";
 RL Electrophoresis 19:837-844(1998).
 RN [8]
 RN X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 24-171.
 RX MEDLINE=20015380; PubMed=10545325;
 RA Vogt J., Schulz G.E.;
 RT "The structure of the outer membrane protein OmpX from *Escherichia*
 RT coli reveals possible mechanisms of virulence";
 RL Structure 7:1301-1309(1999).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
 CC -1- SIMILARITY: BELONGS TO THE AIL/OMPX/PAGC/LOM FAMILY.
 CC -----
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 CC -----
 DR EMBL; L37088; AAA66329.1; -;
 DR EMBL; AE000183; AAC73901.1; -;
 DR EMBL; D90718; BAA35486.1; -;
 DR EMBL; D90719; BAA35496.1; -;
 DR EMBL; AE005262; AAG55186.1; -;
 DR EMBL; AP002553; BAB34315.1; -;
 DR EMBL; U04242; AAA21856.1; -;
 DR PDB; 1QJ8; 10-OCT-99.
 DR PDB; 1QJ9; 06-OCT-99.
 DR Ecogen; EG12135; ompX.
 DR InterPro: IPR000758; Enterovir_OMP.
 DR PRINTS: PR00316; ENTEROVIR_OMP.
 DR PROSITE: PS00694; ENT_VIR_OMP_1; 1.
 DR PROSITE: PS00695; ENT_VIR_OMP_2; 1.
 KW Outer membrane; Transmembrane; Signal; 3D-structure;
 KW Complete proteome.
 FT SIGNAL 1 23
 FT CHAIN 24 171 OUTER MEMBRANE PROTEIN X.
 FT DOMAIN 24 33 POTENTIAL.
 FT DOMAIN 34 45 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 46 55 POTENTIAL.
 FT DOMAIN 56 59 PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 60 69 POTENTIAL.
 FT DOMAIN 70 84 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 85 94 POTENTIAL.
 FT DOMAIN 95 99 PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 100 109 POTENTIAL.
 FT DOMAIN 110 128 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 129 138 POTENTIAL.
 FT DOMAIN 139 143 PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 144 153 POTENTIAL.
 FT DOMAIN 154 159 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 160 171 POTENTIAL.
 FT CONFLICT 10 L -> M (IN REF. 6).
 SQ SEQUENCE 171 AA; 18603 MW; 77CE1245DAE81462 CRC64;

Query Match 43.7%; Score 38; DB 1; Length 171;
 Best Local Similarity 54.5%; Pred. No. 13;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 2 SYQHDLRATGE 12
 Db 120 TYKHDTSDYGF 130
 ID IAPL_ASEB7 STANDARD; PRT; 224 AA.
 AC 065138; 012627; 012628; 012630; 012631; 012904; 012905;
 AC 012906; 012907; 012908;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE IAP-like protein p27.
 GN A224L OR 4CL.
 OS African swine fever virus (strain BA71V) (ASFV),
 OS African swine fever virus (strain E-70 / isolate MS16) (ASFV),
 OS African swine fever virus (strain E-75) (ASFV),
 OS African swine fever virus (isolate Haiti 811) (ASFV), and
 OS African swine fever virus (isolate Lisbon 60 / Lis60) (ASFV).
 OC Viruses; dsDNA viruses, no RNA stage; Asfarviridae;
 OC African swine fever-like viruses.
 OX NCBI_TaxID=10498, 82813, 33713, 82814, 82815;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RA Yanez R.J., Rodriguez J.M., Nogal M.L., Yuste L., Enriquez C.,
 RA Rodriguez J.F., Vinuela E.;
 RT "Analysis of the complete nucleotide sequence of African swine fever
 RT virus";
 RL Virology 208:249-278(1995).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=E-70, E-75, HAITI 811, LIS60, AND MS16;
 RX MEDLINE=97288303; PubMed=9143281;
 RA Neilan J.G., Lu Z., Kutish G.F., Zsak L., Burrage T.G., Borca M.V.,
 RA Carrillo C., Rock D.L.;
 RT "A BIR motif containing gene of African swine fever virus, 4CL, is
 RT nonessential for growth in vitro and viral virulence";
 RL Virology 230:252-264(1997).
 CC -1- FUNCTION: NOT ESSENTIAL FOR GROWTH OR VIRULENCE. DOES NOT HAVE
 CC ANTIAPOPTOTIC FUNCTION.
 CC -1- SIMILARITY: CONTAINS 1 BIR REPEAT.
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 CC -----
 DR EMBL; U18466; AAA65263.1; -;
 DR EMBL; U91733; AAB58388.1; -;
 DR EMBL; U91734; AAB58389.1; -;
 DR EMBL; U91735; AAB58390.1; -;
 DR EMBL; U91736; AAB58391.1; -;
 DR EMBL; U91739; AAB58394.1; -;
 DR InterPro: IPR001370; BIR.
 DR Pfam: PF00653; BIR; 1.
 DR PROSITE: PS01282; BIR_REPEAT_1; 1.
 DR PROSITE: PS0143; BIR_REPEAT_2; 1.
 FT REPEAT 29 92 BIR.
 SQ SEQUENCE 224 AA; 26618 MW; 49E81A325EDA00C9 CRC64;

Query Match 43.7%; Score 38; DB 1; Length 224;
 Best Local Similarity 50.0%; Pred. No. 18;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;


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OS Ictalurid herpesvirus 1 (Channel catfish virus) (CCV).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OX NCBI_TaxID=10401;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-AUBURN 1;
RX MEDLINE=92087490; PubMed=1727613;
RA Davison A.J.;
RT "Channel catfish virus: a new type of herpesvirus.";
RL Virology 186:9-14(1992).
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CC -----
CC DR EMBL: M75136; AAA88147.1; -.
CC PIR: I36790; I36790.
CC KM Hypothetical protein.
CC SQ SEQUENCE 335 AA; 37898 MW; 051B9B66F52C1E3 CRC64;

Query Match 44.8%; Score 39; DB 1; Length 335;
Best Local Similarity 63.6%; Pred. No. 18;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 HDLRAYGFWR 15
   :|||  |||
Db 249 YDLRSCSCWRL 259

RESULT 8
YGCN_ECOLI STANDARD; PRT; 423 AA.
ID YGCN_ECOLI
AC Q46904;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable electron transfer flavoprotein-quinone oxidoreductase ygcN
DE (EC 1.5.5.-).
GN YGCN OR B2766.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
CC -----
CC -1- FUNCTION: PROBABLY ACCEPTS ELECTRONS FROM YGCO/YGCR AND REDUCES
CC A QUINONE.
CC -1- COFACTOR: FAD (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE ETF-OO / FIXC FAMILY.
CC -----
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CC -----
CC DR EMBL: U29579; AAA69276.1; ALT_INIT.

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DR EMBL: AE000360; AAC75808.1; ALT_INIT.
DR EcoGene; EG3121; ygcN.
DR InterPro: IPR000205; NAD_binding.
KM Hypothetical protein; Oxidoreductase; FAD; Flavoprotein;
KM Complete proteome.
FT NP_BIND 7 21 FAD (ADP PART) (POTENTIAL).
SQ SEQUENCE 423 AA; 46393 MW; 346ED1A132F31DEC CRC64;

Query Match 44.8%; Score 39; DB 1; Length 423;
Best Local Similarity 46.2%; Pred. No. 23;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 YQHDLRAYGFWR 15
   :|||  |||
Db 400 FWHHLRRGWL 412

RESULT 9
BIB_DROME STANDARD; PRT; 700 AA.
ID BIB_DROME
AC P23645;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neurogenic protein big brain.
GN BIB.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90245091; PubMed=1692392;
RA Rao Y., Jan L.Y., Jan Y.N.;
RT "Similarity of the product of the Drosophila neurogenic gene big
RT brain to transmembrane channel proteins.";
RL Nature 345:163-167(1990).
CC -1- FUNCTION: MAY MEDIATE INTERCELLULAR COMMUNICATION; MAY FUNCTIONS
CC BY ALLOWING THE TRANSPORT OF CERTAIN MOLECULES(S) AND THEREBY
CC SENDING A SIGNAL FOR AN EXODERMAL CELL TO BECOME AN EPIDERMAL CELL
CC INSTEAD OF A NEUROBLAST. MUTATION IN BIB GENE UNDERLIES "Big
CC BRAIN" DEVELOPMENT.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE MIP/AQUAPORIN FAMILY (TC 1.A.8).
CC -----
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CC -----
CC DR EMBL: X53275; CAB37863.1; -.
CC PIR: S09699; S09699.
CC FLYBASE: FBgn0000180; bib.
DR InterPro: IPR000425; MIP.
DR Pfam: PF00230; MIP; 1.
DR PRINTS: PR00783; MINTINSICP.
DR PROSITE: PS00221; MIP; 1.
KM Developmental protein; Neurogenesis; Transport; Transmembrane.
FT TRANSMEM 72 93 POTENTIAL.
FT TRANSMEM 98 118 POTENTIAL.
FT TRANSMEM 144 167 POTENTIAL.
FT TRANSMEM 190 208 POTENTIAL.
FT TRANSMEM 214 234 POTENTIAL.
FT TRANSMEM 257 273 POTENTIAL.
FT DOMAIN 439 451 POLY-GLN.
FT DOMAIN 487 534 GIN-RICH.
FT DOMAIN 658 690 POLY-GLN.
SQ SEQUENCE 700 AA; 76951 MW; 3390A683F96D5B6B CRC64;

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RP SEQUENCE FROM N.A.
RC STRAIN=CV, COLUMBIA;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman K.L., Barnstead M.E., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.C., Konning C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pal G., Van Aken S., Umeyam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Cressy T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana."
RL Nature 402:761-768(1999).
CC -I- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.
CC -I- SUBCELLULAR LOCATION: Cytoplasmic (By similarity)
CC -I- SIMILARITY: BELONGS TO THE GST SUPERFAMILY. ZETA FAMILY.
CC -----
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CC -----
DR EMBL: AC005312; AAC78520.1; -
DR Mendel: 38453; Arath:1313;38453.
DR InterPro: IPR004046; GST_C.
DR InterPro: IPR004045; GST_N.
DR Pfam: PF00043; GST_C; 1.
DR Pfam: PF02798; GST_N; 1.
DR Transferase.
KM ACT SITE 20
FT SEQUENCE 223 AA; 25352 MW; AAE7E85746610512 CRC64;
SQ
Query Match 46.0%; Score 40; DB 1; Length 223;
Best Local Similarity 50.0%; Pred. No. 8;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 3 YQHDRLRAYGFW 14
DB 8 YQAKLKLYSYMR 19
RESULT 5
YQBL_CAEEL STANDARD: PRT; 451 AA.
AC Q09255;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Hypothetical 51.0 kDa protein C30612.1 in chromosome II.
GN C30612.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Lareille P.;
RL Submitted (JUL-1995) to the EMBL/Genbank/DBJ databases.
CC -----
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CC -----

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DR EMBL: U21319; AAC46670.1; -
DR WormPep: C30612.1; CE01832.
KM Hypothetical protein.
SQ SEQUENCE 451 AA; 51017 MW; 6AAAFD326751C1 CRC64;
Query Match 46.0%; Score 40; DB 1; Length 451;
Best Local Similarity 77.8%; Pred. No. 17;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 SYQHDRLRAY 10
DB 61 SYQHDLSAF 69
RESULT 6
YIHX_ECOLI STANDARD: PRT; 199 AA.
ID YIHX_ECOLI
AC P32145;
DT 01-OCT-1993 (Rel. 27, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein yihx.
GN YIHX OR B385.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=93347969; PubMed=8346018;
RA Plunkett G., III, Burland V.D., Daniels D.L., Blattner F.R.;
RT "Analysis of the Escherichia coli genome. III. DNA sequence of the
RT region from 87.2 to 89.2 minutes."
RL Nucleic Acids Res. 21:3391-3398(1993).
CC -----
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CC -----
DR EMBL: L19201; AAB03018.1; ALT_INIT.
DR EMBL: AE000464; AAD13447.1; ALT_INIT.
DR PIR: S40829; S40829.
DR Ecogene: EG11850; yihx.
DR InterPro: IPR001454; Hydrolase.
DR Pfam: PF00702; Hydrolase; 1.
KM Hypothetical protein; Complete proteome.
SQ SEQUENCE 199 AA; 22732 MW; 9451EA891DFC0D2 CRC64;
Query Match 44.8%; Score 39; DB 1; Length 199;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 RSYQHDRLRAYGF 12
DB 145 RIYQHVLAQEGF 156
RESULT 7
VG44_HSV11 STANDARD: PRT; 335 AA.
ID VG44_HSV11
AC Q00124;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Hypothetical gene 44 protein.
GN 44.

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FT TRANSEM 423 443 POTENTIAL.
SQ SEQUENCE 459 AA; 49941 MW; B2EPD15C8EA94E CRC64;

Query Match 49.4%; Score 43; DB 1; Length 459;
Best Local Similarity 50.0%; Pred. No. 5.2;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 SYQHDLRAYGFW 13
: | : | | | |
Db 416 AYRDMGTYGFW 427

RESULT 2
SYLM_NEUCR STANDARD; PRT; 994 AA.
ID SYLM_NEUCR

AC P15181;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Leucyl-tRNA synthetase, mitochondrial precursor (EC 6.1.1.4)
DE (leucine--tRNA ligase) (LeuRS).
GN LEU-5 OR 99H12.170.

OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.

NCBI_TaxID=5141;

RP SEQUENCE FROM N.A.

RX MEDLINE:90097874; PubMed:2574823;

RA Chow C.M., Metzgerberg R.L., Rajbhandary U.L.;

RT "Nuclear gene for mitochondrial leucyl-tRNA synthetase of Neurospora

crassa: isolation, sequence, chromosomal mapping, and evidence that

the leu-5 locus specifies structural information.";

RL Mol. Cell. Biol. 9:4631-4644(1989).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=OR74A.

RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,

RA Nyakatura G., Mewes H.-W., Mannhaupt G.;

RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.

CC -1- CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP +

CC diphosphate + L-leucyl-tRNA(Leu).

CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.

CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-tRNA SYNTHETASE FAMILY.

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CC -----

DR EMBL: M30472; AAA35599.1; -

DR EMBL: AL451018; CAC18253.1; -

DR PIR: A33474; SYNCML.

DR InterPro: IPR002300; tRNA-synt_1a.

DR InterPro: IPR001412; tRNA-synt_1.

DR InterPro: IPR002302; tRNA-synt_1eu.

DR Pfam: PF00133; tRNA-synt_1.1.

DR PRINTS: PR00985; TRNASYNTH1EU.

DR PROSITE: PS00178; AA-tRNA-LIGASE_1; 1.

KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;

KW Mitochondrion; Transit peptide.

FT TRANSL 1 52 MITOCHONDRION.

FT CHAIN 53 994 LEUCYL-tRNA SYNTHETASE.

FT SITE 93 103 "HIGH" REGION.

FT STATE 697 701 "KMSKS" REGION.

FT BINDING 700 701 ATP (BY SIMILARITY).

SQ SEQUENCE 994 AA; 109853 MW; 2ADB26302A8465F9 CRC64;

Query Match 48.3%; Score 42; DB 1; Length 994;
Best Local Similarity 60.0%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 HDLRAYGFW 14
| | | | : | |
Db 403 HDLRDHAFWK 412

RESULT 3
RL5_NEUCR STANDARD; PRT; 301 AA.
ID RL5_NEUCR

AC 059953;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 60S ribosomal protein L5 (CPR4).

GN CRP-4.

OS Neurospora crassa.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Sordariales; Sordariaceae; Neurospora.

NCBI_TaxID=5141;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=74-OR23-1A;

RA de la Serna I.L., Cujec T.P., Shi Y., Tyler B.M.;

RT "Non-coordinate regulation of 5S rRNA genes and the gene encoding the

5S rRNA-binding ribosomal protein homolog in Neurospora crassa.";

RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: THIS PROTEIN BINDS 5S RNA (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE L18P FAMILY OF RIBOSOMAL PROTEINS.

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CC -----

DR EMBL: AF054907; AAC09000.1; -

DR InterPro: IPR001149; Ribosomal_L18p.

DR Pfam: PF00861; Ribosomal_L18p.1.

DR PRINTS: PR00058; RIBOSOMAL15.

DR PRODOM: PD001394; Ribosomal_L18p.1.

KW Ribosomal protein; rRNA-binding.

SQ SEQUENCE 301 AA; 34411 MW; 289B0F0D1672A5F9 CRC64;

Query Match 47.1%; Score 41; DB 1; Length 301;
Best Local Similarity 60.0%; Pred. No. 7.4;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 SYQHDLRAYG 11
: | | : | | | |
Db 78 AYSHELRAYG 87

RESULT 4
GT21_ARATH STANDARD; PRT; 223 AA.
ID GT21_ARATH

AC 092VQ4;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Probable glutathione S-transferase zeta-class 1 (EC 2.5.1.18).

GN AT2G03380 OR T16F16.17.

OS Arabidopsis thaliana (mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;

RN [1]

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 15, 2002, 11:47:41 ; Search time 18.67 Seconds

(without alignments)
31.108 Million cell updates/sec

Title: US-09-613-092a-6

Perfect score: 87

Sequence: 1 RSYQHDLRAYGFWRLL 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues 105224

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
1	43	49.4	459	1	NORM_NEIMA
2	42	48.3	994	1	SYM_NEUCR
3	41	47.1	301	1	RIS_NEUCR
4	40	46.0	223	1	GT2L_ANATH
5	40	46.0	451	1	YOB1_CAEEL
6	39	44.8	199	1	YIHX_ECOLI
7	39	44.8	335	1	VG44_HSV1
8	39	44.8	423	1	YGCN_ECOLI
9	39	44.8	700	1	BIB_DROME
10	39	44.8	1135	1	VG1M_TSW1
11	38	43.7	171	1	OMPX_ECOLI
12	38	43.7	224	1	IAPL_ASFB7
13	38	43.7	224	1	IAPL_ASFC3
14	38	43.7	224	1	IAPL_ASFCH
15	38	43.7	238	1	IAPL_ASFMB
16	38	43.7	459	1	NORM_NEIMB
17	38	43.7	978	1	YSX7_CAEEL
18	38	43.7	1192	1	LMG2_MOUSE
19	38	43.7	1193	1	LMG2_HUMAN
20	37	42.5	142	1	ELIS_ADE04
21	37	42.5	319	1	EXOM_RHIME
22	37	42.5	331	1	YJ43_SYNY3
23	37	42.5	453	1	OP2_MAIZE
24	37	42.5	514	1	AMT2_LYCES
25	37	42.5	667	1	GR78_APICA
26	37	42.5	715	1	PERE_HUMAN
27	37	42.5	716	1	PERE_MOUSE
28	37	42.5	745	1	PERM_MOUSE
29	37	42.5	877	1	PERM_HUMAN
30	37	42.5	877	1	AGLU_HORVU
31	37	42.5	941	1	CHRD_XENLA
32	37	42.5	999	1	MPD_HELPY
33	37	42.5	1001	1	MPD_HELPY

34	37	42.5	1613	1	VIT2_CAEEL	P05690 caenorhabdi
35	37	42.5	1616	1	VIT1_CAEEL	P55155 caenorhabdi
36	37	42.5	2329	1	YJ16_CAEEL	P34369 caenorhabdi
37	36	41.4	68	1	Y002_BHP1	P51701 bacterioph
38	36	41.4	97	1	YA9_HAETN	P57347 haemophilus
39	36	41.4	301	1	Y186_MYCPN	P75265 mycoplasma
40	36	41.4	331	1	HPIC_TREPA	P083152 treponema
41	36	41.4	347	1	YPPG_ECOLI	P76559 escherichia
42	36	41.4	403	1	YLD1_CAEEL	P003566 caenorhabdi
43	36	41.4	474	1	YBL2_SFVL	P29170 simian foam
44	36	41.4	559	1	Y876_MYCTU	P010564 mycobacteri
45	36	41.4	571	1	YRIQ_CAEEL	P90794 caenorhabdi

ALIGNMENTS

RESULT	ID	NORM_NEIMA	STANDARD	PRT	459 AA.
AC	09J27:				
DT	16-OCT-2001 (rel. 40, Last sequence update)				
DT	16-OCT-2001 (rel. 40, Last annotation update)				
DE	Probable multidrug resistance protein norm (Na(+)/drug antiporter)				
DE	(Multidrug-efflux transporter).				
GN	NORM OR NMA1022.				
OS	Neisseria meningitidis (serogroup A).				
OC	Bacteria; Proteobacteria; Beta subdivision; Neisseriaceae; Neisseria.				
OX	NCBI_Taxid=65699;				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Z491 / SEROGROUP A / SEROTYPE 4A;				
RX	MEDLINE=20222556; PubMed=10761919;				
RA	Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,				
RA	Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,				
RA	Davies R.M., Davis P., Devlin K., Fellwell T., Hamlin N., Holtroyd S.,				
RA	Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,				
RA	Rajadream M.A., Rutherford K.M., Simmonds M., Skelton J.,				
RA	Whitehead S., Spratt B.G., Barrell B.G.;				
RT	"Complete DNA sequence of a serogroup A strain of Neisseria				
RT	meningitidis 22491."				
RL	Nature 404:502-506 (2000).				
CC	-1- FUNCTION: FUNCTIONS AS A NA(+)/DRUG ANTIPORTER (BY SIMILARITY).				
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane				
CC	(Potential).				
CC	-1- SIMILARITY: BELONGS TO THE MULTI ANTIMICROBIAL EXTRUSION (MATE)				
CC	FAMILY. NORM (TC 2.A.66.1.1) SUBFAMILY.				
CC	-----				
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CC	-----				
DR	EMBL: AL162754; CAB84291.1; "				
DR	InterPro: IPR002528; UPF0013.				
DR	Pfam: PF01554; UPF0013; 2.				
KW	Transport; Sodium transport; Transmembrane; Inner membrane;				
KW	Complete proteome.				
FT	TRANSMEM 20 40				POTENTIAL.
FT	TRANSMEM 53 73				POTENTIAL.
FT	TRANSMEM 100 120				POTENTIAL.
FT	TRANSMEM 132 152				POTENTIAL.
FT	TRANSMEM 168 188				POTENTIAL.
FT	TRANSMEM 202 222				POTENTIAL.
FT	TRANSMEM 252 272				POTENTIAL.
FT	TRANSMEM 285 305				POTENTIAL.
FT	TRANSMEM 325 345				POTENTIAL.
FT	TRANSMEM 358 378				POTENTIAL.
FT	TRANSMEM 395 415				POTENTIAL.